

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 March 2003 (27.03.2003)

PCT

(10) International Publication Number
WO 03/025138 A2

- (51) International Patent Classification⁷: **C12N** (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).
- (21) International Application Number: PCT/US02/29560
- (22) International Filing Date:
17 September 2002 (17.09.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|------------|--------------------------------|----|
| 60/323,469 | 17 September 2001 (17.09.2001) | US |
| 60/323,887 | 20 September 2001 (20.09.2001) | US |
| 60/350,666 | 13 November 2001 (13.11.2001) | US |
| 60/355,145 | 8 February 2002 (08.02.2002) | US |
| 60/355,257 | 8 February 2002 (08.02.2002) | US |
| 60/372,246 | 12 April 2002 (12.04.2002) | US |
- (71) Applicant (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway, Boulevard, South San Francisco, CA 94080 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062
- (74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Declaration under Rule 4.17:**
— of inventorship (Rule 4.17(iv)) for US only
- Published:**
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/323,469, filed September 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed
10 November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of
15 such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the
20 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is
25 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases.
30 Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for
5 improving the diagnosis and treatment of cancer patients.

Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in
10 normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells
15 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current
20 treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

25 The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a
30 cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targeting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abelloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

- al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows
5 for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a
10 causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have
15 similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in
20 expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenesis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung
25 cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript"
30 refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of
5 or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino
10 sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a
15 "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing,
20 including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and
25 autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a
30 bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

5 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
10 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
15 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

20 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
25 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a
30 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA
5 in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are
10 described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves
15 first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are
20 extended in both directions along each sequence for as far as the cumulative alignment score can be increased.—Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the
25 cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E)
30 of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

5 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than
10 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a
15 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

20 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site,
25 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid
30 chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
5 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
10 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
15 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
20 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
25 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants
30 refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am.

- Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568;
- 5 Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994)
- 10 Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in
- 15 Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.
- 20 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly
- 25 matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.
- 30 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

5 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage
10 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with
15 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

 The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid,
20 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all.
25 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant
30 for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second
5 sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed
10 in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

15 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of
20 hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of
25 the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides)
30 and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although
5 annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec,
10 and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This
15 occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background.
20 Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that
25 modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation;
30 growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 5 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen 10 recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself 15 is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate 20 that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

25 For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH 30 Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

- 5 A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a
10 portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

- In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression
15 profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue
20 from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

- The identification of sequences that are differentially expressed in cancer versus non-
25 cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the
30 known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be
5 done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

10 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred
15 embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained
20 using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips
25 comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined
30 below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold
5 change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally
10 provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug
15 structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets
20 relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be
25 maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for
30 clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological
5 conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available.
10 For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to
15 association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of
20 peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or
25 dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the

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al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and

Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor

5 (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford

University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques

Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps,

Sequences, and Genomes Chap and Hall.

10 The present invention provides a computer database comprising a computer and
software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with
data specifying the source of the target-containing sample from which each sequence specificity
record was obtained.

 In an exemplary embodiment, at least one of the sources of target-containing sample is
15 from a control tissue sample known to be free of pathological disorders. In a variation, at least
one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another
tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate
one or more of the following parameters for each target species in a sample: (1) a unique
identification code, which can include, e.g., a target molecular structure and/or characteristic
20 separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute
and/or relative quantity of the target species present in the sample.

 The invention also provides for the storage and retrieval of a collection of target data in
a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-
optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble
25 memory devices, and other data storage devices, including CPU registers and on-CPU data
storage arrays. Typically, the target data records are stored as a bit pattern in an array of
magnetic domains on a magnetizable medium or as an array of charge states or transistor gate
states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and
a charge storage area, which may be on the transistor). In one embodiment, the invention
30 provides such storage devices, and computer systems built therewith, comprising a bit pattern
encoding a protein expression fingerprint record comprising unique identifiers for at least 10
target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can
5 include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible
10 (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
15 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit
20 pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database
25 comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute
30 the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the
5 Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

10 An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets
15 in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino
20 acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in
25 England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may
30 have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain
5 containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous
10 transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and
15 number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin
20 receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on
25 receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated
30 molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein.

- 5 In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment.
- 10 Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

- It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through
- 15 recombinant means by adding an appropriate signal sequence.

- In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to
- 20 various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or
- 25 altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL
- 30 mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer
20 sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is
5 derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known
10 (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or
15 attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example,
20 photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix
25 GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative
30 amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other
5 components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-
10 cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of
15 purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription
20 or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than
25 about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

30 Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative
5 cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes:
10 substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis
15 using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

20 While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined
25 sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions
30 may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional
5 imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine,
10 phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the
15 scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-
20 associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally
25 be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g.,
30 WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the
10 nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may
5 reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.)
10 Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the
15 recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized
20 antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
25 immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding
30 sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the
10 following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene
5 expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to,
10 quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene
15 expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as
20 being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays
25 are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can
30 be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for
10 each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens
15 are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
20 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.
30

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5–48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

- 5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.
- 10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

- In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
- 15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

- In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
- 20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

- 25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

- 30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid
5 complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
10 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

15 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense
20 oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to
25 the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific
30 manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

 The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al.(1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

 Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

 Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number
5 of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)
15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
 5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
 10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
 15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
 20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
 25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bordetella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
 30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may
5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated
10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or
15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A-68, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

5	blood vessels/angiogenesis: hemangiomas, lymphangiomas, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
10	bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma bone marrow: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma
15	breast: ductal carcinoma in situ, lobular carcinoma in situ cervix: cancer of the cervix, vagina, or vulva colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
20	esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrodigestive carcinomas (e.g., cancers of the stomach, colon, or rectum) fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
25	head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomylipoma, oncocytoma leukocytes: acute lymphoblastic leukemia/lymphoma, malignant transformation of immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, or lymphoblasts, arthritis, inflammation, wound healing
30	liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
35	ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
40	pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
45	skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
50	stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
55	uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

Tables 2B-66C list accession numbers for Pkeys lacking UnigenelD's for Tables 2A-66C, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 2C-66C list genomic positioning for Pkeys lacking UnigenelD's and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 2A: ABOUT 1031 GENES UP-REGULATED IN ACUTE LYMPHOCYTIC LEUKEMIA (ALL)
Table 2A lists about 1031 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult tissues was greater than or equal to 1.7. The "average" leukemia level was set to the 75th percentile amongst various ALL samples. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigenel number
Unigene Title: Unigene gene title
R1: Ratio of leukemia to normal body tissue

Pkey	ExAcc	UnigenelD	Unigene Title	R1
100458	S74019	Hs.247979	pre-B lymphocyte gene 1	46.8
113089	T40707	Hs.270862	ESTs	20.4
105956	R06428	Hs.226351	ESTs	15.8
101447	M21305		gb:Human alpha satellite and satellite 3	13.8
113009	T23699	Hs.7246	ESTs	12.5
126947	Z40778	Hs.191837	ESTs	11.4
100893	BE245294	Hs.180789	S164 protein	11.1
101050	AU077324	Hs.1832	neuropeptide Y	11.0
132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein	10.7

5	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8	10.4
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	9.1
	112727	T91029	Hs.15069	ESTs	9.0
	109788	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	8.7
	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.8
10	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	7.7
	109384	AA219172	Hs.86849	ESTs	7.6
	112602	AW004045	Hs.203365	ESTs	6.6
	125278	AI218439	Hs.129998	enhancer of polycomb 1	6.5
	112167	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	6.4
15	116355	AA789133	Hs.88650	ESTs	5.8
	123440	AI733692	Hs.112488	ESTs	5.5
	100918	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	5.4
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	5.4
	109260	AW978515	Hs.131915	KIAA0863 protein	5.4
20	129213	AI146494	Hs.109525	ESTs, Weakly similar to IROX2_HUMAN IROQU	5.4
	120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens	5.4
	105498	H68279	Hs.24937	transformer-2 alpha (htra-2 alpha)	5.1
	114840	AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	5.0
	103304	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	4.9
25	113983	W87415	Hs.55296	HLA-B associated transcript-1	4.8
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	4.8
	120712	AF193339	Hs.102506	eukaryotic translation initiation factor	4.8
	107794	AA019255		gb:ze56e10.s1 Soares retina N2b4HR Homo	4.7
	135101	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	4.6
30	129898	AI672731	Hs.13256	ESTs	4.6
	113494	T91451	Hs.86538	ESTs	4.6
	115004	AA329340	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-	4.5
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.5
	112326	R55822	Hs.4268	ESTs	4.4
35	105169	BE245294	Hs.180789	S164 protein	4.4
	117048	H89732	Hs.230113	EST	4.3
	123133	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	4.3
	111394	AA412227	Hs.16131	hypothetical protein FLJ12876	4.3
	106112	AL117518	Hs.3686	KIAA0978 protein	4.2
40	114414	AW152166	Hs.182113	ESTs	4.2
	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	4.2
	114995	AA769266	Hs.193657	ESTs	4.2
	123338	AA504249	Hs.187585	ESTs	4.1
	126666	AA648886	Hs.151999	ESTs	4.1
45	112908	BE281000	Hs.3530	TLS-associated serine-arginine protein 2	4.1
	116640	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.0
	108292	AW975746	Hs.188652	KIAA1702 protein	4.0
	131724	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.0
	119772	AJ250839	Hs.58241	gene for serine/threonine protein kinase	4.0
50	134453	AJ272141	Hs.83484	SRV (sex determining region Y)-box 4	4.0
	123562	AA177088	Hs.190065	ESTs	4.0
	103226	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	3.9
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	3.9
	119873	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.9
55	115553	AJ275986	Hs.71414	transcription factor (SMIF gene)	3.9
	131844	AI419294	Hs.324342	ESTs	3.8
	123360	AA532718	Hs.178604	ESTs	3.8
	111180	AI798851	Hs.283108	hemoglobin, gamma G	3.8
	129426	AF077953	Hs.111323	Protein inhibitor of activated STAT X	3.8
60	105434	AA252111	Hs.15200	ESTs	3.8
	119073	BE245360	Hs.279477	ESTs	3.8
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	3.7
	119325	T51136	Hs.90489	ESTs	3.7
	115898	AA448488	Hs.336629	ribosomal protein L44	3.7
65	119830	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	3.7
	104584	AA704538	Hs.193777	ESTs	3.6
	105212	AA205334	Hs.324278	Homo sapiens mRNA; cDNA DKFZp566M063 (f	3.6
	109223	AW000714	Hs.65818	ESTs	3.6
	112605	R79374	Hs.29852	ESTs	3.5
70	105733	AA767669	Hs.10242	ESTs	3.5
	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	3.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	3.5
	127834	AW301022	Hs.337631	EST	3.5
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	3.5
75	115185	BE299677	Hs.105461	hypothetical protein FLJ20357	3.5
	113921	AW978530	Hs.28355	hypothetical protein FLJ22402	3.5
	115835	AA521410	Hs.41371	ESTs	3.5
	123503	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.4
80	128743	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	3.4
	117031	H88353		gb:yy21a02.s1 Morton Fetal Cochlea Homo	3.4
	123149	AI734179	Hs.105676	ESTs	3.4
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.4
	103158	BE242587	Hs.118651	hematopoietically expressed homeobox	3.4
	107599	AW664072	Hs.60136	ESTs	3.4
	125556	AB033064	Hs.334806	KIAA1238 protein	3.4
	103331	AI825463	Hs.147996	protein kinase, X-linked	3.4

	114387	AI655141	Hs.107720	ESTs, Weakly similar to A54295 interfer	3.4
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.4
	100305	NM_004941	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.4
5	129818	T71092	Hs.172572	hypothetical protein FLJ20093	3.3
	133445	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.3
	132111	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.3
	105292	AF128542	Hs.166846	polymerase (DNA directed), epsilon	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
10	118922	AW205193	Hs.91065	hypothetical protein DKFZp761B2423	3.2
	132344	AW977189	Hs.45719	KIAA0823 protein	3.2
	129889	AA810932	Hs.131899	ESTs, Weakly similar to T00370 hypotheti	3.2
	123670	AI189844	Hs.112708	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.2
15	105289	AB020638	Hs.103000	KIAA0831 protein	3.2
	105583	AA278907	Hs.3530	TLS-associated serine-arginine protein	3.2
	104796	BE620712	Hs.33026	hypothetical protein PP2447	3.2
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	3.2
	134174	AF283770	Hs.79530	CD79A antigen (immunoglobulin-associated	3.2
20	126077	M78772	Hs.210836	ESTs	3.1
	133733	AK000476	Hs.75798	hypothetical protein	3.1
	124847	W07701	Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,	3.1
	127879	AA768098	Hs.189079	ESTs	3.1
	113108	AW516695	Hs.8438	ESTs	3.1
25	110343	AW136703	Hs.17268	ESTs	3.1
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.1
	111676	AB040882	Hs.109778	KIAA1449 protein	3.1
	127311	AA492582	Hs.322404	hypothetical protein MGC4175	3.1
	108830	AA131743	Hs.193352	ESTs	3.1
30	111330	BE247767	Hs.18166	KIAA0870 protein	3.1
	104246	AF016032	Hs.201377	lysosomal apyrase-like 1	3.1
	126568	AA011616	Hs.269877	ESTs	3.1
	124724	H20816	Hs.112423	Homo sapiens mRNA; cDNA DKFZp586i1420 (f	3.1
	114794	AI751157	Hs.101395	hypothetical protein MGC11352	3.1
35	134599	X99226	Hs.284153	Fanconi anemia, complementation group A	3.0
	130314	NM_014674	Hs.154332	KIAA0212 gene product	3.0
	100265	D38521	Hs.112396	KIAA0077 protein	3.0
	115005	AI760825	Hs.111339	ESTs	3.0
	123433	AW450922	Hs.112478	ESTs	3.0
40	127798	AA737068	Hs.294078	ESTs	3.0
	117403	H84455	Hs.40639	ESTs	3.0
	107111	AI298448	Hs.22670	chromodomain helicase DNA binding protei	3.0
	105898	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.0
	108358	M81933	Hs.1634	cell division cycle 25A	3.0
45	132066	AI929392	Hs.181195	DnaJ (Hsp40) homolog, subfamily B, membe	2.9
	130303	BE245294	Hs.180789	S164 protein	2.9
	104596	AF067804	Hs.15423	hypothetical protein HDCMC04P	2.9
	112197	NM_003655	Hs.5637	ESTs	2.9
	132809	AF036144	Hs.5734	meningioma expressed antigen 5 (hyaluron	2.9
50	100877	X80821	Hs.27973	KIAA0874 protein	2.9
	108147	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	2.9
	133674	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	2.9
	129001	AA443323	Hs.107812	BPOZ protein	2.9
	131920	BE002320	Hs.287864	Homo sapiens cDNA FLJ14030 fis, clone HE	2.9
55	134709	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro	2.8
	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	115839	BE300266	Hs.28935	transducin-like enhancer of split 1, hom	2.8
	129969	N57818		gb:yy59d07.s1 Soares fetal liver spleen	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
60	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.8
	129294	AF172940	Hs.184542	CGI-127 protein	2.8
	104518	H20816	Hs.112423	Homo sapiens mRNA; cDNA DKFZp586i1420 (f	2.7
	107796	AA058848	Hs.60797	ESTs	2.7
	106331	AB037742	Hs.24336	KIAA1321 protein	2.7
65	127692	AI021912	Hs.187983	ESTs	2.7
	131916	AA025976	Hs.34569	ESTs	2.7
	124971	T23900	Hs.151001	hypothetical protein FLJ14728	2.7
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.7
	118348	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	2.7
70	113219	T59257	Hs.269528	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	131720	Z68128	Hs.3109	Rho GTPase activating protein 4	2.7
	109593	AW196801	Hs.6685	thyroid hormone receptor interactor 8	2.7
	135359	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.7
	131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.7
75	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.7
	121073	H46199	Hs.112184	DKFZP586J0619 protein	2.7
	125069	H81306	Hs.194485	ESTs	2.7
	116456	AI381911	Hs.334859	KIAA1814 protein	2.7
80	124271	AW293223	Hs.8928	hypothetical protein FLJ20291	2.7
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.7
	115866	AW062629	Hs.52081	KIAA0867 protein	2.7
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	2.7
	124494	N54831	Hs.271381	ESTs, Weakly similar to I38022 hypothet	2.7
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19w	2.7

	120510	AI796395	Hs.111377	ESTs	2.6
	129781	AA306090	Hs.124707	ESTs	2.6
	122698	AA456112	Hs.99410	ESTs	2.6
5	106995	AB023139	Hs.37892	KIAA0922 protein	2.6
	105502	BE464016	Hs.238956	ESTs	2.6
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.6
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	2.6
10	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	2.6
	111219	N68836	Hs.19247	ESTs, Moderately similar to ALUC_HUMAN	2.6
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.6
	125626	AI038854	Hs.180789	S164 protein	2.6
	111189	N67603	Hs.272130	ESTs, Weakly similar to S65824 reverse	2.6
15	113146	BE151985	Hs.5722	hypothetical protein FLJ23316	2.6
	125562	AI494372	Hs.98958	hypothetical protein FLJ23058	2.6
	102263	U29171	Hs.75852	casein kinase 1, delta	2.6
	118835	AA535246	Hs.50852	ESTs	2.6
	103141	X66113	Hs.75584	polymyositis/scleroderma autoantigen 2 (2.6
20	109598	R40515	Hs.21248	ESTs	2.6
	127262	AA828125		gb:cd71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.6
	129620	D79338	Hs.239720	CCR4-NOT transcription complex, subunit	2.6
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.6
	123255	AA830335	Hs.105273	ESTs	2.6
25	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.6
	109638	AW977747	Hs.119120	E3 ubiquitin ligase SMURF1	2.6
	119896	AA731836	Hs.137319	ESTs	2.6
	134770	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	2.6
	119403	AL117554	Hs.119908	nucleolar protein NOP58	2.6
30	129563	AF119664	Hs.27299	transcriptional regulator protein	2.6
	111719	AI655806	Hs.179262	ESTs	2.6
	103982	AA218558	Hs.7905	sorting nexin 9	2.6
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.5
35	131426	AL122045	Hs.26703	CCR4-NOT transcription complex, subunit	2.5
	131938	AF176085	Hs.34956	neural polypyrimidine tract binding prot	2.5
	102450	U48251	Hs.75871	protein kinase C binding protein 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	126339	AA152106	Hs.4859	cyclin L ania-6a	2.5
	118967	AI668670	Hs.216756	ESTs	2.5
40	123110	AA486256	Hs.193510	EST	2.5
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.5
	113247	T63856	Hs.193430	ESTs, Weakly similar to 2109260A B cell	2.5
	122024	AA431296	Hs.139433	ESTs	2.5
	106657	AW854339	Hs.33476	hypothetical protein FLJ11937	2.5
45	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	2.5
	111836	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.5
	121470	AA558958	Hs.324751	ESTs	2.5
	120132	W57554	Hs.125019	ESTs	2.5
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.5
50	118122	AI186671	Hs.48008	ESTs	2.5
	106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.5
	129948	AI537162	Hs.263988	ESTs	2.5
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	2.5
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
55	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.5
	100512	D13317	Hs.78915	GA-binding protein transcription factor,	2.5
	105393	AF167570	Hs.256583	interleukin enhancer binding factor 3, 9	2.5
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.5
	106890	AA489245	Hs.88500	mitogen-activated protein kinase 8 inte	2.5
60	104276	AW965275	Hs.284288	hap0256 protein	2.5
	113283	T66813	Hs.12947	EST	2.5
	118078	N54321	Hs.47790	EST	2.5
	120796	AI247356	Hs.96820	ESTs	2.5
	106265	AA412176	Hs.236463	Homo sapiens mRNA; cDNA DKFZp586l0521 (f	2.5
65	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	106508	AI205785	Hs.30348	ESTs	2.5
	104568	AW629981	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.5
	103698	AA001021	Hs.6685	thyroid hormone receptor interactor 8	2.5
	113947	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_	2.5
70	132112	AL021938	Hs.40154	jumonji (mouse) homolog	2.5
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.4
	117265	AA451966	Hs.43005	RAB9-like protein	2.4
	107834	AA253162	Hs.40838	ESTs	2.4
	113119	T47910		gb:zb18b11.s1 Stratagene fetal spleen (9	2.4
75	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.4
	120548	AA280356	Hs.187634	ESTs	2.4
	121545	AA412442	Hs.98132	ESTs	2.4
	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	126589	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.4
80	115475	AB033085	Hs.40193	hypothetical protein KIAA1259	2.4
	103760	AA642973	Hs.183842	ubiquitin B	2.4
	127889	AI147408	Hs.144941	ESTs	2.4
	124457	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.4
	113721	AF143885	Hs.18190	EST	2.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.4
	123530	AA608705	Hs.187772	ESTs	2.4
	123592	AA805331	Hs.112637	ESTs	2.4
5	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.4
	116728	F13687	Hs.227976	EST	2.4
	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	2.4
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2	2.4
	127841	AW136558	Hs.125246	ESTs	2.4
10	102737	R51790	Hs.239483	Human clone 23933 mRNA sequence	2.4
	129573	D38552	Hs.1191	KIAA0073 protein	2.4
	133095	BE046490	Hs.180677	zinc finger protein 162	2.4
	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
15	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.4
	129059	AW069534	Hs.279583	CGI-81 protein	2.4
	134092	AA218558	Hs.7905	sorting nexin 9	2.4
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.4
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.4
20	128468	T23625	Hs.150580	putative translation initiation factor	2.4
	127407	AW089514	Hs.279581	heterogeneous nuclear ribonucleoprotein	2.4
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.4
	113518	AW367788	Hs.323954	postmeiotic segregation increased 2-lik	2.4
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.4
25	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferase	2.4
	100114	X02308	Hs.82962	thymidylate synthetase	2.4
	125038	AA812234	Hs.270134	hypothetical protein FLJ20280	2.4
30	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.4
	132380	AW373665	Hs.46853	ESTs	2.4
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.3
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.3
35	134839	D63479	Hs.115907	diacylglycerol kinase, delta (130kD)	2.3
	105734	AI952797	Hs.10888	hypothetical protein FLJ21709	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	118349	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	101194	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.3
40	130588	AL030996	Hs.16411	hypothetical protein LOC57187	2.3
	101875	BE241753	Hs.74592	special AT-rich sequence binding protein	2.3
	118751	N74210	Hs.50454	ESTs	2.3
	125174	W51835	Hs.231082	EST	2.3
	105966	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	2.3
45	104624	AA353125	Hs.184721	ESTs	2.3
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	123423	AA598484		gb:ae3804.s1 Gessler Wilms tumor Homo s	2.3
	128531	H03721	Hs.2953	ribosomal protein S15a	2.3
50	108876	AI733860	Hs.191453	ESTs	2.3
	130216	BE301883	Hs.152707	glioblastoma amplified sequence	2.3
	132232	AI522273	Hs.42640	ESTs	2.3
	132664	AI740461	Hs.54542	ESTs	2.3
	105991	AA215701	Hs.186541	ESTs, Weakly similar to I38022 hypothi	2.3
55	100253	D38024	Hs.157425	double homeobox, 2	2.3
	105574	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.3
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.3
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	2.3
	132786	BE083422	Hs.56851	hypothetical protein MGC2568	2.3
60	104952	AW076098	Hs.74316	desmoplakin (DPI, DPII)	2.3
	119127	AA708035	Hs.12248	ESTs	2.3
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.3
	107592	AA694264	Hs.60049	ESTs	2.3
	113378	T80738	Hs.14757	ESTs	2.3
65	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.3
	106898	AA490069	Hs.306676	Homo sapiens cDNA FLJ14302 fis, clone PL	2.3
	130734	AW137091	Hs.18624	KIAA1052 protein	2.3
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.3
	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.3
70	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.3
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.3
	105777	R42755	Hs.23096	ESTs	2.3
	115306	AA280288	Hs.88746	ESTs	2.3
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.3
75	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.3
	121520	AA412163	Hs.164785	ESTs	2.3
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.3
	105700	AW580830	Hs.35254	hypothetical protein FLB6421	2.3
	120820	AA347417	Hs.96869	EST	2.3
80	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.3
	107711	W96141	Hs.220687	ESTs	2.3
	102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr	2.3
	131868	AW408296	Hs.33532	zinc finger protein 151 (pHZ-67)	2.3
	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.3

	118865	AA736405	Hs.54530	ESTs	
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.3
	133772	BE379867	Hs.76038	isopentenyl-diphosphate delta isomerase	2.3
5	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.3
	103437	AV655598	Hs.184211	peptidase (mitochondrial processing) bet	2.3
	123060	AA482027	Hs.142569	ESTs, Weakly similar to I38022 hypotheti	2.3
	125466	R08234	Hs.180461	ESTs	2.3
	100892	BE245294	Hs.180789	S164 protein	2.3
10	121613	AA416879	Hs.193195	ESTs, Weakly similar to 2109260A B cell	2.3
	133665	AL036883	Hs.75450	delta sleep inducing peptide, immunoreac	2.2
	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	126153	H85692	Hs.40730	ESTs	2.2
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.2
15	104960	AA558677	Hs.8928	hypothetical protein FLJ20291	2.2
	113941	AA531016	Hs.22399	hypothetical protein FLJ14824	2.2
	112540	R69751		gb:yl40a10.s1 Soares placenta Nb2HP Homo	2.2
	105322	T87179	Hs.16346	ESTs, Weakly similar to S57447 HPBR11-7	2.2
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.2
20	134733	N87353	Hs.89421	CBF1 interacting corepressor	2.2
	114620	AA642974		gb:nr60h01.s1 NCL_CGAP_Tym3 Homo sapiens	2.2
	123451	AI793211	Hs.165372	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.2
	105561	AA262881	Hs.323836	ESTs, Weakly similar to alternatively s	2.2
25	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	2.2
	130362	BE513050	Hs.279681	heterogeneous nuclear ribonucleoprotein	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.2
	131392	AA235153	Hs.26320	TRABID protein	2.2
30	128845	AW503976	Hs.10649	basement membrane-induced gene	2.2
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.2
	126973	W46653	Hs.251928	nuclear pore complex interacting protein	2.2
	103156	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	2.2
	103163	AU077018	Hs.3235	keratin 4	2.2
35	109252	BE440157	Hs.85944	ESTs	2.2
	131163	AA099524	Hs.23754	ESTs	2.2
	115292	AA279956	Hs.88672	ESTs	2.2
	122591	AI188219	Hs.99311	ESTs, Weakly similar to H5J2_HUMAN DNAB	2.2
	124977	F04819	Hs.190452	KIAA0365 gene product	2.2
40	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	2.2
	100370	D79989	Hs.184884	KIAA0167 gene product	2.2
	128992	H04150	Hs.107708	ESTs	2.2
	129928	AI338993	Hs.134535	ESTs	2.2
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
45	133910	AW835281	Hs.77500	ubiquitin specific protease 4 (proto-onc	2.2
	106288	AB037742	Hs.24336	KIAA1321 protein	2.2
	134125	NM_014781	Hs.50421	KIAA0203 gene product	2.2
	101379	X02994	Hs.1217	adenosine deaminase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
50	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	2.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	2.2
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2	2.2
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.2
	133195	AI434760	Hs.279949	KIAA1007 protein	2.2
55	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.2
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.2
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.2
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.2
	131320	AA505691	Hs.145696	splicing factor (CC1.3)	2.2
60	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	2.2
	103634	BE541733	Hs.180877	H3 histone, family 3B (H3.3B)	2.2
	134624	AF035119	Hs.8700	deleted in liver cancer 1	2.2
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.2
	115556	AL031778	Hs.797	nuclear transcription factor Y, alpha	2.2
65	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.2
	100415	D86970	Hs.75822	TGFB1-induced anti-apoptotic factor 1	2.2
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.2
	129501	AI631811	Hs.180403	STRIN protein	2.2
	127251	AA936428	Hs.128638	ESTs	2.2
70	100613	X52078	Hs.101047	transcription factor 3 (E2A immunoglobul	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
	128897	AW979134	Hs.10700	hypothetical protein	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128804	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.2
75	125585	AW298113	Hs.92909	SON DNA binding protein	2.2
	129584	AV656017	Hs.184325	CGI-76 protein	2.2
	114461	AA531187	Hs.125705	ESTs	2.2
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.2
80	109339	AA314554	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	2.2
	129179	AW969025	Hs.109154	ESTs	2.2
	106711	BE390125	Hs.143187	hypothetical protein	2.2
	106424	H61005	Hs.37902	ESTs	2.2
	123949	AA621665	Hs.208957	EST	2.2
	127256	AI738610	Hs.267957	ESTs, Moderately similar to ALU8_HUMAN	2.2

5	104868	AF173867	Hs.28906	glucocorticoid modulatory element bindin	2.2
	132984	BE539199	Hs.62112	zinc finger protein 207	2.2
	126383	AB032977	Hs.6298	KIAA1151 protein	2.2
	130557	H51825	Hs.268911	ESTs, Weakly similar to S65824 reverse	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
10	105715	BE621800	Hs.29444	putative small membrane protein NID67	2.2
	124691	R05835	Hs.110153	ESTs	2.2
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.2
	117040	AW970600	Hs.303261	ESTs	2.2
	128767	M85169	Hs.1050	pleckstrin homology, Sec7 and coiled/coi	2.2
15	120602	AA808018	Hs.109302	ESTs	2.2
	107182	AI311782	Hs.20013	GCIIP-interacting protein p29	2.2
	107357	U63973	Hs.103501	rhodopsin kinase	2.2
	125499	H10543		gb:ym04c06.r1 Soares infant brain 1NIB H	2.1
	126872	AW450979		gb:UH-H-BI3-ata-a-12-0-UI.s1 NCL_CGAP_Su	2.1
20	113233	T61955	Hs.279867	GGI-59 protein	2.1
	128367	AW611791	Hs.150742	ESTs	2.1
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.1
	114021	AW235215	Hs.16145	ESTs	2.1
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.1
25	134966	AW402389	Hs.920	modulator recognition factor I	2.1
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	2.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.1
	109639	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	2.1
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.1
30	134869	AL157518	Hs.90421	PRO2463 protein	2.1
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.1
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.1
	120906	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TIT3 com	2.1
	134354	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.1
35	106048	AW883367	Hs.301732	hypothetical protein MGC5306	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
	115348	AA281562	Hs.292100	ESTs	2.1
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	2.1
	107121	AB015427	Hs.250493	zinc finger protein 219	2.1
40	118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HE	2.1
	135051	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.1
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	2.1
	126661	AA009835	Hs.269521	ESTs	2.1
	129270	AA357185	Hs.109918	ras homolog gene family, member H	2.1
45	125568	AW615396	Hs.105613	ESTs	2.1
	132867	AF226667	Hs.58553	CTP synthase II	2.1
	124656	AW297702	Hs.102915	ESTs	2.1
	128954	AA346839	Hs.209100	DKFZP434C171 protein	2.1
	132985	AL045579	Hs.62113	KIAA0717 protein	2.1
50	119247	BE269047	Hs.65234	hypothetical protein FLJ20596	2.1
	106686	N66397	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	2.1
	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	2.1
	121170	BE246743	Hs.288529	hypothetical protein FLJ22635	2.1
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.1
55	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.1
	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.1
	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.1
	101183	AA442324	Hs.795	H2A histone family, member O	2.1
	100420	D86983	Hs.118893	Melanoma associated gene	2.1
60	129879	AK001698	Hs.13109	Ran binding protein 11	2.1
	122311	NM_014913	Hs.131915	KIAA0863 protein	2.1
	130666	R85474	Hs.16073	ESTs	2.1
	113517	AI874223	Hs.293560	ESTs	2.1
	115810	AA426026	Hs.187615	ESTs	2.1
65	108743	AI580150	Hs.71074	ESTs	2.1
	129255	AI961727	Hs.109804	H1 histone family, member X	2.1
	120766	AA764879	Hs.12570	tubulin-specific chaperone d	2.1
	126893	AJ252060	Hs.26320	TRABID protein	2.1
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	2.1
70	105865	BE279383	Hs.26557	plakophilin 3	2.1
	120999	AI972375	Hs.29626	hypothetical brain protein my038	2.1
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.1
	117997	N52090	Hs.47420	EST	2.1
	104333	D82418	Hs.29626	hypothetical brain protein my038	2.1
75	134315	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	2.1
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	2.1
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	112563	AW961220	Hs.29282	mitogen-activated protein kinase kinase	2.1
80	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
	133912	H42679	Hs.77522	major histocompatibility complex, class	2.1
	134076	AF086215		gb:Homo sapiens full length insert cDNA	2.1
	116665	F04405		gb:HSC2S8082 normalized infant brain cDN	2.1
	133562	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	2.1
	129092	O56365	Hs.63525	poly(rC)-binding protein 2	2.1
	106869	AW975362	Hs.292679	ESTs	2.1

5	130820	AL353934	Hs.288798	hypothetical protein FLJ21012	2.1
	126277	AB037847	Hs.15441	Crm (Cramped Drosophila)-like	2.1
	106392	BE350058	Hs.36787	chromodomain helicase DNA binding protei	2.1
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	2.1
	120734	AA299948		gb:EST12544 Uterus tumor I Homo sapiens	2.1
10	113070	AB032977	Hs.6298	KIAA1151 protein	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
	123869	AA620824	Hs.112923	EST	2.1
	106145	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	2.1
	109061	AA160896		gb:zo79c07.s1 Stralagene pancreas (93720	2.1
15	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	123132	AI061582	Hs.324179	Homo sapiens cDNA FLJ12371 fis, clone MA	2.1
	117452	N34687	Hs.44054	ninein (GSK3B interacting protein)	2.1
	128538	R44214	Hs.101189	ESTs	2.1
20	111945	R40663	Hs.124944	ESTs	2.1
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.1
	124362	AL046406	Hs.103483	KIAA1798 protein	2.1
	129198	N57532	Hs.109315	KIAA1415 protein	2.1
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.1
25	115643	AA404276	Hs.123253	hypothetical protein FLJ22009	2.0
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	2.0
	115355	AA262292	Hs.88445	ESTs	2.0
	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.0
	125360	AW898892	Hs.189741	ESTs	2.0
30	104926	BE298808	Hs.33363	DKFZP434N093 protein	2.0
	119468	AI911535	Hs.6657	hypothetical protein bK1048E9.5	2.0
	132891	BE267143	Hs.59271	U2(RNU2) small nuclear RNA auxiliary fac	2.0
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	2.0
	105335	AW291165	Hs.25447	ESTs	2.0
35	106727	AA357001	Hs.34045	hypothetical protein FLJ20764	2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	2.0
	128408	AI183407	Hs.143704	EST	2.0
	132311	AI765559	Hs.20072	myosin regulatory light chain interactin	2.0
40	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	116379	AA448588	Hs.71252	hypothetical protein DKFZp761C169	2.0
	105474	AL134843	Hs.219614	f-box and leucine-rich repeat protein 11	2.0
	108922	AA115268	Hs.269263	ESTs	2.0
	123720	AA609734	Hs.112755	EST	2.0
45	128902	AA036637	Hs.107052	ESTs	2.0
	113226	AI821008	Hs.10697	ESTs	2.0
	105798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
	106665	BE090009	Hs.323164	hypothetical protein MGC2217	2.0
	105952	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	2.0
50	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.0
	112972	AI684745	Hs.165983	hypothetical C2H2 zinc finger protein FL	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
	116176	AA311152	Hs.288708	hypothetical protein FLJ21562	2.0
	126457	AA007489	Hs.50382	ESTs	2.0
55	112610	AW500106	Hs.23643	serine/threonine protein kinase MASK	2.0
	109249	AA194730	Hs.268189	hypothetical protein FLJ20436	2.0
	121292	AA401807		gb:zv65f11.s1 Soares_tetal_fetus_Nb2HF8_	2.0
	128605	AW058113	Hs.102402	Mad4 homolog	2.0
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	2.0
60	134674	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	2.0
	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.0
	116411	AA608897	Hs.321618	hypothetical protein FLJ12525	2.0
	111576	T88827	Hs.15489	ESTs	2.0
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.0
65	112662	R85436	Hs.268814	ESTs	2.0
	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (f	2.0
	101045	J05614		gb:Human proliferating cell nuclear anti	2.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.0
70	119849	AI074585	Hs.58440	ESTs	2.0
	124395	N29963	Hs.272095	ESTs, Weakly similar to I38022 hypotheti	2.0
	131600	NM_004377	Hs.29331	cameline palmitoyltransferase I, muscle	2.0
	112774	R95770	Hs.35455	ESTs	2.0
	109751	AB033492	Hs.6679	hHDC for homolog of Drosophila headcase	2.0
75	102377	U40343	Hs.29656	cyclin-dependent kinase inhibitor 2D (p1	2.0
	115197	R18656	Hs.6749	ESTs	2.0
	102808	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DE	2.0
	128869	AA768242	Hs.80518	hypothetical protein	2.0
	111229	AW389845	Hs.110855	ESTs	2.0
80	129330	AL079310	Hs.92260	high-mobility group protein 2-like 1	2.0
	105448	NM_001186	Hs.154276	BTB and CNC homology 1, basic leucine zi	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	102337	AI814663	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	2.0
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.0
	107902	AA026627	Hs.61358	ESTs	2.0
	129340	H75334	Hs.11050	F-box only protein 9	2.0
	101097	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	2.0

5	124864	AW970168	Hs.185706	ESTs	2.0
	118485	AA508515	Hs.291049	ESTs	2.0
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	2.0
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
	118677	AW971146	Hs.293187	ESTs	2.0
10	100020				2.0
	123252	AW968776	Hs.287586	Homo sapiens cDNA FLJ13648 fis, clone PL	2.0
	134977	AL044963	Hs.306121	leukocyte receptor cluster (LRC) encoded	2.0
	115334	AA702972	Hs.65300	ESTs	2.0
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bindi	2.0
15	129101	NM_013403	Hs.108665	zinedin	2.0
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.0
	111018	AI287912	Hs.3628	mitogen-activated protein kinase kinase	2.0
	105933	AF078544	Hs.194686	solute carrier family 25 (mitochondrial	2.0
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.0
20	120861	AA350394	Hs.96952	ESTs	2.0
	132430	AW973652	Hs.283105	ESTs	2.0
	115026	AA251972	Hs.188718	ESTs	2.0
	128660	AA011597	Hs.177398	ESTs	2.0
	134554	AI184316	Hs.85273	retinoblastoma-binding protein 6	2.0
25	109592	AI198059	Hs.26370	ESTs	2.0
	123636	AA609263		gb:af13c08.s1 Soares_testis_NHT Homo sap	2.0
	132610	AA160511	Hs.5326	amino acid system N transporter 2; porcu	2.0
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	120467	AW292562	Hs.187628	ESTs	2.0
30	126046	AA804957	Hs.119840	ESTs	2.0
	128179	AW293689	Hs.127116	ESTs	2.0
	123349	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona	2.0
	106208	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
	125832	AA628600	Hs.117587	ESTs	2.0
35	133317	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	2.0
	132886	AW978168	Hs.5912	F-box only protein 7	2.0
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.0
	133149	AA370045	Hs.6607	AXIN1 up-regulated	2.0
	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	2.0
40	106487	AI697340	Hs.135265	Homo sapiens clone FLB8436 PRO2277 mRNA,	2.0
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.0
	120592	AA830664	Hs.143974	ESTs	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	101887	AW967413	Hs.83958	transducin-like enhancer of split 4, hom	2.0
45	125324	R07785		gb:yf15c06.r1 Soares fetal liver spleen	2.0
	133906	BE386038	Hs.77492	heterogeneous nuclear ribonucleoprotein	2.0
	113408	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	2.0
	115613	AW136951	Hs.173946	hypothetical protein FLJ10486	2.0
	107468	AA740979	Hs.91389	ESTs	2.0
50	100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.0
	120476	NM_014922	Hs.104305	death effector filament-forming Ced-4-l	2.0
	117160	AA322302	Hs.183302	PCTAIRE protein kinase 2	2.0
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tu	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
55	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	2.0
	133207	AI561173	Hs.67688	ESTs	2.0
	122053	AI637498	Hs.98745	ESTs	2.0
	121080	AA617830	Hs.28310	ESTs	2.0
	113316	T70318	Hs.268581	ESTs	2.0
60	113137	AW952129	Hs.293225	ESTs, Weakly similar to FLDED-1 [H.sapie	1.9
	100416	AW505086	Hs.196914	minor histocompatibility antigen HA-1	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	103872	AI816078	Hs.21756	translation factor sui1 homolog	1.9
	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	1.9
65	126082	H81188	Hs.269571	ESTs	1.9
	124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	1.9
	123385	BE149685	Hs.17767	KIAA1554 protein	1.9
	103138	X65965		gb:H.sapiens SOD-2 gene for manganese su	1.9
	104867	AA278898	Hs.225979	hypothetical protein similar to small G	1.9
70	128668	AI754363	Hs.103422	Homo sapiens cDNA FLJ14630 fis, clone NT	1.9
	125826	M20681	Hs.7594	solute carrier family 2 (facilitated glu	1.9
	113701	T97301	Hs.18026	ESTs	1.9
	134447	M58603	Hs.83428	nuclear factor of kappa light polypeptid	1.9
	128895	AW467000	Hs.106985	ESTs	1.9
75	112719	AI200957	Hs.19301	Homo sapiens, Similar to Nedd-4-like ubi	1.9
	102552	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	1.9
	131186	Z70200	Hs.246112	KIAA0788 protein	1.9
	133347	BE257758	Hs.71475	acid cluster protein 33	1.9
	133388	AW245631	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
80	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.9
	100336	N76101	Hs.8127	KIAA0144 gene product	1.9
	113479	AI023133	Hs.10739	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	123783	AA610112		gb:af19g05.s1 Soares_total_fetus_Nb2HFB_	1.9
	113016	NM_014007	Hs.127649	KIAA0414 protein	1.9
	132761	AI815537	Hs.323502	nuclear RNA export factor 1	1.9
	128536	AW955085	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.9

	126663	AW518478	Hs.181297	ESTs	1.9
	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	106742	AW591428	Hs.27556	hypothetical protein FLJ22405	1.9
5	129793	AW207000	Hs.126857	Homo sapiens cDNA FLJ12936 fis, clone NT	1.9
	105888	AW970572	Hs.9247	protein kinase, AMP-activated, alpha 1 c	1.9
	101892	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	1.9
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.9
	126751	AI378328	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.9
10	129111	AL080155	Hs.226372	DKFZP434J154 protein	1.9
	128750	T80270	Hs.104788	hypothetical protein LOC55565	1.9
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	100157	D14661	Hs.119	Wilms' tumour 1-associating protein	1.9
15	125845	AK001440	Hs.131840	hypothetical protein FLJ10578	1.9
	134682	AW882645	Hs.88044	sprouty (Drosophila) homolog 1 (antagoni	1.9
	106565	NM_014892	Hs.227602	KIAA1116 protein	1.9
	106706	AB037810	Hs.18760	KIAA1389 protein	1.9
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	1.9
20	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.9
	123264	AI681270	Hs.99824	BCE-1 protein	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9
	104995	AK001690	Hs.16390	hypothetical protein FLJ10035	1.9
	133424	AA350994	Hs.20281	KIAA1700	1.9
25	132450	AA100012	Hs.48827	hypothetical protein FLJ12085	1.9
	131803	U73737	Hs.284289	vitiligo-associated protein VIT-1	1.9
	116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa	1.9
	113815	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	1.9
	100245	AL039248	Hs.3094	KIAA0063 gene product	1.9
30	113677	Z70200	Hs.246112	KIAA0788 protein	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
	134937	AI251449	Hs.171939	ESTs	1.9
	134506	AW247364	Hs.84285	ubiquitin-conjugating enzyme E2i (homolo	1.9
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.9
35	115261	AA938293	Hs.60088	hypothetical protein MGC11314	1.9
	125198	W69474	Hs.323140	ESTs	1.9
	115317	AA303799	Hs.300141	ribosomal protein L39	1.9
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	1.9
	117329	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H	1.9
40	116353	AB032966	Hs.131728	KIAA1140 protein	1.9
	114459	AW445217	Hs.103362	ESTs	1.9
	133903	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.9
	116083	AA455706	Hs.44581	heat shock protein hsp70-related protein	1.9
	130037	AI498631	Hs.111334	ferritin, light polypeptide	1.9
45	102273	BE391815	Hs.75981	ubiquitin specific protease 14 (tRNA-gua	1.9
	120452	AL022328	Hs.104335	hypothetical protein IMAGE3510317	1.9
	116432	BE271922	Hs.71243	ESTs, Weakly similar to zinc finger prot	1.9
	115916	AI052731	Hs.91910	ESTs	1.9
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	1.9
50	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	1.9
	105693	BE250951	Hs.181368	U5 snRNP-specific protein (220 kD), orth	1.9
	102316	U34301		gb:Human nonmuscle myosin heavy chain II	1.9
	131422	AW607731	Hs.26670	Human PAC clone RP3-515N1 from Zq11.2-q	1.9
	128434	AI190914	Hs.143880	ESTs	1.9
55	117086	AA581602	Hs.41840	ESTs	1.9
	102006	AL048967	Hs.172207	non-POU-domain-containing, octamer-bindi	1.9
	121335	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_	1.9
	105905	AA401533	Hs.19440	ESTs	1.9
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	1.9
60	109875	H03260	Hs.30385	ESTs	1.9
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.9
	126203	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.9
	122530	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	1.9
	124506	BE273688	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
65	130525	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.9
	127226	AL036559	Hs.3463	ribosomal protein S23	1.9
	106465	AA971576	Hs.225951	topoisomerase-related function protein 4	1.9
	106970	AA521368	Hs.24252	ESTs	1.9
	134275	AI878910	Hs.3688	cisplatin resistance-associated overexpr	1.9
70	126825	AA100230		gb:z81c01.s1 Stratagene colon (937204)	1.9
	132443	AW246148	Hs.268371	hypothetical protein FLJ20274	1.8
	104631	AA002064	Hs.18920	ESTs	1.8
	111468	H62647	Hs.205481	ESTs	1.8
	114317	AA524839	Hs.469	succinate dehydrogenase complex, subunit	1.8
75	126158	N55989	Hs.16390	hypothetical protein FLJ10035	1.8
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.8
	119229	T03229		gb:FB5C2 Fetal brain, Stratagene Homo sa	1.8
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.8
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.8
80	100967	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.8
	105149	BE089288	Hs.8958	Homo sapiens cDNA FLJ12024 fis, clone HE	1.8
	104542	R29657		gb:F1-1179D 22 week old human fetal live	1.8
	124236	AF086006		gb:Homo sapiens full length insert cDNA	1.8
	127155	AA284993		gb:z123e10.r1 Soares ovary tumor NbHOT H	1.8

	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.8
	107021	AK001342	Hs.14570	hypothetical protein FLJ22530	1.8
	110023	AW294701	Hs.31040	ESTs	1.8
5	114899	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	1.8
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	1.8
	110384	H45282	Hs.268798	ESTs	1.8
	132693	BE244200	Hs.55075	KIAA0410 gene product	1.8
	127684	AA668631	Hs.32556	KIAA0379 protein	1.8
10	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	104249	AF004231	Hs.22405	leukocyte immunoglobulin-like receptor,	1.8
	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.8
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	1.8
	100417	NM_014003	Hs.78054	pre-mRNA splicing factor similar to S. c	1.8
	120532	AA262354	Hs.186648	ESTs, Weakly similar to I38022 hypotheti	1.8
15	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	100739	M59287	Hs.2083	CDC-like kinase 1	1.8
	110636	H72868	Hs.19110	ESTs	1.8
	132957	BE244044	Hs.61469	hypothetical protein	1.8
20	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	1.8
	132161	W31634	Hs.180799	hypothetical protein FLJ22561	1.8
	129510	AW968504	Hs.123073	CDC2-related protein kinase 7	1.8
	126805	F32658	Hs.101359	chromosome 6 open reading frame 32	1.8
	129295	U63127	Hs.110121	SEC7 homolog	1.8
25	127823	AW972893	Hs.78869	transcription elongation factor A (SII),	1.8
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	1.8
	111959	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	1.8
	109303	AA199857	Hs.269291	ESTs	1.8
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	1.8
30	127303	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.8
	115982	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.8
	123331	AA497013		gb:ae32g02.s1 Gessler Wilms tumor Homo s	1.8
	111598	R11505	Hs.268912	ESTs	1.8
	121643	AA640987	Hs.193767	ESTs	1.8
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.8
	118761	AW799109	Hs.226755	ESTs	1.8
	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.8
	118103	AA401733	Hs.184134	ESTs	1.8
	134595	NM_002401	Hs.29282	mitogen-activated protein kinase kinase	1.8
40	134212	AA654353	Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
	128033	AI248705	Hs.149321	ESTs	1.8
	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.8
	111122	N63753	Hs.16492	DKFZP564G2022 protein	1.8
	114798	AA159181	Hs.54900	serologically defined colon cancer anti	1.8
45	106349	AW954310	Hs.127270	KIAA1545 protein	1.8
	135358	BE622827	Hs.99486	hypothetical protein FLJ13044	1.8
	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kinase 1	1.8
	116654	Z26324	Hs.79204	ESTs, Weakly similar to I38022 hypotheti	1.8
	124554	N65961		gb:za27d03.s1 Soares fetal liver spleen	1.8
50	120259	AW014786	Hs.192742	hypothetical protein FLJ12785	1.8
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.8
	125261	W90351	Hs.110134	ESTs, Highly similar to CREB-binding pro	1.8
	135026	N92165	Hs.93231	ESTs	1.8
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.8
55	125768	AI557486	Hs.119122	ribosomal protein L13a	1.8
	114122	R46128	Hs.12751	ESTs	1.8
	133047	AA310600	Hs.63657	peptide:N-glycanase similar to yeast PNG	1.8
	133589	L37368	Hs.75104	RNA-binding protein S1, serine-rich doma	1.8
	130872	U61084	Hs.226307	phorbol (similar to apolipoprotein B m	1.8
60	133498	BE299587	Hs.85301	calcium binding protein P22	1.8
	131144	AA305255	Hs.23528	HSPC038 protein	1.8
	104261	AW248364	Hs.5409	RNA polymerase I subunit	1.8
	115507	AI083668	Hs.50601	hypothetical protein MGC10986	1.8
	109073	T05003	Hs.10056	hypothetical protein FLJ14621	1.8
65	115363	AA214618	Hs.152759	activator of S phase kinase	1.8
	112657	AW844878	Hs.19769	hypothetical protein MGC4174	1.8
	102960	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.8
	125549	R20215		gb:yg18b09.r1 Soares infant brain tNIB H	1.8
	137397	AL133921	Hs.76272	retinoblastoma-binding protein 2	1.8
70	125048	AW440068	Hs.59425	hypothetical protein FLJ23323	1.8
	103403	X95406		gb:H.sapiens cyclin E gene.	1.8
	123546	AA608817	Hs.112597	EST	1.8
	124694	R06108		gb:ye94h05.s1 Soares fetal liver spleen	1.8
	102406	U43177		(NONE)	1.8
75	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	1.8
	123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.8
	118533	N71861	Hs.49413	ESTs	1.8
	123197	AA489250		gb:aa57h12.s1 NCI_CGAP_GCB1 Homo sapiens	1.8
	125656	AW516428	Hs.78687	neutral sphingomyelinase (N-SMase) activ	1.8
80	100154	H60720	Hs.81892	KIAA0101 gene product	1.8
	106876	N52821	Hs.269412	ESTs, Moderately similar to ALU7_HUMAN A	1.8
	128339	AL121087	Hs.296406	KIAA0685 gene product	1.8
	105939	AL137728	Hs.12258	Homo sapiens mRNA; cDNA DKFZp434B0920 (f	1.8
	102495	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.8

	100221	D28383		gb:Human mRNA for ATP synthase B chain,	1.8
	101741	NM_003199	Hs.326198	transcription factor 4	1.8
	101701	NM_002436	Hs.1861	membrane protein, palmitoylated 1 (55kD)	1.8
5	107119	AI375499	Hs.27379	ESTs	1.8
	134362	U47742	Hs.82210	zinc finger protein 220	1.8
	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
	101437	M20681	Hs.7594	solute carrier family 2 (facilitated glu	1.8
	106204	AA188734	Hs.21479	ubiquitin 1	1.8
10	112716	AW590680	Hs.110802	von Willebrand factor	1.8
	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.8
	111369	AA535740	Hs.170263	tumor protein p53-binding protein, 1	1.8
	135204	AF067515	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	1.8
	105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	1.8
15	110997	AW862823	Hs.168052	KIAA0421 protein	1.8
	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	115818	H11695	Hs.322901	disrupter of silencing 10	1.8
	115904	AI167560	Hs.61297	ESTs	1.8
	107510	BE613332	Hs.132055	ESTs, Weakly similar to GNMSLL retroviru	1.8
20	116435	AA186761	Hs.334812	hypothetical protein DKFZp586K0717	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	127426	AA854756	Hs.124076	ESTs	1.8
	125175	W52355	Hs.303030	EST	1.8
	132972	AA034365	Hs.288924	Homo sapiens cDNA FLJ11392 fis, clone HE	1.8
25	125982	R98091		gb:yr30e11.1.1 Soares fetal liver spleen	1.8
	115620	AA399997	Hs.211610	CUG triplet repeat, RNA-binding protein	1.8
	128115	AI435590	Hs.130168	ESTs	1.8
	106880	AI493206	Hs.32425	ESTs	1.7
	101199	L22075	Hs.1666	guanine nucleotide binding protein (G pr	1.7
30	104159	BE386983	Hs.283685	hypothetical protein FLJ20396	1.7
	101368	M13058	Hs.73952	proline-rich protein HaellI subfamily 2	1.7
	103646	AW248439	Hs.2340	junction plakoglobin	1.7
	130717	AA334274	Hs.18368	DKFZP564B0769 protein	1.7
	124981	N25485	Hs.330310	maternal G10 transcript	1.7
35	124770	AA984414	Hs.120429	ESTs	1.7
	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	1.7
	101636	BE392781	Hs.89474	ADP-ribosylation factor 6	1.7
	123553	AI494291	Hs.111977	ESTs	1.7
	127172	AA292208	Hs.251278	KIAA1201 protein	1.7
40	130621	AW513087	Hs.16803	LUC7 (S. cerevisiae)-like	1.7
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	1.7
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.7
	128092	AA904517	Hs.166229	ESTs	1.7
45	128193	AJ224442	Hs.155020	putative methyltransferase	1.7
	113965	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	1.7
	106620	D52562	Hs.296317	KIAA1789 protein	1.7
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.7
	114964	BE085271	Hs.8834	ring finger protein 3	1.7
50	101800	NM_006433	Hs.105806	granulysin	1.7
	130094	NM_001471	Hs.167017	gamma-aminobutyric acid (GABA) B recepto	1.7
	120112	AA180240	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	1.7
	109978	H09356	Hs.22528	ESTs	1.7
	121252	AA393907	Hs.97179	ESTs	1.7
	127768	AW085002	Hs.156187	ESTs	1.7
55	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	100052				1.7
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	1.7
	134333	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (1.7
	123541	AW976511	Hs.112592	ESTs	1.7
60	134191	W26632	Hs.7979	KIAA0736 gene product	1.7
	103305	X82279		gb:H.sapiens Fas, Apo-1 gene (promoter a	1.7
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	1.7
	100598	AL121734	Hs.146409	cell division cycle 42 (GTP-binding prot	1.7
	113610	T93279		gb:ye2501.s1 Stratagene lung (937210) H	1.7
65	105593	AA279341	Hs.174151	aldehyde oxidase 1	1.7
	125317	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	1.7
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.7
	105105	R61532	Hs.87016	hypothetical protein FLJ22938	1.7
	132791	AB029551	Hs.7910	RING1 and YY1 binding protein	1.7
70	116996	H83935	Hs.40535	ESTs	1.7
	133335	BE251012	Hs.263812	nuclear distribution gene C (Anidulans)	1.7
	120959	BE247692	Hs.102469	putative nuclear protein	1.7
	105621	AL040058	Hs.6375	uncharacterized hypothalamus protein HT0	1.7
	106181	AI803651	Hs.191608	ESTs	1.7
75	125661	AA491830	Hs.25689	ESTs	1.7
	127585	AA604144	Hs.190632	ESTs	1.7
	112035	AI955289	Hs.300759	ribosomal protein L36	1.7
	102870	M64437	Hs.234799	breakpoint cluster region	1.7
	108039	AA280319	Hs.288840	PRO1575 protein	1.7
80	125898	AK001823	Hs.92287	Homo sapiens mRNA: cDNA DKFZp564C2478 (f	1.7
	114740	N70103		gb:za53e10.s1 Soares fetal liver spleen	1.7
	120304	AA192469	Hs.271838	ESTs	1.7
	103433	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7

	105269	AF174499	Hs.6764	histone deacetylase 6	1.7
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (1.7
	133579	X75346	Hs.75074	mitogen-activated protein kinase-activat	1.7
5	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.7
	129601	AB032964	Hs.115726	KIAA1138 protein	1.7
	113739	AA356599	Hs.173904	ESTs	1.7
	100840	U04816	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	1.7
	122878	AA847744	Hs.99640	ESTs	1.7
	119495	BE144608	Hs.55533	ESTs	1.7
10	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	109891	H04757	Hs.323176	ESTs	1.7
	126884	U49436	Hs.286236	KIAA1856 protein	1.7
	132977	AA093322	Hs.301404	RNA binding motif protein 3	1.7
15	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	1.7
	104730	AW139789	Hs.16370	Homo sapiens cDNA FLJ11652 fis, clone HE	1.7
	102205	BE242291	Hs.197540	hypoxia-inducible factor 1, alpha subunit	1.7
	112945	AW138458	Hs.20787	Homo sapiens cDNA: FLJ21688 fis, clone C	1.7
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.7
20	107157	AW853745	Hs.286035	hypothetical protein FLJ22686	1.7
	133229	AL137480	Hs.6834	KIAA1014 protein	1.7
	129912	AF155096	Hs.107213	hypothetical protein FLJ20585	1.7
	119811	AW137640	Hs.231444	Homo sapiens, Similar to hypothetical pr	1.7
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	1.7
25	133134	AF198620	Hs.65648	RNA binding motif protein 8A	1.7
	115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.7
	133817	AW578716	Hs.7644	H1 histone family, member 2	1.7
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.7
	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	1.7
30	121009	NM_001533	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.7
	125546	H09950		gb:ym01d12r1 Soares infant brain 1N1B H	1.7
	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	119015	N95490	Hs.29700	hypothetical protein FLJ20094	1.7
	100058				1.7
35	116655	AF271732	Hs.68090	bridging integrator-3	1.7
	119898	R93325	Hs.58690	ESTs	1.7
	105021	H07960	Hs.306044	CGI-05 protein	1.7
	102098	N25485	Hs.330310	maternal G10 transcript	1.7
	126730	AA442429		gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_	1.7
40	113427	T85105	Hs.15471	ESTs	1.7
	122317	T85253	Hs.290874	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.7
	130503	BE208491	Hs.295112	KIAA0618 gene product	1.7
	117348	N24157		gb:yx96b12.s1 Soares melanocyte 2NbHM Ho	1.7
	127033	AF169301	Hs.9098	sulfate transporter 1	1.7
45	128554	AW972147	Hs.101395	hypothetical protein MGC11352	1.7
	124733	R20547	Hs.100830	ESTs	1.7
	106310	R98185	Hs.17240	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp434i0623 (f	1.7
	101075	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	1.7
50	126659	T16245		gb:N1B1005R Normalized infant brain, Ben	1.7
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	1.7
	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.7
	104188	AA478423	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	1.7
	134750	L25073	Hs.11139	cold shock domain protein A	1.7
55	106826	BE253927	Hs.24983	hypothetical protein from EUROIMAGE 2021	1.7
	113511	T89578	Hs.189740	ESTs	1.7
	111070	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
	129710	AJ277841	Hs.120963	ELG protein	1.7
60	132833	U78525	Hs.57783	eukaryotic translation initiation factor	1.7
	125775	AW514585	Hs.29205	alpha integrin binding protein 63	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	100487	AJ076640	Hs.15243	nucleolar protein 1 (120kD)	1.7
	119302	T25725		gb:ESTDIR152 CD34+DIRECTIONAL Homo sapie	1.7
65	128245	AA993101	Hs.170486	ESTs	1.7
	130322	NM_014247	Hs.154545	PDZ domain containing guanine nucleotide	1.7
	135363	AW589601	Hs.119	Wilms' tumour 1-associating protein	1.7
	125181	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.7
	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	1.7
70	127206	AW816490	Hs.337508	ESTs	1.7
	121880	AW946155	Hs.7750	hypothetical protein AL133206	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	114601	AA075566		gb:zm8806.s1 Stratagene ovarian cancer	1.7
	126278	AA417302	Hs.63042	DKFZp554J157 protein	1.7
75	120964	AA398085	Hs.142390	ESTs	1.7
	133634	AL035071	Hs.234279	microtubule-associated protein, RP/EB fa	1.7
	107025	AA825523	Hs.21255	ESTs, Weakly similar to T38022 hypotheti	1.7
	105638	AA493453	Hs.247817	H2B histone family, member A	1.7
	135398	M16029	Hs.287270	ret proto-oncogene (multiple endocrine	1.7
	115794	AA424900	Hs.112227	membrane-associated nucleic acid binding	1.7
80	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.7
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.7
	130868	AB037855	Hs.171917	hypothetical protein FLJ11085	1.7
	110493	AI247707	Hs.36915	ESTs	1.7

5	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.7
	128764	AW024282	Hs.104938	hypothetical protein MGC15906	1.7
	134065	X78992	Hs.78909	butyrate response factor 2 (EGF-response	1.7
	101082	BE616731	Hs.80645	interferon regulatory factor 1	1.7
	130945	U20582	Hs.2149	actin like protein	1.7
10	106974	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.7
	126752	AI073373	Hs.326923	EST, Weakly similar to I38022 hypothetical	1.7
	133327	AL390127	Hs.7104	Kruppel-like factor 13	1.7
	127005	T81309	Hs.251654	insulin-like growth factor 2 (somatomedi	1.7
	105615	AA281959	Hs.5210	glia maturation factor, gamma	1.7
15	116295	AA742596	Hs.91216	ESTs, Weakly similar to 2004399A chromos	1.7
	111587	AI125867	Hs.20734	ESTs	1.7
	104570	AW978870	Hs.131828	ESTs	1.7
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.7
	130430	W27893	Hs.150580	putative translation initiation factor	1.7
20	119244	AW407564	Hs.275865	ribosomal protein S18	1.7
	131152	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	1.7
	133419	BE242676	Hs.73172	growth factor independent 1	1.7
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.7
	116482	AW207000	Hs.126857	Homo sapiens cDNA FLJ12936 fis, clone NT	1.7
25	132555	AW500131	Hs.171763	CD22 antigen	1.7
	125840	AB028986	Hs.12064	ubiquitin specific protease 22	1.7
	115416	AA283893	Hs.337079	ESTs	1.7
	120041	AA830882	Hs.59368	ESTs	1.7
	126295	AI281459	Hs.270114	ESTs	1.7
30	122528	AA449804	Hs.292154	stromal cell protein	1.7
	Table 2B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
35	Pkey	CAT number	Accession		
	106451	13766_27	AA079195 AA084955 AA126308 AA084956		
	124236	46919_1	AF086006 H64722 H65212 H66282		
	115982	173_2	W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353		
			AW088477 AI887846 AW502624 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618		
40	116665	1394292_1	AI124782 AA889402 AA765804 AA765530 AA055698 AA594019 AI267368 AA456946 R93354 AF264624 AW668618 AA601493		
	125165	1852047_1	F04405 BE173130		
	125324	1692163_1	W45350 W45406		
	126053	1601238_1	R07785 T85948 T86972		
	125499	1562851_1	H64450 H64464		
45	126127	1205826_1	H10543 R11878		
	125546	356478_1	N95428 W24040 AW751366 H81987		
	125549	1702179_1	H09950 R18413 AA570553 AW973425		
	125761	1744008_1	R20215 R18767		
	127155	200358_1	R68351 R68364		
50	125957	1583542_1	AA284993 AA478122 AA477923		
	125982	1766315_1	H41694 H45213		
	127245	226662_1	R98091 W92898		
	127248	227560_1	AA323958 AA370268		
	127262	231725_1	AA364195 AA325029 AW962050		
55	126659	1541209_1	AA828125 AA834883 AA330555		
	127303	258778_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006		
	127315	37938_1	AA366951 AA470999 AA469425		
	126730	297653_1	AF116622 AI114507 AA640834 AA377999		
	103898	187213_3	AA442429 T19477		
60	126872	142696_1	AA248884		
	112540	1605263_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367		
	127705	966283_2	BE011368 BE011362 BE011215 BE011365 BE011363		
	121335	279548_1	R69751 R70467 H69771 H80879 H80878		
	120734	208882_1	AJ003322 AJ003324		
65	114620	32062_8	AA404418 AI217248		
	122652	26401_30	AA299948 AA299949		
	123636	genbank_AA609263	AA642974 AA084223		
	100842	ligr_HT4398	AA454641		
	116548	genbank_D20433	AA609263		
70	123783	genbank_AA610112	U05597		
	125032	genbank_T74884	D20433		
	123808	genbank_AA620552	AA610112		
	102316	entrez_U34301	T74884		
	102406	entrez_U43177	AA620552		
75	134076	40321_1	U34301		
	104542	genbank_T47910	U43177		
	104799	genbank_AA029703	AF085215 W02702 AA284288 W25655		
	127954	135151_1	R29657		
	120809	genbank_AA346495	T47910		
80	113610	genbank_T93279	AA029703		
	113947	genbank_W84768	F06298 R18057		
	101045	entrez_J05614	AA346495		
			T93279		

129969	genbank_N57818	
117031	genbank_H88353	
101447	entrez_M21305	
124540	genbank_N63232	
124554	genbank_N65961	
117348	genbank_N24157	
117357	genbank_N24829	
124677	genbank_R01073	
124694	genbank_R08108	
103138	entrez_X65965	
103305	entrez_X82279	
103392	entrez_X94563	
103403	entrez_X95406	
119229	genbank_T03229	
119302	genbank_T25725	
126825	430458_1	AA100230 AA100274
105225	genbank_AA211777	
121292	genbank_AA401807	
112853	genbank_T02843	T02843
121387	genbank_AA405854	
114601	genbank_AA075566	
100221	entrez_D28383	D28383
123197	genbank_AA489250	AA489250
114740	379876_1	N70103 N70020 AW383189 AI207469 W00935 W00906 AA551569 AI343637 AA135199
123331	genbank_AA497013	
107794	genbank_AA019255	
100554	tigr_HT2241	M95923
123423	genbank_AA598484	
123474	genbank_AA599209	
109061	genbank_AA160896	

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hematopoietic Tissues

Table 3A lists about 1346 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hematopoietic tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult hematopoietic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 85th percentile amongst various ALL samples. The "average" normal adult hematopoietic tissue level was set to the 75th percentile amongst various non-malignant hematopoietic tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of leukemia to hematopoietic tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
129498	AA449789	Hs.75511	connective tissue growth factor	57.88
100458	S74019	Hs.247979	pre-B lymphocyte gene 1	49.45
133774	X54079	Hs.76067	heat shock 27kD protein 1	48.42
102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr	41.49
130650	AB040951	Hs.284208	DKFZP434N161 protein	35.88
132922	AF249745	Hs.6066	Rho guanine nucleotide exchange factor	35.74
112254	AA852097	Hs.25829	ras-related protein	33.28
106706	AB037810	Hs.18760	KIAA1389 protein	32.39
101050	AU077324	Hs.1832	neuropeptide Y	30.68
102455	U48705	Hs.75562	discoidin domain receptor family, member	26.81
101838	BE243845	Hs.75511	connective tissue growth factor	25.46
113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	24.69
134125	NM_014781	Hs.50421	KIAA0203 gene product	24.63
106943	AW888222	Hs.9973	tensin	23.14
130069	AI754813	Hs.146428	collagen, type V, alpha 1	23.06
119073	BE245360	Hs.279477	ESTs	22.53
130444	M12125	Hs.300772	tropomyosin 2 (beta)	21.96
100420	D86983	Hs.118893	Melanoma associated gene	21.05
114324	AF084481	Hs.26077	Wolfram syndrome 1 (wolframin)	18.95
101400	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	18.46
102759	NM_005100	Hs.788	A kise (PRKA) anchor protein (gravin)	17.88
100893	BE245294	Hs.180789	S164 protein	16.75
131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.60
106410	AB037787	Hs.26229	neurotigin 2	16.51
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8	15.60
131524	AB040927	Hs.301804	KIAA1494 protein	15.01
107794	AA019255		gb:ze56e10.s1 Soares refi N2b4HR Homo	14.78
129213	AI146494	Hs.109525	ESTs, Weakly similar to IRIX2_HUMAN IROQU	14.76
116068	AA328041	Hs.194329	hypothetical protein FLJ21174	14.24
134416	X68264	Hs.211579	melanoma cell adhesion molecule	14.06
134545	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	14.03
114009	AI248544	Hs.103000	KIAA0831 protein	13.93
115110	AK001671	Hs.11387	KIAA1453 protein	13.75
130107	AF112977	Hs.172887	phytanoyl-CoA hydroxylase (Refsum diseas	13.60
133558	X68945	Hs.748	fibroblast growth factor receptor 1 (fms	13.60
100871	T85231	Hs.179661	tubulin, beta 5	13.50
101462	AL035668	Hs.73853	bone morphogenetic protein 2	13.48
120809	AA346495		gb:EST52657 Fetal heart II Homo sapiens	13.33

5	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin)	13.25
	103460	AI021993	Hs.14331	S100 calcium-binding protein A13	13.25
	102460	U48959	Hs.211582	myosin, light polypeptide kise	13.14
	100168	H73444	Hs.394	adrenomedullin	13.09
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	13.00
	130103	Y13492	Hs.149098	smoothelin	12.92
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript)	12.03
	113632	T94907	Hs.188572	ESTs	11.85
10	118951	NM_000448	Hs.73958	recombination activating gene 1	11.73
	100305	NM_004941	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	11.63
	109737	AA055415	Hs.13233	ESTs, Moderately similar to A47582 B-cell	11.55
	122577	AA829725	Hs.334437	hypothetical protein MGC4248	11.49
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	11.40
15	132303	BE177330	Hs.325093	Homo sapiens cD: FLJ21210 fis, clone C	11.37
	103176	AL021154	Hs.76884	inhibitor of D binding 3, dominant neg	11.17
	108358	MB1933	Hs.1634	cell division cycle 25A	11.15
	104584	AA704538	Hs.193777	ESTs	11.12
	106777	AF037261	Hs.33787	vinexin beta (SH3-containing adaptor mol	11.08
20	121054	AW976570	Hs.97387	ESTs	10.90
	119400	T92767		gb:ye27d06.s1 Stratagene lung (937210) H	10.83
	126610	AI911353	Hs.191391	ESTs	10.83
	134555	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	10.80
	131555	T47364	Hs.278613	interferon, alpha-inducible protein 27	10.79
25	130979	NM_012446	Hs.169833	single-stranded-D-binding protein	10.70
	113783	AL359588	Hs.7041	hypothetical protein DKFZp7628226	10.65
	123503	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	10.60
	117031	H88353		gb:yu21a02.s1 Morton Fetal Cochlea Homo	10.45
	100752	T81309	Hs.251664	insulin-like growth factor 2 (somatomedi	10.44
30	102618	AL037672	Hs.81071	extracellular matrix protein 1	10.36
	113089	T40707	Hs.270862	ESTs	10.33
	132089	W22007	Hs.39122	hypothetical protein MGC15737	10.29
	101663	NM_003528	Hs.2178	H2B histone family, member Q	10.23
	104876	AI933128	Hs.25220	like-glycosyltransferase	10.23
35	106370	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	10.18
	129406	AB018255	Hs.111138	KIAA0712 gene product	10.18
	115354	AA281636	Hs.334827	ESTs	10.13
	123077	AA485229	Hs.105649	ESTs	10.05
	131273	AW206008	Hs.283378	Homo sapiens cD: FLJ21778 fis, clone H	9.95
40	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	9.83
	133699	BE501689	Hs.75617	collagen, type IV, alpha 2	9.80
	110855	AB007928	Hs.28169	KIAA0459 protein	9.65
	111826	R35975		gb:yh91b07.s1 Soares placenta Nb2HP Homo	9.58
	126947	Z40778	Hs.191837	ESTs	9.50
45	116674	AI768015	Hs.92127	ESTs	9.48
	129087	AI348027	Hs.108557	hypothetical protein PP1057	9.46
	114837	BE244930	Hs.166895	ESTs	9.45
	120009	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	9.45
50	112483	AW969785	Hs.285885	Homo sapiens cD FLJ11321 fis, clone PL	9.40
	103487	AA743603	Hs.172108	nucleoporin 88kD	9.30
	105675	AL390083	Hs.271277	hypothetical protein from EUROMIMAGE 3636	9.28
	129158	NM_004413	Hs.109	dipeptidase 1 (rel)	9.23
	114394	T34462	Hs.103291	neuritin	9.17
	133331	Y14487	Hs.738	ribosomal protein L14	9.11
55	114787	AA156509	Hs.231892	ESTs, Weakly similar to S65657 alpha-1C-	9.10
	125502	AW977181	Hs.194718	zinc finger protein 265	9.03
	132325	N37065	Hs.44856	hypothetical protein FLJ12116	9.01
	127968	AA830201	Hs.124347	ESTs	9.00
	114605	AL157423	Hs.306478	Homo sapiens mR; cD DKFZp76100511 (f	8.93
60	114875	AA235609	Hs.236443	Homo sapiens mR; cD DKFZp564N1063 (f	8.93
	129898	AI672731	Hs.13256	ESTs	8.89
	106263	W21493	Hs.28329	hypothetical protein FLJ14005	8.89
	117130	AA748850	Hs.125830	bladder cancer overexpressed protein	8.88
	105553	AA256756	Hs.31178	ESTs	8.85
65	103657	Z73677		gb:H.sapiens gene encoding plakophilin 1	8.83
	105831	AA329449	Hs.247302	twisted gastrulation	8.82
	106375	AW872878	Hs.289072	hypothetical protein FLJ22175	8.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	8.75
	123433	AW450922	Hs.112478	ESTs	8.67
70	134558	NM_001773	Hs.85289	CD34 antigen	8.67
	115893	AI652127	Hs.48419	ESTs	8.67
	128621	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mR, comp	8.60
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	8.58
	112554	R71489	Hs.29196	EST	8.55
75	129969	N57818		gb:yu59d07.s1 Soares fetal liver spleen	8.53
	131558	AA453208	Hs.28726	RAB9, member RAS oncogene family	8.45
	134027	Z97630	Hs.226117	H1 histone family, member 0	8.45
	134138	AB023169	Hs.7935	KIAA0952 protein	8.43
	120030	AI076355	Hs.58694	ESTs	8.43
80	101005	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 o	8.33
	115423	AI499516	Hs.89303	ESTs	8.33
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	8.30
	131965	W79283	Hs.35962	ESTs	8.30
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	8.28

5	108886	AW248434	Hs.91521	hypothetical protein	8.26
	107985	T40064	Hs.71968	Homo sapiens mR: cD DKFZp564F053 (fr	8.25
	114239	AL137667	Hs.267445	Homo sapiens mR: cD DKFZp434B231 (fr	8.23
	124281	AJ333756	Hs.111801	arsene resistance protein ARS2	8.23
	117099	H93699		gbcyv16a11.s1 Soares fetal liver spleen	8.20
	119432	AL120247	Hs.40109	KIAA0872 protein	8.15
	115957	AI745379	Hs.42911	ESTs	8.15
	132355	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	8.13
10	108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.10
	131694	NM_000246	Hs.3076	MHC class II transactivator	8.05
	104897	N33937	Hs.10336	ESTs	8.03
	120266	AJ807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	8.03
	130404	AI672727	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	8.00
15	115729	AA417812	Hs.38775	ESTs	8.00
	127216	AI798703	Hs.143702	ESTs, Weakly similar to S70029 probable	7.95
	131693	AW963776	Hs.110796	SAR1 protein	7.93
	113107	AI821027	Hs.8429	ESTs	7.90
	122282	BE246331	Hs.98401	Homo sapiens mR full length insert cDN	7.90
20	111040	AJ435502	Hs.14931	ESTs	7.90
	127987	AI022103	Hs.124511	ESTs	7.90
	125317	Z95348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	7.88
	105242	AI564857	Hs.27888	ESTs, Weakly similar to serine/threonine	7.75
25	100421	D86985	Hs.79276	KIAA0232 gene product	7.71
	114359	NM_016929	Hs.283021	chloride intracellular channel 5	7.70
	119772	AJ250839	Hs.58241	gene for serine/threonine protein kine	7.70
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.65
	134361	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	7.57
	105476	AL117352	Hs.120828	Human D sequence from clone RP5-876B10	7.55
30	113289	T66900	Hs.188446	ESTs	7.50
	122707	NM_002039	Hs.239706	GRB2-associated binding protein 1	7.50
	130055	AJ568248	Hs.146355	v-abl Abelson murine leukemia viral onco	7.49
	108766	AF145713	Hs.61490	schwannomin-interacting protein 1	7.45
	107957	Z36842	Hs.57548	ESTs	7.45
35	123116	AW190412	Hs.183738	FERM, RhoGEF (ARHGEF) and pleckstrin dom	7.38
	123190	AA489212	Hs.105228	EST	7.38
	129574	AA026815	Hs.11463	UMP-CMP kine	7.38
	115274	C01566	Hs.86671	ESTs	7.35
	102571	U60115	Hs.239069	four and a half LIM domains 1	7.34
40	116845	AA649530		gbms44f05.s1 NCL CGAP_Alv1 Homo sapiens	7.33
	134851	AB011124	Hs.90232	KIAA0552 gene product	7.33
	101780	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	7.28
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN A	7.28
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	7.25
45	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c	7.23
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	7.20
	127692	AI021912	Hs.187983	ESTs	7.18
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	7.18
	107727	AA149707	Hs.173091	ubiquitin-like 3	7.14
50	118089	AI762507	Hs.47878	ESTs	7.12
	106025	AV653785	Hs.173334	ELL-RELATED R POLYMERASE II, ELONGATIO	7.10
	122111	AW593206	Hs.98785	Ksp37 protein	7.08
	119674	VW60379	Hs.57773	ESTs	7.05
	126607	W87425	Hs.114688	ESTs	7.05
55	121545	AA412442	Hs.98132	ESTs	7.05
	113287	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	7.03
	126672	AA255692	Hs.203631	ESTs, Weakly similar to alternatively sp	7.00
	132087	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho	6.97
	118697	N22706	Hs.43234	ESTs	6.97
60	100295	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	6.95
	101188	L20320	Hs.184298	cyclin-dependent kine 7 (homolog of Xe	6.95
	121481	AA411931		gbzu03g05.s1 Soares_testis_NHT Homo sap	6.95
	113003	AW292315	Hs.7215	ESTs	6.93
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor	6.91
65	113529	AI190741	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	6.90
	132887	AA195831	Hs.273385	guanine nucleotide binding protein (G pr	6.90
	113560	T91015	Hs.268626	ESTs	6.85
	123440	AI733692	Hs.112488	ESTs	6.83
	130390	AA490770	Hs.182382	ESTs	6.83
70	133889	U48959	Hs.211582	myosin, light polypeptide kine	6.83
	113573	R89379	Hs.15990	ESTs	6.80
	112453	R63899	Hs.28455	ESTs	6.78
	125221	AA236115	Hs.120785	ESTs	6.78
	134081	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	6.77
75	127610	AA960867	Hs.150271	ESTs, Highly similar to unmed protein	6.75
	105486	AW449258	Hs.6187	ESTs	6.75
	107796	AA058848	Hs.60797	ESTs	6.71
	132754	AI752244	Hs.75309	eukaryotic translation elongation factor	6.71
	105806	AF206019	Hs.110347	REV1 (yeast homolog)-like	6.70
80	110837	H03109	Hs.108920	HT018 protein	6.65
	117698	N62293	Hs.45107	ESTs	6.65
	128994	AF205849	Hs.107740	Kruppel-like factor 2 (lung)	6.65
	129131	AB026436	Hs.177534	dual specificity phosphatase 10	6.65
	108528	AA650558	Hs.325202	ESTs, Highly similar to GBAS_HUMAN GUANI	6.62

	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	6.61
	129389	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	6.60
	125278	AI218439	Hs.129998	enhancer of polycomb 1	6.59
5	124667	W24320	Hs.102941	Homo sapiens cD: FLJ21531 fts, clone C	6.59
	105640	AA001021	Hs.6685	thyroid hormone receptor interactor 8	6.58
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	6.58
	105808	AI133161	Hs.286131	CGI-101 protein	6.53
	120087	AF186780	Hs.79219	RaiGDS-like gene; KIAA0959 protein	6.52
10	100514	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase	6.50
	108378	AI368460	Hs.74815	platelet-derived growth factor receptor,	6.50
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	6.50
	115673	AA406341	Hs.269908	Homo sapiens cD FLJ11991 fts, clone HE	6.48
	133410	Y07847	Hs.73088	RAS-related on chromosome 22	6.48
	131281	AA251716	Hs.25227	ESTs	6.46
15	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mR, complete cds	6.45
	128766	AW160432	Hs.296460	craniofacial development protein 1	6.45
	114530	AA601038	Hs.191797	ESTs, Weakly similar to S55657 alpha-1C-	6.43
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	6.40
20	120593	AA748355	Hs.193522	ESTs	6.40
	125832	AA628600	Hs.117587	ESTs	6.38
	129537	NM_004605	Hs.1179	TATA box binding protein (TBP)-associate	6.38
	115302	AL109719	Hs.47578	ESTs	6.33
	126137	AA312594	Hs.99115	hypothetical protein FLJ20689	6.30
25	114465	BE521056	Hs.131731	hypothetical protein FLJ11099	6.29
	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	6.29
	127380	AF070554	Hs.15535	Homo sapiens clone 24582 mR sequence	6.26
	106956	R06428	Hs.226351	ESTs	6.25
	105962	AW880358	Hs.339808	hypothetical protein FLJ10120	6.25
30	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	6.23
	111116	AK002039	Hs.26243	Homo sapiens cD FLJ11177 fts, clone PL	6.23
	127282	AA347158	Hs.185780	ESTs	6.23
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	6.21
	101664	AA436989	Hs.121017	H2A histone family, member A	6.20
35	103317	X83441	Hs.166091	ligase IV, D, ATP-dependent	6.20
	133894	AW021236	Hs.180433	rTS beta protein	6.19
	109260	AW978515	Hs.131915	KIAA0863 protein	6.18
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6	6.18
	132050	AI267615	Hs.38022	ESTs	6.18
40	113009	T23699	Hs.7246	ESTs	6.17
	118835	AA535246	Hs.50852	ESTs	6.16
	125626	AI038854	Hs.180789	S164 protein	6.15
	117086	AA581602	Hs.41840	ESTs	6.14
	101960	AL036287	Hs.194662	calponin 3, acidic	6.13
45	104488	N56191	Hs.106511	protocadherin 17	6.13
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	6.13
	127894	AL121053	Hs.5534	Homo sapiens cD FLJ12961 fts, clone NT	6.13
	113595	T92056	Hs.290240	ESTs, Moderately similar to ALU2_HUMAN A	6.10
	120784	AW752101	Hs.16580	hypothetical protein FLJ11026	6.10
50	115004	AA329340	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	6.08
	129740	BE165866	Hs.83623	nuclear receptor subfamily 1, group 1, m	6.05
	117483	N72185	Hs.44189	ESTs	6.04
	103815	BE245294	Hs.180789	S164 protein	6.03
	122040	AA847758	Hs.111030	ESTs	6.03
55	109538	AW977747	Hs.119120	E3 ubiquitin ligase SMURF1	6.02
	112727	T91029	Hs.15069	ESTs	6.01
	120273	AA176688	Hs.269284	ESTs	6.00
	122127	AW207175	Hs.106771	ESTs	6.00
	126046	AA804957	Hs.119840	ESTs	5.99
60	119774	AB032977	Hs.6298	KIAA1151 protein	5.98
	106265	AA412176	Hs.236463	Homo sapiens mR; cD DKFZp586i0521 (f	5.98
	111987	NM_015310	Hs.6763	KIAA0942 protein	5.98
	123619	AA602964		gb:nc097c02.s1 NCL_CGAP_Pr2 Homo sapiens	5.96
	128122	AI267491	Hs.160593	ESTs	5.95
65	128473	T78277	Hs.100293	O-linked N-acetylglucosamine (Glc) tr	5.95
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11	5.94
	122468	AA448172	Hs.137687	ESTs, Highly similar to K6B1_HUMAN RIBOS	5.93
	101801	M86407	Hs.1216	actinin, alpha 3	5.93
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	5.92
70	108908	AA136569	Hs.10848	KIAA0187 gene product	5.90
	121470	AA558958	Hs.324751	ESTs	5.90
	131938	AF176085	Hs.34956	neural polypyrimidine tract binding prot	5.89
	109613	H47315	Hs.27519	ESTs	5.89
	109384	AA219172	Hs.86849	ESTs	5.88
75	118559	N68456	Hs.49519	ESTs	5.88
	102010	U02687	Hs.385	fms-related tyrosine kinase 3	5.85
	105921	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypothi	5.85
	124298	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.85
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	5.84
80	103331	AI825463	Hs.147996	protein kinase, X-linked	5.82
	135052	AL136653	Hs.93675	decidual protein induced by progesterone	5.80
	115219	AA262776	Hs.269314	Homo sapiens cD FLJ14123 fts, clone MA	5.78
	121899	R55341	Hs.50421	KIAA0203 gene product	5.78
	135217	AA453880	Hs.9658	hypothetical protein FLJ11790	5.77

	123973	C14805		gb:C14805 Clontech human aorta polyA+ mR	5.77
	112605	R79374	Hs.29852	ESTs	5.76
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.75
5	129889	AA810932	Hs.131899	ESTs, Weakly similar to T00370 hypotheti	5.75
	102638	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	5.73
	121501	AA470687	Hs.104772	ESTs	5.73
	124921	R93082	Hs.332635	ESTs	5.70
	109850	AI150548	Hs.23155	ESTs	5.70
10	120594	AW136478	Hs.5094	ring finger protein 10	5.70
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	5.70
	100455	AW888941	Hs.75789	N-myc downstream regulated	5.69
	106565	NM_014892	Hs.227602	KIAA1116 protein	5.68
	120912	AA376690	Hs.187650	ESTs	5.68
15	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	5.68
	107606	AF207989	Hs.330425	Homo sapiens, Similar to G protein-coupl	5.67
	106597	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	5.66
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	5.65
	100064			AFX control - TrpnX-3	5.63
20	108758	AA127395	Hs.222414	ESTs	5.63
	101392	NM_002507	Hs.1827	nerve growth factor receptor (TNFR super	5.61
	102211	BE314524	Hs.78776	putative transmembrane protein	5.60
	107427	W26975	Hs.46736	hypothetical protein FLJ23476	5.60
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	5.60
25	111764	AA420368	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	5.58
	119405	T93865	Hs.91085	ESTs	5.58
	126464	AI990046	Hs.54780	transcription termination factor, R po	5.58
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	5.58
	123255	AA830335	Hs.105273	ESTs	5.57
	122861	AA335721	Hs.119394	ESTs	5.56
30	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	5.55
	132906	BE613337	Hs.234896	geminin	5.55
	109001	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	5.55
	115816	BE042915	Hs.287588	Homo sapiens cD FLJ13675 fis, clone PL	5.55
35	128401	R01865	Hs.268586	ESTs	5.53
	129296	AI051967	Hs.110122	ESTs	5.53
	120314	T10013	Hs.221040	HBS1 (S. cerevisiae)-like	5.51
	132815	AI815189	Hs.57475	sex comb on midleg homolog 1	5.50
	113983	W87415	Hs.55296	HLA-B associated transcript-1	5.50
40	105002	AA224244	Hs.182704	ESTs, Moderately similar to altertivel	5.49
	132025	AA011117	Hs.3745	milk fat globule-EGF factor 8 protein	5.49
	110732	AW070838	Hs.174174	KIAA0601 protein	5.48
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	5.48
	126758	AI559444	Hs.293960	ESTs	5.48
45	129426	AF077953	Hs.111323	Protein inhibitor of activated STAT X	5.47
	103217	NM_001841	Hs.73037	carbinoid receptor 2 (macrophage)	5.46
	132261	U80743	Hs.306094	trinucleotide repeat containing 12	5.45
	105586	AA865118	Hs.191538	ESTs	5.43
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-link	5.43
50	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	5.43
	134092	AA218558	Hs.7905	sorting nexin 9	5.41
	119316	AI114630	Hs.208334	Homo sapiens cD: FLJ21874 fis, clone H	5.38
	108019	AI017773	Hs.249159	adrenergic, alpha-2A-, receptor	5.38
	109421	AW604652	Hs.332442	ESTs	5.38
55	111929	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	119718	W69216	Hs.92848	ESTs	5.38
	106154	BE540255	Hs.6994	Homo sapiens cD: FLJ22044 fis, clone H	5.35
	108544	W39433	Hs.23971	hypothetical protein DKFZp547N043	5.35
	119580	AL079310	Hs.92260	high-mobility group protein 2-like 1	5.35
60	126777	AL157491	Hs.145211	Homo sapiens mR: cD DKFZp434K1111 (f	5.35
	112944	H18063	Hs.13254	ESTs	5.34
	103149	NM_006201	Hs.171834	PCTAIRE protein kase 1	5.34
	132437	AA152106	Hs.4859	cyclin L antia-6a	5.33
	103860	AW976877	Hs.38057	ESTs	5.33
65	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	5.33
	129914	NM_012421	Hs.13321	rearranged L-myc fusion sequence	5.33
	130309	AF067804	Hs.15423	hypothetical protein HDCCMC04P	5.31
	116312	BE379794	Hs.65403	hypothetical protein	5.30
	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	5.28
70	125583	AA195667	Hs.86022	ESTs	5.28
	130591	N59646	Hs.169745	crumbs (Drosophila) homolog 1	5.28
	116355	AA789133	Hs.88650	ESTs	5.26
	115553	AJ275988	Hs.71414	transcription factor (SMIF gene)	5.26
	122802	AI687303	Hs.285529	G protein-coupled receptor 49	5.25
75	128495	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	5.24
	117667	U59305	Hs.44708	Ser-Thr protein kase related to the my	5.23
	127890	AA294934	Hs.293902	ESTs, Weakly similar to ISHUS protein d	5.22
	134843	AA428520	Hs.90061	progesterone binding protein	5.21
	120968	AA528283	Hs.292737	ESTs	5.21
80	102076	BE299197	Hs.179665	cyclin-dependent kase inhibitor 1A (p2	5.20
	100934	J03019	Hs.99913	adrenergic, beta-1-, receptor	5.20
	112667	BE538516	Hs.15423	hypothetical protein HDCCMC04P	5.20
	119304	AW249266	Hs.98493	X-ray repair complementing defective rep	5.20
	131868	AW408296	Hs.33532	zinc finger protein 151 (pH2-67)	5.20

5	105914	AW245680	Hs.9701	growth arrest and D-damage-inducible,	5.18
	102258	NM_001546	Hs.34853	inhibitor of D binding 4, dominant neg	5.18
	103850	AA187101	Hs.213194	hypothetical protein MGC10895	5.18
	112516	T83909		gb:yd67f10.r1 Soares fetal liver spleen	5.18
	133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	5.18
10	135180	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	5.18
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.18
	134801	S76825	Hs.89695	insulin receptor	5.17
	133362	AK001519	Hs.7194	CGI-74 protein	5.17
	135206	AB024703	Hs.96334	ring finger protein 11	5.15
15	111480	R06453	Hs.19706	ESTs	5.15
	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo	5.15
	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass	5.15
	127140	AI273507	Hs.303966	ESTs	5.15
	109223	AW000714	Hs.65818	ESTs	5.14
20	103656	Z73497	Hs.247802	Human D sequence from clone U240C2 on	5.14
	133388	AW245631	Hs.182447	heterogeneous nuclear ribonucleoprotein	5.12
	100511	M76676	Hs.116840	ESTs	5.10
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	5.10
	109937	AI084066	Hs.20072	myosin regulatory light chain interactin	5.10
25	122996	AI436216	Hs.191715	ESTs, Weakly similar to ZN91_HUMAN ZINC	5.10
	128242	AA992626	Hs.269755	ESTs, Moderately similar to ALU5_HUMAN A	5.10
	112374	NM_016323	Hs.26663	cyclin-E binding protein 1	5.10
	124506	BE273688	Hs.182447	heterogeneous nuclear ribonucleoprotein	5.10
	104216	AB002313	Hs.3989	plexin B2	5.09
30	135051	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.08
	131629	Z45794	Hs.238809	ESTs	5.08
	111722	R23924	Hs.23596	EST	5.07
	107034	AF257770	Hs.20930	poly(rC)-binding protein 4	5.06
	110243	H26683		gb:yl14g03.s1 Soares breast 2NbHBst Homo	5.05
35	125837	AW968123	Hs.333513	small inducible cytokine subfamily E, me	5.05
	130300	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	5.05
	103957	AL120051	Hs.144700	ephrin-B1	5.04
	112678	AI418466	Hs.33665	ESTs	5.03
	124963	F06600	Hs.101375	Homo sapiens mR; cD DKFZp434H205 (tr	5.03
40	131379	AK001123	Hs.26176	hypothetical protein FLJ10261	5.03
	109451	N32264	Hs.44330	ESTs	5.02
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	5.02
	131038	W87778	Hs.169388	hypothetical protein DKFZp761H2024	5.01
	101208	L25081	Hs.179735	ras homolog gene family, member C	5.01
45	104973	NM_015310	Hs.6763	KIAA0942 protein	4.99
	103141	X66113	Hs.75584	polymyositis/scleroderma autoantigen 2 (4.98
	111260	AB033035	Hs.51965	KIAA1209 protein	4.98
	128142	T67162	Hs.135127	ESTs, Weakly similar to unmed protein	4.98
	113857	AW243158	Hs.5297	DKFZP564A2416 protein	4.96
50	105292	AF128542	Hs.166846	polymerase (D directed), epsilon	4.95
	114341	AF270491	Hs.28249	hepatocellular carcinoma-associated anti	4.95
	100615	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.95
	103208	AW411340	Hs.31314	retinoblastoma-binding protein 7	4.95
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.95
55	125321	T86652	Hs.178294	ESTs	4.95
	101145	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	4.95
	100551	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mR, complete	4.93
	126182	AA721331	Hs.293771	ESTs	4.93
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	4.93
60	133969	AA569112	Hs.78	GA-binding protein transcription factor,	4.93
	120873	AA358015		gb:EST66864 Fetal lung III Homo sapiens	4.92
	125219	AI804331	Hs.99423	ATP-dependent R helicase	4.91
	102790	BE245277	Hs.154195	E4F transcription factor 1	4.90
	129486	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.89
65	130381	L47345	Hs.155202	transcription elongation factor B (SIII)	4.88
	132389	AA310393	Hs.190044	ESTs	4.88
	100260	D38491	Hs.322478	KIAA0117 protein	4.88
	109585	N59650	Hs.27252	ESTs	4.88
	111603	R11529	Hs.20634	EST	4.88
70	120514	AA258335		gb:zr59b02.s1 Soares_NhHMPu_S1 Homo sapi	4.88
	130314	NM_014674	Hs.154332	KIAA0212 gene product	4.86
	108958	AF142482	Hs.203846	TEA domain family member 3	4.86
	126503	W86610	Hs.185736	ESTs	4.85
	100406	AI962060	Hs.118397	AE-binding protein 1	4.85
75	116238	AV660717	Hs.47144	DKFZP586N0819 protein	4.84
	105288	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DJ	4.83
	118753	AA346206	Hs.50471	ESTs, Weakly similar to T14267 Xln prote	4.82
	113070	AB032977	Hs.6298	KIAA1151 protein	4.81
	107908	AF087999	Hs.42826	ESTs	4.80
80	119678	AI658666	Hs.6106	R binding motif protein 4	4.80
	100415	D86970	Hs.75822	TGFB1-induced anti-apoptotic factor 1	4.79
	126360	F12374		gb:HSC398101 normalized infant brain cDN	4.78
	133101	AK000299	Hs.180952	dyctin 4 (p62)	4.78
	103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	4.78
	107666	AA010611	Hs.60418	EST	4.78
	108030	AI378523	Hs.62011	ESTs	4.78
	131479	D86181	Hs.273	galactosylceramidase (Krabbe disease)	4.78

5	133140	AF180581	Hs.6582	Rho guanine exchange factor (GEF) 12	4.78
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	4.78
	106288	AB037742	Hs.24336	KIAA1321 protein	4.76
	101524	NM_000448	Hs.73958	recombination activating gene 1	4.75
	113095	AA828380	Hs.126733	ESTs	4.75
10	114924	AI338053	Hs.87329	HSPC072 protein	4.75
	127543	AK000787	Hs.157392	Homo sapiens cD FLJ20780 fis, clone CO	4.75
	115866	AW052629	Hs.52081	KIAA0867 protein	4.75
	101382	AU076772	Hs.1279	complement component 1, r subcomponent	4.74
	126509	R47400	Hs.23850	ESTs	4.74
15	127930	AA809572	Hs.123304	ESTs	4.73
	127824	AI911516	Hs.127811	ESTs	4.73
	110049	H12449	Hs.31159	EST, Weakly similar to ALUB_HUMAN !!! A	4.73
	127115	H77859	Hs.65450	reticulon 4	4.73
	104727	N81203	Hs.20047	zinc finger protein, subfamily 2A (FYVE	4.72
20	127532	AJ003429		gb:AJ003429 Selected chromosome 21 cD	4.71
	127304	AI741577	Hs.99962	proteoglycan 2, bone marrow (tural kil	4.70
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.70
	114969	AW162998	Hs.24684	KIAA1376 protein	4.70
	115125	AA193588	Hs.85888	ESTs	4.70
25	118348	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	4.70
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	4.70
	130881	AA809875	Hs.25933	ESTs	4.70
	132074	AA478486	Hs.3852	KIAA0368 protein	4.70
	106897	AF039023	Hs.167496	RAN binding protein 6	4.69
30	131121	AA120865	Hs.23136	ESTs	4.69
	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	4.68
	112868	AW388359	Hs.10667	ESTs	4.68
	116877	AA708958	Hs.168732	ESTs	4.68
	131241	BE501914	Hs.24654	Homo sapiens cD FLJ11640 fis, clone HE	4.68
35	132027	AF151020	Hs.181444	hypothetical protein	4.68
	133323	BE336654	Hs.70937	H3 histone family, member A	4.68
	114269	AA175769	Hs.23450	mitochondrial ribosomal protein S25	4.67
	122713	AI089443	Hs.99436	ESTs	4.67
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.66
40	134453	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.66
	115510	BE299339	Hs.72249	three-PDZ containing protein similar to	4.66
	115322	L08895	Hs.78995	MADS box transcription enhancer factor 2	4.66
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	4.65
	104674	AI935962	Hs.26289	ESTs	4.65
45	106276	AA625947	Hs.25750	ESTs	4.65
	108216	AA524743	Hs.44883	ESTs	4.65
	120376	AA227469		gb:zr18a07.s1 Stratagene NT2 neuro pr	4.65
	121743	AA397636		gb:z179e09.r1 Soares_testis_NHT Homo sap	4.65
	128011	AI347067	Hs.124636	ESTs	4.65
50	123454	AA868510	Hs.112496	ESTs	4.64
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	4.64
	120484	AA253170	Hs.96473	EST	4.63
	127046	AA321948	Hs.293968	ESTs	4.63
	133184	AA001021	Hs.6685	thyroid hormone receptor interactor 8	4.63
55	123184	BE247767	Hs.18166	KIAA0870 protein	4.62
	106627	AK000706	Hs.15125	hypothetical protein FLJ20699	4.61
	115475	AB033085	Hs.40193	hypothetical protein KIAA1259	4.61
	119468	AI911535	Hs.6657	hypothetical protein bK1048E9.5	4.59
	133662	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	4.58
60	113941	AA531016	Hs.22399	hypothetical protein FLJ14824	4.58
	131590	R46277	Hs.250638	Homo sapiens mR full length insert cDN	4.58
	128795	AA531287	Hs.105805	ESTs	4.58
	116480	C14088	Hs.169476	glyceraldehyde-3-phosphate dehydrogese	4.58
	111713	C75253	Hs.220950	ESTs	4.58
65	113721	AF143885	Hs.18190	EST	4.57
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	102009	BE245149	Hs.82643	protein tyrosine kase 9	4.55
	135242	AI583187	Hs.9700	cyclin E1	4.55
	127580	BE548749	Hs.148016	ESTs	4.55
70	109785	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	4.53
	109700	F09609		gb:HSC33H092 normalized infant brain cDN	4.53
	124882	AI698652	Hs.101539	ESTs	4.53
	131765	AW381270	Hs.194110	hypothetical protein PRO2730	4.53
	115684	NM_006577	Hs.284284	ESTs, Highly similar to beta-1,3-N-acety	4.52
75	102034	AI903474	Hs.230	fibromodulin	4.52
	109776	R43665	Hs.12257	ESTs	4.50
	111650	R16722	Hs.124246	ESTs	4.50
	132993	AB023154	Hs.62264	KIAA0937 protein	4.49
	129017	AA115333	Hs.107968	ESTs	4.49
80	132902	AI936442	Hs.59838	hypothetical protein FLJ10808	4.48
	114814	AB006622	Hs.182536	KIAA0284 protein	4.48
	120839	AA348913		gb:EST55442 Infant adrel gland II Homo	4.48
	101434	AV650066	Hs.1430	coagulation factor XI (plasma thrombopla	4.48
	102018	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	4.48
	104619	AA001635	Hs.287414	transcriptioal intermediary factor 1 ga	4.48
	106716	AA931198	Hs.238928	HT002 protein; hypertension-related calc	4.48
	126020	H79863	Hs.114243	ESTs	4.48

5	119899	AI057404	Hs.58698	ESTs	4.47
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tum	4.46
	125695	W22529	Hs.30942	ephrin-B2	4.46
	105715	BE621800	Hs.29444	putative small membrane protein NID67	4.45
	117169	R87866	Hs.95120	ESTs, Weakly similar to HZHU hemoglobin	4.45
10	102757	AW955454	Hs.30942	ephrin-B2	4.45
	120637	AA811804		gb:rob39a05.s1 NCL_CGAP_GCB1 Homo sapiens	4.45
	131579	N62922	Hs.29088	ESTs	4.45
	135287	U82670	Hs.9786	zinc finger protein 275	4.45
	112540	R69751		gb:yl40a10.s1 Soares placenta Nb2HP Homo	4.45
15	125724	AL360190	Hs.295978	Homo sapiens mR full length insert cDN	4.44
	115498	AA291070		gb:zs46a08.s1 NCL_CGAP_GCB1 Homo sapiens	4.43
	102263	U29171	Hs.75852	casein kise 1, delta	4.43
	124312	H94647	Hs.102329	ESTs	4.43
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mR sequence	4.43
20	115955	AF263513	Hs.44198	intracellular membrane-associated calciu	4.43
	103562	NM_002702	Hs.2815	POU domain, class 6, transcription facto	4.42
	100169	AL037228	Hs.82043	D123 gene product	4.40
	108928	AA143802	Hs.71781	ESTs	4.40
	125908	AF265555	Hs.250646	baculoviral IAP repeat-containing 6	4.40
25	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.40
	129512	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.40
	134570	U66615	Hs.172280	SW/SNF related, matrix associated, aci	4.40
	135073	W55956	Hs.94030	Homo sapiens mR; cD DKFZp586E1624 (f	4.40
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	4.40
30	128793	AB011125	Hs.105749	KIAA0553 protein	4.40
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	4.38
	126144	H84455	Hs.40639	ESTs	4.38
	130783	X07282	Hs.171495	relinoic acid receptor, beta	4.38
	135192	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io	4.38
35	100284	D43767	Hs.66742	small inducible cytokine subfamily A (Cy	4.37
	117269	N21621	Hs.91142	KH-type splicing regulatory protein (FUS	4.36
	104261	AW248364	Hs.5409	R polymerase 1 subunit	4.35
	108609	BE409857	Hs.69499	hypothetical protein	4.35
	126319	D81689		gb:HUM184E05B Human fetal brain (TFujiwa	4.35
40	127445	AA906286	Hs.193942	ESTs	4.35
	130772	BE270640	Hs.19192	cyclin-dependent kise 2	4.35
	134625	AA977638	Hs.184389	ESTs	4.35
	135397	L14922	Hs.166563	replication factor C (activator 1) 1 (14	4.35
	128070	AA886944	Hs.303908	ESTs	4.35
45	135045	AI494054	Hs.93589	hypothetical protein DKFZp564B1162	4.33
	101881	NM_004957	Hs.754	foliopolyglutamate synthase	4.33
	129838	AB007863	Hs.185140	KIAA0403 protein	4.33
	130974	NM_003528	Hs.2178	H2B histone family, member Q	4.33
	107763	AA018220	Hs.106730	chromosome 22 open reading frame 3	4.32
50	129818	T71092	Hs.172572	hypothetical protein FLJ20093	4.31
	129407	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	4.30
	110846	BE277343	Hs.297875	endoplasmic reticulum chaperone SIL1, ho	4.30
	111433	R01452	Hs.40193	hypothetical protein KIAA1259	4.30
	114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.30
55	115853	AW978561	Hs.191548	ESTs	4.30
	116165	AI184751	Hs.75874	pregnancy-associated plasma protein A	4.30
	126911	AA428049	Hs.1501	syndecan 2 (heparan sulfate proteoglycan	4.30
	131230	NM_005865	Hs.274407	protease, serine, 16 (thymus)	4.30
	100349	D64110	Hs.77311	BTG family, member 3	4.29
60	100175	BE258769	Hs.32500	acetyl-Coenzyme A acyltransferase 2 (mit	4.29
	105335	AW291165	Hs.25447	ESTs	4.29
	122507	BE567620	Hs.99210	ESTs	4.28
	105397	AA814807	Hs.7395	hypothetical protein FLJ23182	4.28
	133674	AW851121	Hs.75497	Homo sapiens cD: FLJ22139 fis, clone H	4.28
65	102826	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.28
	103272	NM_006680	Hs.2838	malic enzyme 3, DP(+)-dependent, mitoc	4.28
	111887	R38635	Hs.12328	KIAA1005 protein	4.28
	120336	N85785	Hs.181165	eukaryotic translation elongation factor	4.28
	133736	D49958	Hs.75819	glycoprotein M6A	4.28
70	130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	4.27
	119830	AW054922	Hs.53478	Homo sapiens cD FLJ12366 fis, clone MA	4.27
	108758	AB014564	Hs.22616	KIAA0664 protein	4.25
	109709	F09749	Hs.187405	ESTs	4.25
	110463	H52931	Hs.165067	ESTs	4.25
75	124472	N52517	Hs.102670	EST	4.25
	109770	R40322	Hs.248420	ESTs, Moderately similar to A47582 B-cel	4.24
	131487	F13036	Hs.27373	Homo sapiens mR; cD DKFZp564O1763 (f	4.23
	107216	D51069	Hs.211579	melanoma cell adhesion molecule	4.23
	123562	AA177088	Hs.190065	ESTs	4.23
80	125986	W02410	Hs.205555	ESTs	4.23
	126221	N20514	Hs.172965	ESTs	4.23
	127092	T26985		gb:NIBT065H01R Infant brain, LLNL array	4.23
	132349	AW975654	Hs.181286	serine protease inhibitor, Kazal type 1	4.23
	118946	N92834		gb:zb67R03.s1 Soares_fetal_lung_NbHL19W	4.22
	101531	AI199711	Hs.576	fucoosidase, alpha-L- 1, tissue	4.21
	105322	T87179	Hs.16346	ESTs, Weakly similar to S57447 HPBRIL-7	4.21
	104219	AB002323	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	4.20

5	102825	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	4.20
	103571	AI675749	Hs.211608	nucleoporin 153kD	4.20
	106942	AA995351	Hs.31314	retinoblastoma-binding protein 7	4.20
	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.20
	123107	AA225048	Hs.104207	ESTs	4.20
	132659	Z75190	Hs.54481	low density lipoprotein receptor-related	4.20
	130084	AI929377	Hs.173724	creatine kinase, brain	4.19
	114553	BE219860	Hs.22505	hypothetical protein FLJ10159	4.18
10	129528	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.18
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	4.18
	110637	AI241470	Hs.268982	ESTs	4.18
	127520	T51239		gb:yb20d12.s1 Stratagene fetal spleen (9	4.18
	130322	NM_014247	Hs.154545	PDZ domain containing guanine nucleotide	4.17
	104768	D82319	Hs.11056	RALBP1 protein	4.17
15	123360	AA532718	Hs.178604	ESTs	4.17
	133110	AA808177	Hs.65228	ESTs	4.16
	130923	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	4.16
	109878	BE620775	Hs.4866	Homo sapiens cD FLJ14387 fis, clone HE	4.16
20	119265	BE539706	Hs.285363	ESTs	4.16
	124214	H58608	Hs.151323	ESTs	4.15
	106193	AA057478	Hs.23272	ESTs	4.15
	105169	BE245294	Hs.180789	S164 protein	4.15
	123204	AA610002	Hs.44296	hypothetical protein FLJ22324	4.15
25	131600	NM_004377	Hs.29331	camitine palmitoyltransferase I, muscle	4.14
	131365	M93415	Hs.26014	activin A receptor, type II	4.14
	121993	AW297880	Hs.98661	ESTs	4.14
	110779	AI391472	Hs.12561	ESTs, Highly similar to C212_HUMAN 28.3	4.13
	126383	AB032977	Hs.6298	KIAA1151 protein	4.13
30	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	4.13
	131475	AA992841	Hs.27263	KIAA1458 protein	4.13
	128933	NM_002050	Hs.334695	GATA-binding protein 2	4.12
	113141	AI493276	Hs.9187	ESTs	4.11
	134833	L20965	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	4.11
35	106461	AI630759	Hs.17481	Homo sapiens clone 24606 mR sequence	4.10
	128056	AI990131	Hs.276973	potassium large conductance calcium-acti	4.10
	114757	AW970579	Hs.291031	ESTs	4.10
	134653	AI765883	Hs.87385	ESTs	4.09
	100472	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	4.08
40	103102	X61177	Hs.68876	interleukin 5 receptor, alpha	4.08
	106779	BE276013	Hs.172364	Homo sapiens mR for FLJ00086 protein,	4.08
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.08
	130178	U20982	Hs.1516	insulin-like growth factor-binding prote	4.07
	124659	AI680737	Hs.289068	Homo sapiens cD FLJ11918 fis, clone HE	4.07
45	127861	AW295020	Hs.198529	ESTs	4.07
	112129	AB037715	Hs.183639	hypothetical protein FLJ10210	4.07
	100918	AK001335	Hs.31137	protein tyrosine phosphatase; receptor I	4.06
	124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	4.05
	102722	F13271	Hs.79981	Human clone 23560 mR sequence	4.05
50	111117	AB037721	Hs.173871	KIAA1300 protein	4.05
	122506	AA449120	Hs.99209	ESTs	4.05
	126392	AI356294	Hs.3280	caspase 6, apoptosis-related cysteine pr	4.05
	130760	AW379130	Hs.18953	phosphodiesterase 9A	4.05
	104220	AB002324	Hs.301094	KIAA0326 protein	4.05
55	112774	R95770	Hs.35455	ESTs	4.04
	111128	AW505364	Hs.19074	LATS (large tumor suppressor, Drosophila	4.04
	113146	BE151985	Hs.5722	hypothetical protein FLJ23316	4.04
	124940	AF068846	Hs.103804	heterogeneous nuclear ribonucleoprotein	4.03
	105498	H68279	Hs.24937	transformer-2 alpha (htra-2 alpha)	4.03
60	112631	R62040		gb:yj06b06.s1 Soares placenta Nb2HP Homo	4.03
	118244	N62516	Hs.48556	ESTs	4.03
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	4.03
	129232	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	4.03
	134192	H01345	Hs.24139	Homo sapiens cD: FLJ23137 fis, clone L	4.03
65	131893	BE336886	Hs.3416	adipose differentiation-related protein	4.02
	116793	T77781		gb:yd20a11.s1 Soares fetal liver spleen	4.02
	125674	AL036166	Hs.323378	coated vesicle membrane protein	4.01
	116640	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.01
	105057	AA134233	Hs.336942	Homo sapiens cD: FLJ21488 fis, clone C	4.00
70	105158	AW976357	Hs.234545	hypothetical protein NUF2R	4.00
	116245	AB033107	Hs.42796	KIAA1281 protein	4.00
	119946	AA932283	Hs.58925	ESTs	4.00
	121975	AA740679	Hs.98631	ESTs	4.00
	132037	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cD 2700	4.00
75	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	4.00
	109468	NM_015310	Hs.6763	KIAA0942 protein	3.99
	106829	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	3.99
	134682	AW882645	Hs.88044	sprouty (Drosophila) homolog 1 (antagoni	3.98
	105966	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.98
80	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	3.98
	102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	3.98
	104146	AW880614	Hs.146381	R binding motif protein, X chromosome	3.98
	111465	AI968256	Hs.15470	putative ring zinc finger protein NY-REN	3.98
	126499	AK001779	Hs.110445	CGF-97 protein	3.98

5	134388	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.98
	105554	BE616694	Hs.288042	hypothetical protein FLJ14299	3.97
	115206	AW183695	Hs.186572	ESTs	3.96
	103853	AF272390	Hs.111782	myosin 5C	3.96
	110542	H58373	Hs.332938	hypothetical protein MGC5370	3.96
	106797	AI768801	Hs.169943	Homo sapiens cD FLJ13569 fis, clone PL	3.96
	130589	AL110226	Hs.16441	DKFZP434H204 protein	3.95
	122788	AI828638	Hs.99514	hypothetical protein FLJ20574	3.95
10	104518	H20816	Hs.112423	Homo sapiens mR; cD DKFZp5661420 (f	3.95
	130640	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	3.95
	110847	N30169	Hs.279807	ESTs, Weakly similar to 2004399A chromos	3.95
	116156	AA461045	Hs.50701	ESTs	3.95
	122096	AA431162	Hs.98690	ESTs	3.95
15	122160	AI769281	Hs.97439	ESTs	3.95
	123930	AA740878	Hs.112982	ESTs	3.95
	126280	Z19417		gb:HSB268122 STRATAGENE Human skeletal m	3.95
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.95
	134757	AA913267	Hs.211576	IL2-inducible T-cell kine	3.95
20	117296	AL133427	Hs.42506	Homo sapiens mR full length insert cDN	3.95
	112261	AL050297	Hs.300861	ESTs, Highly similar to T08701 hypotheti	3.95
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	3.94
	131844	AI419294	Hs.324342	ESTs	3.94
	101607	X60111	Hs.1244	CD9 antigen (p24)	3.94
25	121613	AA416879	Hs.193195	ESTs, Weakly similar to 2109260A B cell	3.94
	115815	AW905328	Hs.180842	ribosomal protein L13	3.93
	125684	AW589427	Hs.158849	Homo sapiens cD: FLJ21663 fis, clone C	3.93
	126783	AA083531		gb:zn09d10.s1 Stratagene hNT neuron (937	3.93
	129201	H18359	Hs.109390	ESTs	3.93
30	128954	AA346839	Hs.209100	DKFZP434C171 protein	3.92
	122939	AA477141		gb:zu37g06.s1 Soares ovary tumor NbHOT H	3.92
	130348	AB032957	Hs.210850	KIAA1131 protein	3.92
	125847	AW161885	Hs.249034	ESTs	3.91
	120452	AL022328	Hs.104335	hypothetical protein IMAGE3510317	3.91
35	123143	AA487595		gb:aa95e02.s1 Stratagene fetal reti 93	3.91
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mR, partial cds	3.91
	106605	AW772298	Hs.21103	Homo sapiens mR; cD DKFZp564B076 (fr	3.90
	126714	AF114491	Hs.137354	egf-like module containing, mucin-like,	3.90
40	121611	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	3.90
	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	3.90
	101356	AW878229	Hs.80642	sigl transducer and activator of trans	3.89
	133668	L77964	Hs.271980	mitogen-activated protein kine 6	3.89
	109114	BE622787	Hs.84045	hypothetical protein FLJ20288	3.88
45	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol	3.88
	107850	AA022910	Hs.295446	ESTs, Moderately similar to B10024C cyto	3.88
	130907	AA322866	Hs.21107	neurofilin	3.88
	101679	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.88
	104267	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.88
	112232	BE253927	Hs.24983	hypothetical protein from EUROMAGE 2021	3.88
50	113248	T63857		gb:yc16e01.s1 Stratagene lung (937210) H	3.88
	114044	BE327427	Hs.79953	ESTs	3.88
	115414	AA662240	Hs.283099	AF15q14 protein	3.88
	129598	N30436	Hs.11556	Homo sapiens cD FLJ12566 fis, clone NT	3.88
55	102134	AL036967	Hs.2324	prolamine 2	3.87
	105310	R98185	Hs.17240	ESTs	3.87
	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.86
	110947	AW298410	Hs.21475	ESTs	3.85
	115839	BE300266	Hs.28935	transducin-like enhancer of split 1, hom	3.85
	103534	AW970672	Hs.9247	protein kine, AMP-activated, alpha 1 c	3.85
60	105209	AB023197	Hs.227743	KIAA0980 protein	3.85
	108749	AA127017	Hs.71052	ESTs	3.85
	110565	AI884970	Hs.4983	ESTs	3.85
	110799	AI089660	Hs.323401	dpy-30-like protein	3.85
	117068	H91257	Hs.41391	EST	3.85
65	130956	NM_001135	Hs.2159	aggrecan 1 (chondroitin sulfate proteogl	3.85
	102273	BE391815	Hs.75981	ubiquitin specific protease 14 (IR-gua	3.85
	112960	AL110209	Hs.6770	LCAT-like lysophospholipase	3.84
	114414	AW152166	Hs.182113	ESTs	3.84
	109665	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	3.84
70	106208	AK001674	Hs.22630	cofactor required for Sp1 transcrip	3.84
	122311	NM_014913	Hs.131915	KIAA0863 protein	3.84
	124271	AW293223	Hs.8928	hypothetical protein FLJ20291	3.83
	106650	AL049951	Hs.22370	Homo sapiens mR; cD DKFZp56400122 (f	3.83
	112167	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	3.83
75	122354	AL157579	Hs.153610	KIAA0751 gene product	3.83
	111462	R05296		gb:ye91e08.s1 Soares fetal liver spleen	3.81
	128109	AW269421	Hs.128093	ESTs	3.81
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	3.81
	109210	AA669722	Hs.272137	ESTs	3.81
80	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.80
	106827	AA457456	Hs.11408	hypothetical protein FLJ20435	3.80
	124232	H63391	Hs.339677	ESTs, Weakly similar to I38022 hypotheti	3.80
	126039	AL137523	Hs.181102	p30 DBC protein	3.80
	128022	AW195569	Hs.125906	ESTs	3.80

	132005	AA149707	Hs.173091	ubiquitin-like 3	3.79
	131392	AA235153	Hs.26320	TRABID protein	3.79
	131775	AB014548	Hs.31921	KIAA0648 protein	3.79
5	126257	N99638		gb:za39g11.1 Soares fetal liver spleen	3.79
	121950	AA429515		gb:zw75c05.s1 Soares_testis_NHT Homo sap	3.79
	116067	AA454827	Hs.293637	ESTs	3.78
	104658	AA360954	Hs.27268	Homo sapiens cD: FLJ21933 fis, clone H	3.78
	104493	AW960427	Hs.79059	transforming growth factor, beta recepto	3.77
	100163	W44671	Hs.124	gene predicted from cD with a complete	3.77
10	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kise 1	3.77
	120586	AL031778	Hs.797	nuclear transcription factor Y, alpha	3.76
	128764	AW024282	Hs.104938	hypothetical protein MGC15905	3.75
	111574	AI024145	Hs.188526	ESTs	3.75
	117396	W20128	Hs.296039	ESTs	3.75
15	119052	R10889		gb:yl38d02.s1 Soares fetal liver spleen	3.75
	121806	AA424313	Hs.98402	ESTs	3.75
	122410	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothei	3.75
	126638	AA649257	Hs.188602	ESTs	3.75
	127879	AA768098	Hs.189079	ESTs	3.75
20	121095	AA320134	Hs.196029	Homo sapiens mR for KIAA1657 protein,	3.75
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr	3.74
	101230	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.74
	100200	H94688	Hs.173737	ras-related C3 botulinum toxin substrate	3.73
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	3.73
25	110975	H17012	Hs.14633	ESTs	3.73
	117314	N32498	Hs.42829	ESTs	3.73
	118737	AA199686		gb:zq75g09.r1 Stratagene hNT neuron (937	3.73
	124169	BE079334	Hs.271630	ESTs	3.73
	124580	N68420	Hs.107992	ESTs	3.73
30	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	3.73
	124879	R73588	Hs.101533	ESTs	3.72
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.72
	103644	M13305	Hs.247787	opsin 1 (cone pigments), long-wave-sensi	3.72
	106044	N90344	Hs.149436	kinesin family member 5B	3.71
35	127867	C18530		gb:C18530 Human placenta cD (TFujiwara	3.71
	133828	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	3.71
	107387	D86983	Hs.118893	Melanoma associated gene	3.71
	104160	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.71
40	106098	BE278344	Hs.7970	DKFZP4348027 protein	3.70
	133691	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan	3.70
	120717	AA904681	Hs.154434	ESTs, Weakly similar to unknown [H.sapie	3.70
	119263	T15977		gb:I82328 Infant brain, Benlo Soares Hom	3.70
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.70
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	3.70
	110708	N33878	Hs.306117	KIAA0306 protein	3.70
	114357	R41677	Hs.6107	Homo sapiens cD FLJ14839 fis, clone OV	3.70
	115285	AW972872	Hs.293736	ESTs	3.70
	123034	AL359571	Hs.44054	ninein (GSK3B interacting protein)	3.70
50	126396	T06298	Hs.153326	EST	3.70
	132597	Y11192	Hs.5299	aldehyde dehydrogenase 5 family, member	3.70
	105823	AI559444	Hs.293960	ESTs	3.70
	102644	T59816	Hs.173311	C18B11 homolog (44.9kD)	3.70
	133513	AF136407	Hs.7446	chromosome 6 open reading frame 5	3.70
55	116450	AI654450	Hs.47274	Homo sapiens mR; cD DKFZp564B176 (fr	3.69
	104596	AF067804	Hs.15423	hypothetical protein HDCMC04P	3.69
	133579	X75346	Hs.75074	mitogen-activated protein kise-activat	3.68
	124556	N29317	Hs.236463	Homo sapiens mR; cD DKFZp586I0521 (f	3.68
	120534	AI635113	Hs.270366	ESTs, Weakly similar to I78865 serine/th	3.68
	103156	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	3.68
60	134992	AA464444	Hs.5831	tissue inhibitor of metalloprotease 1	3.68
	106730	BE467313	Hs.260707	ESTs	3.68
	120880	AA360240	Hs.97019	EST	3.68
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma	3.68
65	126973	W46653	Hs.251928	nuclear pore complex interacting protein	3.67
	103646	AW248439	Hs.2340	junction plakoglobin	3.67
	116333	AF155827	Hs.203963	hypothetical protein FLJ10339	3.67
	120922	AA481003	Hs.97128	ESTs	3.67
	127407	AW089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	3.67
70	106578	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.67
	123000	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mR,	3.67
	101464	AA852431	Hs.51299	DH dehydrogenase (ubiquinone) flavopro	3.67
	101397	M26380	Hs.180878	lipoprotein lipase	3.67
	131135	NM_016569	Hs.267182	TBX3-iso protein	3.66
75	106112	AL117518	Hs.3686	KIAA0978 protein	3.66
	123974	NM_015678	Hs.3821	neurobeachin	3.66
	127742	AW293496	Hs.180138	ESTs	3.66
	112908	BE281000	Hs.3530	TLS-associated serine-arginine protein 2	3.66
	131802	AL137406	Hs.296356	Homo sapiens mR; cD DKFZp434M162 (fr	3.65
80	135162	AI187925	Hs.95667	F-box protein 30	3.65
	124984	BE313210	Hs.223241	eukaryotic translation elongation factor	3.65
	118844	AL035364	Hs.50891	hypothetical protein	3.65
	125429	AI023654	Hs.114191	ESTs	3.65
	125596	R25698		gb:yg44h11.2 Soares infant brain 1N1B H	3.65

5	125792	AA496205	Hs.193700
	126965	AI470523	Hs.139336
	130776	AF167706	Hs.19280
	131949	AK000010	Hs.258798
	116612	C14904	Hs.45184
	123749	AA609949	Hs.112790
	134203	AA161219	Hs.799
	133605	AL038165	Hs.75187
10	109235	AI381800	Hs.300684
	125447	AI582222	Hs.128686
	122942	AI277829	Hs.111862
	122748	AA458822	Hs.193815
	103840	AW975861	Hs.47367
15	105333	AA234831	Hs.246112
	108807	AI652236	Hs.49376
	114699	AA127386	
	126040	Z28444	Hs.24119
	131028	AI879165	Hs.2227
20	131710	NM_015368	Hs.30985
	100164	AW372032	Hs.173714
	120837	BE149656	Hs.306621
	131089	Z42645	Hs.22870
	126428	AA412436	Hs.301885
25	129148	AW501216	Hs.108945
	102337	AI814663	Hs.170133
	104520	AI702384	Hs.76925
	112954	AA928953	Hs.6655
	125197	AF086270	Hs.278554
30	128124	AI125748	Hs.130194
	129553	AW015763	Hs.113065
	123998	AA203429	Hs.79474
	128835	AK001731	Hs.106390
	129226	BE222494	Hs.180919
35	135131	AI582743	Hs.94953
	128955	AA775076	Hs.185807
	100225	D28539	Hs.167185
	101572	AA437199	Hs.656
	102277	U31099	Hs.158326
40	103667	Z80788	Hs.247815
	112373	AW963357	Hs.7847
	119284	AL041224	Hs.65379
	125422	AA903229	Hs.153717
	126381	M76665	Hs.275215
45	129168	AI132988	Hs.109052
	123133	AA487264	Hs.154974
	128789	AW368576	Hs.139851
	104172	AA476418	
	134263	AW973443	Hs.8086
50	101759	M80244	Hs.184601
	104942	NM_016348	Hs.10235
	123443	BE244537	Hs.167382
	110707	AI239832	Hs.15617
	105787	AI492261	Hs.32450
55	112940	AK001757	Hs.281348
	115301	T11832	Hs.127797
	125978	N68443	Hs.35608
	128002	AI985897	Hs.125293
	119847	H81136	Hs.334604
60	134595	NM_002401	Hs.29282
	121309	AA293834	Hs.97312
	122679	AA811286	Hs.192837
	106061	AA565356	Hs.13250
	127207	AA377165	Hs.44833
65	129563	AF119664	Hs.27299
	105951	R48700	Hs.20733
	115643	AA404276	Hs.123253
	130473	U11690	Hs.1572
	104246	AF016032	Hs.201377
70	120562	BE244580	Hs.302267
	101211	AA355357	Hs.283429
	100774	J05581	Hs.89603
	108407	AA075519	
	113538	AI554947	Hs.15167
75	113876	AI799751	Hs.5635
	110731	NM_014899	Hs.188006
	125845	AK001440	Hs.131840
	112945	AW138458	Hs.20787
	131686	NM_012296	Hs.30687
80	125413	AI887951	Hs.74566
	129360	AI000534	Hs.110708
	128819	R38007	Hs.77578
	101973	U41514	Hs.80120
	103616	NM_002647	Hs.32971

Homo sapiens mR; cD DKFZp586i0324 (f	3.65
ATP-binding cassette, sub-family C (CFTR	3.65
cysteine-rich motor neuron 1	3.65
hypothetical protein FLJ20003	3.65
Homo sapiens cD FLJ12284 fis, clone MA	3.65
EST	3.65
diphtheria toxin receptor (heparin-bindi	3.64
translocase of outer mitochondrial membr	3.64
calicoronin gene-related peptide-receptor	3.64
ESTs	3.63
KIAA0590 gene product	3.63
ESTs	3.63
KIAA1785 protein	3.63
KIAA0788 protein	3.63
hypothetical protein FLJ20644	3.63
gb:zn90d09.r1 Stratagene lung carcinoma	3.63
Homo sapiens mR; cD DKFZp586G2222 (f	3.63
CCAAT/enhancer binding protein (C/EBP),	3.63
pannexin 1	3.63
MORF-related gene X	3.62
Homo sapiens cD FLJ11963 fis, clone HE	3.62
Homo sapiens mR full length insert cDN	3.62
ESTs	3.62
KIAA0515 protein	3.61
forkhead box O1A (rhabdomyosarcoma)	3.61
hypothetical protein FLJ14981	3.60
Homo sapiens EST from clone 208499, full	3.60
heterochromatin-like protein 1	3.60
ESTs	3.60
ESTs	3.60
tyrosine 3-monooxygenase/tryptophan 5-mo	3.60
Homo sapiens mR; cD DKFZp586H0924 (f	3.59
inhibitor of D binding 2, dominant neg	3.59
Homo sapiens, Similar to complement comp	3.59
Homo sapiens, Similar to PRO0478 protein	3.58
glutamate receptor, metabotropic 5	3.58
cell division cycle 25C	3.58
prostaglandin D2 receptor (DP)	3.58
H4 histone family, member L	3.58
ESTs	3.58
ESTs	3.58
ESTs	3.58
hydroxysteroid (11-beta) dehydrogenase 1	3.58
chromosome 14 open reading frame 2	3.58
Homo sapiens mR; cD DKFZp667N064 (fr	3.57
caveolin 2	3.57
gb:zx02a12.s1 Soares_tetal_fetus_Nb2HF8_	3.57
R (guanine-7-) methyltransferase	3.57
solute carrier family 7 (cationic amino	3.56
chromosome 5 open reading frame 4	3.56
triuretic peptide receptor A/guanylate	3.56
ESTs, Weakly similar to ALU4_HUMAN ALU S	3.55
ESTs	3.55
hypothetical protein FLJ10895	3.55
Homo sapiens cD FLJ11381 fis, clone HE	3.55
ESTs	3.55
ESTs	3.55
Homo sapiens mR for KIAA1870 protein,	3.55
mitogen-activated protein kinase kinase	3.55
ESTs	3.54
ESTs, Weakly similar to ALU5_HUMAN ALU S	3.54
ESTs	3.54
ESTs	3.54
transcriptional regulator protein	3.54
Homo sapiens cD: FLJ22356 fis, clone H	3.53
hypothetical protein FLJ22009	3.53
faciogenital dysplasia (Aarskog-Scott sy	3.53
lysosomal	3.53
hypothetical protein FLJ10330	3.53
SMC (mouse) homolog, X chromosome	3.53
mucin 1, transmembrane	3.53
gb:zm87h09.s1 Stratagene ovarian cancer	3.53
ESTs, Weakly similar to S37482 finger pr	3.53
ESTs	3.53
KIAA0878 protein	3.52
hypothetical protein FLJ10578	3.51
Homo sapiens cD: FLJ21686 fis, clone C	3.51
GRB2-associated binding protein 2	3.51
dihydropyrimidine-like 3	3.51
sarcoglycan, epsilon	3.50
ubiquitin specific protease 9, X chromos	3.50
UDP-N-acetyl-alpha-D-galactosamine:polyp	3.50
phosphoinositide-3-kinase, class 3	3.50

5	105535	AI459519	Hs.297681
	118767	AI038653	Hs.50500
	126634	AW361109	Hs.43627
	130851	R65282	Hs.20247
	134353	AL138201	Hs.82120
	111394	AA412227	Hs.16131
	102696	BE540274	Hs.239
	113037	R17268	Hs.259873
10	111028	H59346	Hs.30151
	131688	AI935413	Hs.30692
	115613	AW135951	Hs.173946
	116975	H81076	Hs.269001
	100210	D25361	Hs.3104
	110147	H18700	Hs.268799
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	119088	R39261	Hs.90790
	120347	AA211068	Hs.120247
	122702	AI220089	Hs.99439
20	125552	H09701	Hs.278366
	126461	AI381659	Hs.267086
	128572	AA933022	Hs.256583
	118397	BE139479	Hs.161492
	127999	AW978827	Hs.69851
25	132066	AI929392	Hs.181195
	105693	BE250951	Hs.181368
	128874	H06245	Hs.106801
	119984	AA230228	Hs.59197
	104000	AI146527	Hs.80475
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	101045	J05614	Hs.94834
	120149	AA227609	Hs.21255
	107025	AA825523	Hs.2563
	101716	AF050658	Hs.75730
35	102899	AI815559	Hs.101340
	123075	AW293133	Hs.239307
	124695	AA594979	Hs.22891
	127669	N28989	Hs.126857
	129793	AW207000	Hs.59601
40	120095	AA693774	Hs.29724
	110915	BE092285	Hs.179825
	130542	U64675	Hs.752
	100488	BE273749	Hs.272572
	115027	AA743331	Hs.155478
45	119298	NM_001241	Hs.152316
	126486	AI065133	Hs.1435
	130021	M24470	Hs.263395
	127166	AW954605	Hs.7644
	114988	AA251089	Hs.74870
50	133817	AW578716	Hs.99872
	133562	M60721	Hs.107882
	105610	AA280072	Hs.816
	129007	AK001521	Hs.92927
	100662	AI368680	Hs.920
55	120159	R60781	Hs.115778
	134966	AW402389	Hs.194283
	100369	D79988	Hs.49
	104260	AF008192	Hs.50334
	100134	AA305746	Hs.65250
60	116015	AA338648	Hs.280858
	119251	T15753	Hs.146847
	127176	BE387162	Hs.103000
	123422	AA598484	Hs.19247
	123094	AA761073	Hs.87779
65	105289	AB020638	Hs.209473
	111219	N68836	Hs.118210
	127963	AI299013	Hs.283108
	109412	BE543313	Hs.93670
	118794	AW517051	Hs.194081
	112040	R43286	Hs.85982
70	111180	AI798851	Hs.6427
	117329	AA524065	Hs.230157
	104371	AI288696	Hs.97579
	109265	AA195285	Hs.287849
	109557	AW452405	Hs.120189
75	120753	AA312551	Hs.111977
	120970	AA398118	Hs.1735
	127094	F13215	Hs.94498
	127746	AI239495	Hs.124027
	123553	AI494291	Hs.26039
80	130652	M31669	
	135101	U82275	
	121799	AI885670	
	112278	Z41698	

serine (or cysteine) protease inhibitor	3.50
ESTs	3.50
SRY (sex determining region Y)-box 22	3.50
ESTs, Weakly similar to S65657 alpha-1C-	3.50
nuclear receptor subfamily 4, group A, m	3.50
hypothetical protein FLJ12876	3.50
forkhead box M1	3.49
axol transport of synaptic vesicles	3.49
ESTs, Weakly similar to I38022 hypothetical	3.49
p21 (CDKN1A)-activated kinase 2	3.49
hypothetical protein FLJ10486	3.48
ESTs	3.48
KIAA0042 gene product	3.48
ESTs	3.48
Homo sapiens cD FLJ10366 fis, clone NT	3.48
Homo sapiens cD: FLJ22930 fis, clone K	3.48
nuclear fragile X mental retardation pro	3.48
ESTs	3.48
ESTs, Weakly similar to I38022 hypothetical	3.48
ESTs	3.48
interleukin enhancer binding factor 3, 9	3.48
ESTs	3.47
nucleolar protein family A, member 1 (H/	3.47
DJ (Hsp40) homolog, subfamily B, membe	3.47
U5 snRNP-specific protein (220 kD), orth	3.47
ESTs, Weakly similar to PC4259 ferritin	3.46
ESTs	3.46
polymerase (R) II (D directed) polyp	3.46
ELK1, member of ETS oncogene family	3.46
gb:Human proliferating cell nuclear anti	3.46
ESTs	3.46
ESTs, Weakly similar to I38022 hypothetical	3.45
tachykinin, precursor 1 (substance K, su	3.45
sigl recognition particle receptor (rd	3.45
ESTs, Weakly similar to A42442 integrin	3.45
tyrosyl-HR synthetase	3.45
solute carrier family 7 (cationic amino	3.45
Homo sapiens cD FLJ12936 fis, clone NT	3.44
ESTs	3.44
hypothetical protein FLJ13187	3.43
RAN binding protein 2-like 1	3.43
FK506-binding protein 1A (12kD)	3.43
hemoglobin, alpha 2	3.43
cyclin T2	3.43
hypothetical protein PRO0971	3.43
guanosine monophosphate reductase	3.43
sema domain, transmembrane domain (TM),	3.42
gb:zs0405.s1 NCI_CGAP_GCB1 Homo sapiens	3.42
H1 histone family, member 2	3.41
H2.0 (Drosophila)-like homeo box 1	3.41
fatal Alzheimer antigen	3.41
hypothetical protein FLJ10659	3.41
SRY (sex determining region Y)-box 2	3.41
putative 47 kDa protein	3.41
modulator recognition factor 1	3.41
KIAA0166 gene product	3.41
putative GR6 protein	3.40
macrophage scavenger receptor 1	3.40
testes development-related NYD-SP22	3.40
EST	3.40
ESTs, Highly similar to A35661 D excis	3.40
gb:ae38104.s1 Gessler Wilms tumor Homo s	3.39
TRAF family member-associated NFKB activ	3.39
KIAA0631 protein	3.39
ESTs, Moderately similar to ALUC_HUMAN I	3.38
Homo sapiens cD: FLJ23087 fis, clone L	3.38
hypothetical protein FLJ10520	3.38
ESTs	3.38
gb:yg17e11.s1 Soares infant brain 1N1B H	3.38
hemoglobin, gamma G	3.38
Homo sapiens cD: FLJ22664 fis, clone H	3.38
ESTs, Weakly similar to I38022 hypothetical	3.38
ESTs	3.38
ESTs	3.38
ESTs	3.38
ESTs, Weakly similar to A46010 X-linked	3.38
ESTs, Weakly similar to T22074 hypothetical	3.38
ESTs	3.38
ESTs	3.37
inhibin, beta B (activin AB beta polypep	3.37
leukocyte immunoglobulin-like receptor,	3.37
SELENOPHOSPHATE SYNTHETASE ; Human selen	3.37
Homo sapiens cD FLJ13937 fis, clone Y7	3.36

5	113401	AA610175	Hs.179647	Homo sapiens cD FLJ12195 fis, clone MA	3.36
	109292	AW975746	Hs.188662	KIAA1702 protein	3.36
	135026	N92165	Hs.93231	ESTs	3.36
	118210	N49233	Hs.46914	ESTs, Weakly similar to A46010 X-linked	3.35
	123476	AA384564	Hs.108829	ESTs	3.35
	111076	N59129	Hs.20851	ESTs	3.35
	111520	AI985369	Hs.301134	ESTs	3.35
	133383	BE313555	Hs.7252	KIAA1224 protein	3.35
10	103731	AA070545		gb:znm70c03.r1 Stratagene neuroepithelium	3.35
	110828	AK002114	Hs.23495	hypothetical protein FLJ11252	3.35
	112520	R68654	Hs.30814	ESTs	3.35
	115725	AW899053	Hs.76917	F-box only protein 8	3.35
	125867	H13331	Hs.123721	ESTs	3.35
15	127719	AJ242163	Hs.22670	chromodomain helicase D binding protei	3.35
	129863	BE379765	Hs.129872	sperm associated antigen 9	3.35
	130816	M61877	Hs.1985	spectrin, alpha, erythrocytic 1 (ellipto	3.35
	130888	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	3.35
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	3.35
20	118986	AF148713	Hs.125830	bladder cancer overexpressed protein	3.35
	101723	U34304		gb:Human nonmuscle myosin heavy chain II	3.34
	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons	3.34
	102856	M26150	Hs.248177	H3 histone family, member L	3.34
25	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.34
	134748	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (reB)	3.34
	109149	AA831179	Hs.40065	hypothetical protein MGC4825	3.33
	115026	AA251972	Hs.188718	ESTs	3.33
	103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	3.33
	111189	N67603	Hs.272130	ESTs, Weakly similar to S65824 reverse t	3.33
30	127076	AI422951	Hs.146162	ESTs	3.33
	124949	AI903210	Hs.336780	tubulin, beta polypeptide	3.33
	111012	AJ077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.33
	113412	AW628660	Hs.44131	KIAA0974 protein	3.33
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	3.33
35	121633	AA417011	Hs.98175	EST	3.33
	124591	N69243	Hs.192974	hypothetical protein FLJ12735	3.33
	130225	AB021179	Hs.15299	HMBA-inducible	3.33
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.33
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	3.33
40	105726	NM_012068	Hs.9754	activating transcription factor 5	3.32
	101867	M96132		gb:Human MHC class II HLA-DR-beta-1*0901	3.32
	105004	BE616023	Hs.25298	KIAA1813 protein	3.32
	100288	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	3.32
45	118349	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.32
	103352	H09366	Hs.78853	uracil-D glycosylase	3.32
	107436	W27720	Hs.12450	protocadherin 9	3.30
	109062	AA160941		gb:zq40d12.s1 Stratagene hNT neuron (937	3.30
	110379	AI300505	Hs.33130	Homo sapiens cD: FLJ23486 fis, clone L	3.30
	111221	AB037782	Hs.15119	KIAA1361 protein	3.30
50	117903	AA768283	Hs.47111	ESTs	3.30
	123265	AA491209		gb:aa47a08.s1 NCL CGAP_GCB1 Homo sapiens	3.30
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	3.30
	111945	R40663	Hs.124944	ESTs	3.30
	126214	AW748336	Hs.168052	KIAA0421 protein	3.30
55	121073	H46199	Hs.112184	DKFZP586J0619 protein	3.30
	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	3.30
	100992	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral	3.30
	134021	L13720	Hs.78501	growth arrest-specific 6	3.30
	126452	R26867		gb:yh52e01.s1 Soares placenta Nb2HP Homo	3.29
60	117195	AI798425	Hs.42710	ESTs	3.29
	127663	AK000452	Hs.10340	hypothetical protein FLJ20445	3.29
	113677	Z70200	Hs.246112	KIAA0788 protein	3.28
	132398	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.28
	109533	AL043979	Hs.259729	KIAA0596 protein	3.28
65	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.28
	104348	H05405	Hs.19221	hypothetical protein DKFZp566G1424	3.28
	113047	AI571940	Hs.7549	ESTs	3.28
	113203	AA743563	Hs.10305	ESTs	3.28
	114503	AL040600	Hs.188083	ESTs	3.28
70	122100	AA431220	Hs.41086	pleckstrin homology domain-containing, f	3.28
	123073	AA485061	Hs.105652	ESTs	3.28
	130253	AI078570	Hs.167473	phosphoglucomutase 5	3.28
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	3.28
	130762	D84371	Hs.1898	paraoxase 1	3.28
75	132360	AW893660	Hs.46440	solute carrier family 21 (organic anion	3.28
	110763	AI928445	Hs.92254	sytoplamin-like 2	3.27
	103437	AV655598	Hs.184211	peptidase (mitochondrial processing) bet	3.27
	114840	AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	3.27
	106888	AA020964	Hs.24734	oxysterol binding protein	3.27
80	129896	BE295568	Hs.13225	UDP-Galactose 4-epimerase	3.26
	113459	T80206	Hs.14716	ESTs	3.26
	134332	D86962	Hs.81875	growth factor receptor-bound protein 10	3.26
	117048	H89732	Hs.230113	EST	3.26
	109249	AA194730	Hs.268189	hypothetical protein FLJ20436	3.26

5	134663	W73428	Hs.8750	uncharacterized bone marrow protein BMD4	3.26
	114440	AL046511	Hs.106525	hypothetical protein FLJ12567	3.25
	102196	BE266830	Hs.75238	chromatin assembly factor 1, subunit B (3.25
	109581	R45584	Hs.23025	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.25
	120814	AW867796	Hs.96860	ESTs, Weakly similar to I38022 hypothe	3.25
10	122391	AA446316	Hs.191622	ESTs	3.25
	122553	AA451884	Hs.190121	ESTs	3.25
	124755	R38087	Hs.267690	KIAA1228 protein	3.25
	130943	U20760	Hs.272429	calcium-sensing receptor (hypocalciuric	3.25
	115185	BE299677	Hs.105461	hypothetical protein FLJ20357	3.25
15	114297	AA149707	Hs.173091	ubiquitin-like 3	3.25
	106657	AW854339	Hs.33476	hypothetical protein FLJ11937	3.25
	124320	H95749	Hs.102342	EST	3.25
	124087	H08773	Hs.288590	Homo sapiens cD FLJ11454 fis, clone HE	3.24
	110705	AB007902	Hs.32168	KIAA0442 protein	3.24
20	106508	AI205785	Hs.30348	ESTs	3.24
	112538	AA908813		gb:cg77b06.s1 NCL_CGAP_Ov8 Homo sapiens	3.24
	100130	NM_000304	Hs.103724	peripheral myelin protein 22	3.24
	106017	AA477956	Hs.26268	ESTs	3.24
	113921	AW976530	Hs.28355	hypothetical protein FLJ22402	3.23
25	121520	AA412163	Hs.164785	ESTs	3.23
	129255	AI961727	Hs.109804	H1 histone family, member X	3.23
	125069	H81306	Hs.194485	ESTs	3.23
	119863	AA081218	Hs.58608	Homo sapiens cD FLJ14206 fis, clone NT	3.23
	111273	N70934		gb:za33106.s1 Soares fetal liver spleen	3.23
30	102971	X16609	Hs.183805	ankyrin 1, erythrocytic	3.23
	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothe	3.23
	121770	NM_015902	Hs.278428	progesterin induced protein	3.23
	128972	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypothe	3.23
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso	3.23
35	134835	L04569	Hs.89925	calcium channel, voltage-dependent, L ty	3.23
	103158	BE242587	Hs.118651	hematopoietically expressed homeobox	3.22
	118405	AL117518	Hs.3686	KIAA0978 protein	3.22
	104631	AA002064	Hs.18920	ESTs	3.22
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.22
40	134607	AI675881	Hs.86538	ESTs	3.22
	135114	AW340493	Hs.175043	ancient conserved domain protein 4	3.22
	120191	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mR,	3.22
	105029	AI122691	Hs.13268	ESTs	3.21
	128550	AA418276	Hs.170142	ESTs	3.21
45	119873	AI660149	Hs.44865	lysosomal	3.21
	130115	T47294	Hs.149923	X-box binding protein 1	3.21
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.21
	120259	AW014786	Hs.192742	hypothetical protein FLJ12785	3.21
	110721	H97678	Hs.31319	ESTs	3.21
50	130062	AL049415	Hs.278679	a disintegrin and metalloprotease doma	3.21
	100265	D38521	Hs.112396	KIAA0077 protein	3.20
	100624	AB001025	Hs.9349	ryanodine receptor 3	3.20
	122275	AA437124	Hs.187247	ESTs	3.20
	127089	AA347668		gb:EST54026 Fetal heart II Homo sapiens	3.20
55	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	3.20
	132809	AF036144	Hs.5734	meningioma expressed antigen 5 (hyaluron	3.20
	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	3.20
	128339	AL121087	Hs.296406	KIAA0685 gene product	3.19
	117121	H95044	Hs.321386	EST	3.19
60	124760	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	3.19
	132232	AI522273	Hs.42640	ESTs	3.19
	125919	W26713	Hs.256972	ESTs	3.19
	123324	AB018352	Hs.105399	KIAA0809 protein	3.19
	100157	D14661	Hs.119	Wilms' tumour 1-associating protein	3.19
65	101447	M21305		gb:Human alpha satellite and satellite 3	3.19
	124345	NM_014487	Hs.120766	nucleolar cysteine-rich protein	3.18
	122583	NM_012447	Hs.20132	stromal antigen 3	3.18
	128961	AL133014	Hs.107387	CGI-20 protein	3.18
	111321	AI569766	Hs.13205	ESTs	3.18
70	134977	AL044963	Hs.306121	leukocyte receptor cluster (LRC) encoded	3.18
	131535	N22120	Hs.75277	hypothetical protein FLJ13910	3.18
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos	3.18
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	3.18
	101654	M60298	Hs.733	erythrocyte membrane protein band 4.2	3.18
75	104732	AL079294	Hs.29952	Homo sapiens mR full length insert cDN	3.18
	106857	AB037744	Hs.34892	KIAA1323 protein	3.18
	108301	AA069728	Hs.184582	ribosomal protein L24	3.18
	118042	AI432389	Hs.161465	ESTs	3.18
	120900	AA830712	Hs.291931	ESTs	3.18
80	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	3.18
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.17
	110672	AW612890	Hs.191178	ESTs	3.17
	115665	BE072425	Hs.44579	hypothetical protein FLJ20199	3.17
	127581	AK000680	Hs.266175	phosphoprotein associated with GEMs	3.17
	129584	AV656017	Hs.184352	CGI-76 protein	3.16
	108830	AA131743	Hs.193352	ESTs	3.16
	124443	AI857519	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.16

5	106290	AW961393	Hs.16364	hypothetical protein FLJ10955	3.16
	122787	AI209093	Hs.99512	ESTs	3.16
	133112	T15465	Hs.182231	thyrotropin-releasing hormone	3.16
	116435	AA186761	Hs.334812	hypothetical protein DKFZp586K0717	3.16
	109121	BE389387	Hs.49767	DH dehydrogese (ubiquinone) Fe-S pro	3.16
	126721	AW579621	Hs.125359	Thy-1 cell surface antigen	3.15
	102526	AA203429	Hs.79474	tyrosine 3-monooxygenase/tryptophan 5-mo	3.15
	100512	D13317	Hs.78915	GA-binding protein transcription factor,	3.15
10	105299	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	3.15
	117842	AI984505	Hs.161121	ESTs	3.15
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	3.15
	128639	AW582962	Hs.102897	CGI-47 protein	3.15
	130343	AB040914	Hs.278628	KIAA1481 protein	3.15
15	115706	AB004849	Hs.50748	chromosome 21 open reading frame 18	3.15
	120673	AW968634	Hs.105093	ESTs	3.15
	132116	AW960474	Hs.40289	ESTs	3.15
	116217	AU076474	Hs.123178	translocase of inner mitochondrial membr	3.15
	104926	BE298808	Hs.33363	DKFZP434N093 protein	3.14
20	105297	NM_015905	Hs.183858	transcriptio intermediary factor 1	3.14
	125343	AI475495	Hs.304101	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.14
	115618	H11695	Hs.322901	disrupter of silencing 10	3.14
	124893	AA830185	Hs.269680	ESTs	3.13
	105461	BE530771	Hs.69388	hypothetical protein FLJ20505	3.13
25	126165	AI741816	Hs.125897	ESTs	3.13
	105212	AA205334	Hs.324278	Homo sapiens mR; cD DKFZp566M063 (fr	3.13
	101628	M57506	Hs.72918	small inducible cytokine A1 (I-309, homo	3.13
	107951	AI300077	Hs.61690	ESTs	3.13
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.13
30	117299	N75768		gb:yyw30b07.r1 Morton Felal Cochlea Homo	3.13
	119694	AA041350	Hs.57847	ESTs, Moderately similar to ICE4_HUMAN C	3.13
	124840	R56146	Hs.164515	EST, Weakly similar to AF090930 1 PRO047	3.13
	127433	AW979155	Hs.298275	amino acid transporter 2	3.13
	128337	AI123529	Hs.166592	ESTs	3.13
35	134053	AW626686	Hs.78851	KIAA0217 protein	3.13
	134475	NM_014733	Hs.83790	KIAA0305 gene product	3.13
	128761	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	3.12
	124971	T23800	Hs.151001	hypothetical protein FLJ14728	3.12
	128314	T87479	Hs.291797	ESTs	3.12
40	134695	AB036829	Hs.178347	SKIP for skeletal muscle and kidney enri	3.12
	131333	BE244603	Hs.25726	transposon-derived Buster1 transposase-I	3.12
	119781	AJ278016	Hs.55565	ankyrin repeat domain 3	3.12
	131824	U28838	Hs.32935	TATA box binding protein (TBP)-associate	3.11
	124595	AW194851	Hs.111801	arslete resistance protein ARS2	3.11
45	116115	AL042355	Hs.70202	WD repeat domain 10	3.11
	129415	AI907084	Hs.111243	MADS box transcription enhancer factor 2	3.11
	111552	T97939	Hs.191185	ESTs	3.10
	134861	NM_000937	Hs.171880	polymerase (R) II (D directed) polyp	3.10
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	3.10
50	126536	AA156151		gb:zo48c06.r1 Stralagene endothelial cei	3.10
	128246	AI990512	Hs.214818	DMRT-like family C2	3.10
	106412	AA453734	Hs.10198	ESTs	3.10
	107902	AA026627	Hs.61358	ESTs	3.10
	112495	AI346487	Hs.28739	ESTs	3.09
55	131870	NM_014874	Hs.3363	KIAA0214 gene product	3.09
	105301	AW352357	Hs.7457	MAGE1 protein	3.09
	123670	AI189844	Hs.112708	ESTs, Moderately similar to ZN91_HUMAN Z	3.09
	116474	AW160774	Hs.159154	tubulin, beta, 4	3.09
	112064	AL049390	Hs.22689	Homo sapiens mR; cD DKFZp586O1318 (f	3.09
60	130525	AA361850	Hs.322149	Human clone 137308 mR, partial cds	3.08
	120398	AL133649	Hs.110953	retinoic acid induced 1	3.08
	102735	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni	3.08
	124748	R34617		gb:yh85h12.s1 Soares placenta Nb2HP Homo	3.08
	120755	AA312934	Hs.190745	Homo sapiens cD: FLJ21326 fs, clone C	3.08
65	118895	BE304917	Hs.31097	hypothetical protein FLJ21478	3.08
	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	3.08
	114290	R51383	Hs.25793	ESTs	3.08
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	3.08
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	3.08
70	127766	AA723659	Hs.290607	EST	3.08
	132693	BE244200	Hs.55075	KIAA0410 gene product	3.07
	106812	BE251590	Hs.239370	DKFZP7271051 protein	3.07
	125654	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.07
	111836	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	3.06
	101682	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2	3.06
75	110004	H10413	Hs.268774	ESTs	3.06
	117591	N64777	Hs.44656	ESTs	3.06
	110737	AA335609	Hs.7589	ESTs, Weakly similar to A46010 X-linked	3.06
	134337	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.06
	132450	AA100012	Hs.48827	hypothetical protein FLJ12085	3.06
80	125556	AB033054	Hs.334806	KIAA1238 protein	3.06
	101811	NM_002556	Hs.24734	oxysterol binding protein	3.06
	131530	AA574309	Hs.283402	TCR eta	3.06
	105049	AB032945	Hs.172506	myosin VB	3.06

5	126614	AA701941	Hs.187555	ESTs	3.05	
	130960	AF035621	Hs.21611	kinesin family member 3C	3.05	
	105503	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	3.05	
	107361	U72513	Hs.159486	Human RPL13-2 pseudogene mR, complete	3.05	
	107575	D81886	Hs.59908	ESTs	3.05	
10	116999	H84644	Hs.40707	EST	3.05	
	119554	W38188		(NONE)	3.05	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.05	
	125805	A1160594	Hs.166656	ESTs, Highly similar to S49460 glutamate	3.05	
	127263	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.05	
15	128025	T64877	Hs.108479	ESTs	3.05	
	131090	A1143139	Hs.2288	visinin-like 1	3.05	
	112197	NM_003655	Hs.5637	ESTs	3.05	
	133492	L40397	Hs.74137	transmembrane trafficking protein	3.04	
	118485	AA508515	Hs.291049	ESTs	3.04	
20	113893	AJ373741	Hs.59384	hypothetical protein MGC3047	3.04	
	116911	AW205577	Hs.308435	ESTs, Moderately similar to KIAA0745 pro	3.04	
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	3.04	
	124724	H20816	Hs.112423	Homo sapiens mR; cD DKFZp586I1420 (f	3.04	
	105894	AJ904740	Hs.25691	receptor (calcitonin) activity modifying	3.04	
25	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.04	
	128714	T85231	Hs.179661	tubulin, beta 5	3.04	
	134550	U76376	Hs.87247	harakiri, BCL2-interacting protein (cont	3.04	
	106851	AI458623		gb:lk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.04	
	133445	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.04	
30	102581	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.04	
	127542	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	3.03	
	113043	AI628789	Hs.7483	ESTs	3.03	
	134710	AI433797	Hs.8889	serine hydroxymethyltransferase 1 (solub	3.03	
	119245	AI815733	Hs.114360	transforming growth factor beta-stimulat	3.03	
35	106391	AW959538	Hs.321214	hypothetical protein DKFZp564D0478	3.03	
	114607	AF041260	Hs.129057	breast carcinoma amplified sequence 1	3.03	
	116083	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.03	
	132079	AJ701457	Hs.38694	ESTs	3.03	
	103825	AI571835	Hs.55468	ESTs	3.03	
40	106438	AI141031	Hs.21342	ESTs	3.03	
	124359	N22508	Hs.139315	Homo sapiens cD: FLJ21479 fis, clone C	3.03	
	126384	AW090198	Hs.4779	KIAA1150 protein	3.03	
	127995	AA970953	Hs.128709	ESTs	3.03	
	127981	AA837029	Hs.157463	ESTs	3.02	
45	124417	N34059		gb:yy28h09.s1 Soares fetal liver spleen	3.02	
	124357	N22401		gb:yyw37g07.s1 Morton Fetal Cochlea Homo	3.02	
	105437	AF151076	Hs.25199	hypothetical protein	3.02	
	101158	AW327723	Hs.76122	splicing factor, arginine/serine-rich 4	3.02	
	113897	R91601	Hs.4947	hypothetical protein FLJ22584	3.02	
50	100159	AA285268	Hs.23488	KIAA0107 gene product	3.02	
	106487	AI697340	Hs.135265	Homo sapiens clone FLB8436 PRO2277 mR,	3.02	
	124977	F04819	Hs.190452	KIAA0365 gene product	3.02	
	131631	AA022569	Hs.29802	slit (Drosophila) homolog 2	3.01	
	102259	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	3.01	
55	104399	AL022316	Hs.301947	kraken-like	3.01	
	116536	BE218027	Hs.89969	ESTs	3.00	
	125889	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.00	
	102233	AW163045	Hs.79334	nuclear factor, Interleukin 3 regulated	3.00	
	102628	U90322	Hs.27812	G protein-coupled receptor 23	3.00	
60	112812	H55977	Hs.35810	ESTs	3.00	
	114654	AA101840	Hs.103679	ESTs	3.00	
	118555	N68372		gb:za68c10.s1 Soares_fetal_lung_NbHL19W	3.00	
	120005	W90105	Hs.94942	EST	3.00	
	123596	AA421130	Hs.112640	EST	3.00	
65	126134	AL133033	Hs.4084	KIAA1025 protein	3.00	
	126194	H98755	Hs.302975	ESTs, Weakly similar to Z195_HUMAN ZINC	3.00	
	129778	AK001676	Hs.12457	hypothetical protein FLJ10814	3.00	
	Table 3B:					
	Pkey:	Unique Eos probeset identifier number				
CAT number:	Gene cluster number					
Accession:	Genbank accession numbers					
70	Pkey	CAT number	Accession			
	123619	371681_1	AA602964 AA609200			
	124417	1642364_1	N34059 N46979			
	117299	1632586_1	N75768 N22543			
	116845	393481_1	AA649530 AA659316 H64973			
75	124748	1715080_1	R34617			
	125596	1708455_1	R25698 R56582 R56018			
	126257	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815			
	126280	1572221_1	Z19417 H20866			
	126319	1528523_1	D81689 D81802			
80	104172	273499_1	AA476418 AA393338 AA398747 AA476518			
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752			
			AA076512 AA085119 AA085208 AA085045			
			AA325606 AA099517 N89423			
	126433	127143_1				

	127092	177998_1	T26985 Z44165
	127099	244301_1	AA347668 AW956810 Z44271 F07065 F07064 R13506
	126535	149206_1	AA156151 Z25109 C05177
5	103731	112052_1	AA070545 AA131490 AA131373
	127263	232161_1	AA331156 AA331157 AA331155
	126783	113388_1	AA083531 AA126047 AA074915 AA148649
	118946	1683457_1	N92834 W25061
	127520	656170_1	T51239
10	127532	353907_1	AJ003429 AJ003367 AA564825
	112516	1744223_1	T83909 R68586
	112538	504579_1	AA908813 R70255
	112540	1605263_1	R69751 R70467 H69771 H80879 H80878
	113248	328626_1	T63857 AW971220 AA493469 T63699
15	112631	1746257_1	R82040 R70934
	128360	1540098_1	F12374 T74059
	120514	25532_3	AA258335 AA258499
	127867	1511945_1	C18530 T63953
	120637	200885_1	AA811804 AA809404 AA286907 AW977624
20	121481	123001_1	AA411931 AA411930
	120934	177521_1	AA226198 AA226513 AA383773
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742
			AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
25	121743	274582_1	AA397636 AA421144
	114699	135322_1	AA127386 R15644 AA127404
	106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
	123731	genbank_AA609839	AA609839
	123973	506369_1	C14805
	116793	74964_1	T77781 AW014157 D12422 AI918246 AA452599 AA628404 N35886 AA464593 AW301738 T77780 AI042309 AI095302 H60603
30	109700	genbank_F09609	AW510576 H37814 W61360 AI373286 AI702287 AA152465 AW169067 AW169012 AW340355 AI289311
	118466	genbank_N86741	F09609
	111273	genbank_N70934	N66741
	118555	genbank_N68372	N70934
35	111462	genbank_R05296	N68372
	118720	genbank_N73515	R05296
	118737	382979_1	N73515
	111826	genbank_R35975	AA199686 N73861
40	120376	genbank_AA227469	R35975
	120809	genbank_AA346495	AA227469
	120839	genbank_AA348913	AA346495
	120873	genbank_AA358015	AA348913
	116498	genbank_AA291070	AA358015
	101045	entrez_J05614	AA291070
45	129969	genbank_N57818	J05614
	108407	genbank_AA075519	N57818
	122939	genbank_AA477141	AA075519
	117031	genbank_H88353	AA477141
	124298	genbank_H91679	H88353
50	117099	321871_1	H91679
	101447	entrez_M21305	H93699 H97976 H80036
	124357	genbank_N22401	M21305
	101723	2603_1	N22401
55			U34304 AA355800 M69181 AA375523 AA093590 AA365595 S67247 AI371761 AW351920 AW181991 H28934 W79172 AA653543
			AA122005 W95572 AF086505 C02448 W57668 T11988 W95465 AA425179 F05724 F12205 F06285 R16384 T66222 F08515
			F07288 AA150346 H83264 T86770 N36366 AA337253 H12001 H82899 H69395 H69380 N29054 N30920 T97385 T96819
			AA463807 AL079860 T11987 AA305048 AA149133 T82813 AA029555 AA035109 AA449123 AA340297 AA724155 W05196
			AI859528 AA149134 C16426 C16097 C16587 C16138 C16107 AW021754 C16500 N30019 R55718 R60552 N84522 AI143322
60			AW519024 AA490700 N20675 AW296747 C16068 D58331 C16518 AI141214 N67221 C16423 C16537 C16094 C16152 H28935
			T66152 C16362 AW022425 AA602899 AA694603 H22255 W74368 C16356 AI129361 AI917986 AI582253 AI923898 AI038907
			AW191970 AI678861 C16429 C16345 AI277790 R42325 AI640420 AI004136 AI277797 C16100 F09836 T71212 AA152316
			AW090781 AI055902 T16084 AW022915 C16556 AW473979 T96820 AA476595 N75446 F02570 H69286 T89992 AA907493
			T34275 AA156107 H11758 AI650288 H82900 AI474575 N66718 F04914 AA505470 AA993349 F01973 AI123277 F04729 C16236
			AA879148 AA029574 AA887046 R08127 D57339 AA490477 AI669818 AI190995 AA035507 AL119272 AL135029 AA258725
65			AL079521 N40299 AI630191 N86148 AA341165 T28492 N83749 AI382123 AI065033 AI950411 AI935653 AI275551 AW027482
			AW197337 AI158323 AI335930 AI094099 AI351490 AA258563 AI634763 AI492374 AA983970 AI123565 T72559 F09890
			AA669531 AI445824 T07180 AW084799 AA306254 R60606 W28367 R55928 W27995 AL044845 AA501890 N84045 T97274
			N87532 AL135219 AA116056 T06000 AA116057 T07181 R08126
70	124677	genbank_R01073	R01073
	110243	genbank_H26683	H26683
	101867	entrez_M96132	M96132
	101941	entrez_S77583	S77583
	119052	149538_1	R10889 R10888
	126452	209811_1	R25867 R27438
	119263	genbank_T15977	T15977
75	112040	genbank_R43286	R43286
	103657	entrez_Z73677	Z73677
	119400	genbank_T92767	T92767
	119554	NOT_FOUND_entrez_W38188	W38188
80	123130	genbank_AA487200	AA487200
	123143	genbank_AA487595	AA487595
	121950	genbank_AA429515	AA429515
	123265	genbank_AA491209	AA491209
	114988	genbank_AA251089	AA251089
	107794	genbank_AA019255	AA019255

123422 genbank_AA598484 AA598484
109062 genbank_AA160941 AA160941

5 TABLE 4A: ABOUT 1164 GENES UPREGULATED IN GLIOBLASTOMA

	Pkey:		Unique Eos probeset identifier number	R1	R2
	ExAccn:		Exemplar Accession number, Genbank accession number		
10	UnigeneID:		Unigene number	R1	R2
	Unigene Title:		Unigene gene title		
	R1:		Ratio of brain tumor to body atlas	R1	R2
	R2:		Ratio of brain tumor to normal brain		
	Pkey	ExAccn	UnigeneID	Unigene Title	
15	412719	AW016610	Hs.129911	ESTs	117.8
	428321	AI699994	Hs.301347	ESTs	108.9
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	107.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	99.0
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-L	72.0
20	449494	AW237014	Hs.286650	aquaporin 4	60.0
	439285	AL133916	Hs.298998	ESTs	58.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	54.2
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	53.5
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	49.6
	425088	AA663372	Hs.169395	Homo sapiens cDNA FLJ12015 fis, clone HE	49.5
25	412959	D87458	Hs.75090	KIAA0282 protein	46.3
	447004	AW296968	Hs.157539	ESTs	43.7
	436878	BE465204	Hs.47448	ESTs	39.8
	433551	AI985544	Hs.289048	ESTs	39.7
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	39.3
30	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	39.1
	431725	XG5724	Hs.2839	Norie disease (pseudoglioma)	38.4
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	37.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	37.5
35	439415	F05538	Hs.12825	ESTs	35.4
	409395	U46745	Hs.54435	dystrobrevin, alpha	34.3
	449539	W80363	Hs.58446	ESTs	33.6
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	32.8
	431019	NM_005249	Hs.2714	forkhead box G1B	32.4
40	427540	R12014	Hs.20976	ESTs	32.1
	425057	AA826434	Hs.96944	ESTs	31.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	30.8
	416829	AB013805	Hs.80220	calenin (cadherin-associated protein), d	30.4
	420807	AA280627	Hs.57846	ESTs	30.4
45	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	30.4
	429466	M85835	Hs.12827	ESTs	30.2
	444471	AB020684	Hs.11217	KIAA0877 protein	29.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	28.8
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	27.7
50	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	27.1
	440435	AL042201	Hs.21273	ESTs	26.9
	411078	AI222020	Hs.182364	ESTs, Weakly similar to 25 kDa trypsin i	26.0
	407808	AA663559	Hs.289109	dimethylarginine dimethylaminohydrolase	25.8
	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	25.5
55	421659	NM_014459	Hs.106511	protocadherin 17	25.0
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	24.7
	433332	AI367347	Hs.127809	ESTs	24.6
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	23.8
	419271	N34901	Hs.238532	ESTs	23.6
60	447397	BE247676	Hs.18442	E-1 enzyme	23.1
	439039	AI656707	Hs.48713	ESTs	23.0
	414175	AI308876	Hs.103849	ESTs	22.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	22.0
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	21.6
65	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	21.2
	451468	AW503398	Hs.210047	ESTs	21.0
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	20.8
	443850	AW014723	Hs.134719	ESTs	20.4
	418738	AW388633	Hs.6682	ESTs	20.2
70	449433	AI672096	Hs.9012	ESTs	19.9
	435706	W31254	Hs.7045	GL004 protein	19.7
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	19.7
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	19.6
	442562	BE379584	Hs.34789	ESTs	19.4
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	19.1
75	426320	W47595	Hs.169300	transforming growth factor, beta 2	18.7
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	18.6
	452106	AI141031	Hs.21342	ESTs	18.6
	431173	AW971198	Hs.294068	ESTs	18.6
	422583	AA410506	Hs.118578	H.sapiens mRNA for ribosomal protein L18	18.5
80	419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypept	18.5
	443547	AW271273	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT	18.5
	451592	AI805416	Hs.213897	ESTs	18.4
	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	18.3

	422544	AB018259	Hs.118140	KIAA0716 gene product		
	408096	BE250162	Hs.83785	dihydrofolate reductase	18.2	4.7
	418027	AB037807	Hs.83293	hypothetical protein	18.0	18.0
5	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	18.0	8.2
	429418	AI381028	Hs.99283	ESTs	18.0	18.0
	432527	AW975028	Hs.102754	ESTs	17.8	17.8
	447809	AW207605	Hs.164230	ESTs, Highly similar to phosphodiesteras	17.7	4.2
	419704	AA429104	Hs.45057	ESTs	17.5	4.3
10	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spl	17.4	4.6
	445133	AW157646	Hs.153506	ESTs, Weakly similar to AF150755 1 micro	17.4	2.1
	446659	AI335361	Hs.226376	ESTs	17.3	18.8
	409049	AI423132	Hs.146343	ESTs	17.2	2.8
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	17.2	3.8
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	17.2	11.0
15	438527	AI969251	Hs.143237	ESTs	17.0	6.3
	417791	AW965339	Hs.111471	ESTs	16.9	16.9
	417355	D13168	Hs.82002	endothelin receptor type B	16.8	10.5
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	16.4	16.4
20	419721	NM_001650	Hs.288650	aquaporin 4	16.3	4.2
	427701	AA411101	Hs.221750	ESTs	16.2	4.4
	432435	BE218886	Hs.282070	ESTs	16.1	3.9
	426809	BE313114	Hs.29706	ESTs	16.1	5.7
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	16.0	10.0
25	400859				15.9	15.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	15.7	15.7
	420092	AA814043	Hs.88045	ESTs	15.6	15.6
	449605	AW138581	Hs.198416	ESTs	15.6	5.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	15.5	3.0
30	449611	AI970394	Hs.197075	ESTs	15.3	4.6
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	15.2	15.2
	405238				15.2	5.6
	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	15.1	2.8
	409638	AW450420	Hs.21335	ESTs	15.0	3.5
35	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	14.9	7.1
	416737	AF154335	Hs.79691	LJM domain protein	14.8	5.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	14.7	4.2
	436870	AW204219	Hs.43679	ESTs	14.6	3.0
	443181	AI039201	Hs.54548	ESTs	14.6	2.6
40	436281	AW411194	Hs.120051	ESTs	14.6	3.5
	449448	D60730	Hs.57471	ESTs	14.5	8.5
	422564	AI148006	Hs.222120	ESTs	14.4	4.8
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	14.4	14.4
	428748	AW593206	Hs.98785	ESTs	14.3	2.4
45	452576	AB023177	Hs.29900	KIAA0960 protein	14.2	14.2
	452461	N78223	Hs.108106	transcription factor	14.1	8.1
	449670	F07693	Hs.23869	Homo sapiens mRNA; cDNA DKFp434K2172 (f	14.1	12.8
	436637	AI783629	Hs.26766	ESTs	14.1	14.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	14.0	2.3
50	419078	M93119	Hs.89584	insulinoma-associated 1	13.9	13.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	13.9	2.9
	452355	N54926	Hs.29202	G protein-coupled receptor 34	13.9	4.1
	421452	AI925946	Hs.104530	fetal hypothetical protein	13.9	13.9
	430290	AI734110	Hs.136355	ESTs	13.9	13.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	13.8	13.8
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	13.6	13.6
	416795	AI497778	Hs.168053	ESTs, Highly similar to AF227948 1 HBV p	13.5	13.5
	422025	BE348774	Hs.122554	ESTs	13.5	13.5
	400992				13.3	13.3
60	413174	AA723564	Hs.191343	ESTs	13.3	5.5
	425187	AW014486	Hs.22509	ESTs	13.2	2.5
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	13.1	8.2
	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	13.1	2.7
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	13.0	2.4
65	439519	AA837118	Hs.118366	ESTs	12.9	4.0
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	12.9	7.6
	446657	AI335191	Hs.260702	ESTs, Moderately similar to ALU7_HUMAN A	12.7	3.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.6	12.6
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	12.6	12.6
70	451996	AW514021	Hs.245510	ESTs	12.6	12.6
	400860				12.6	7.0
	439579	AF086400		gb:Homo sapiens full length insert cDNA	12.5	23.1
	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	12.4	12.4
	419948	AB041035	Hs.93847	NADPH oxidase 4	12.4	12.4
75	427304	AA761526	Hs.163853	ESTs	12.4	2.4
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	12.3	12.3
	428137	AA421792	Hs.170999	ESTs	12.2	12.2
	432683	AW995441	Hs.10475	ESTs	12.2	12.2
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	12.2	2.0
80	453884	AA355925	Hs.36232	KIAA0186 gene product	12.1	12.1
	441440	AI807981	Hs.30495	ESTs	12.0	5.2
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	12.0	3.6
	410227	AB009284	Hs.61152	exosmoses (multiple)-like 2	12.0	62.7
	439444	AI277652	Hs.54578	ESTs	11.9	2.9
					11.9	16.5

5	433309	AA807060	Hs.126558	ESTs	11.7	9.0
	439170	AA332355	Hs.165539	ESTs	11.6	9.7
	417160	N76497	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	11.5	7.2
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	11.5	5.8
	410611	AW954134	Hs.20924	KIAA1628 protein	11.5	28.2
	437124	AA554458	Hs.204200	ESTs	11.5	11.5
	418858	AW961605	Hs.21145	Homo sapiens cDNA: FLJ22489 fis, clone H	11.3	11.3
	423600	AI633559	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone H	11.3	2.8
10	429393	AA383024	Hs.201603	ESTs, Highly similar to hypothetical pro	11.3	11.3
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	11.3	3.4
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	11.3	11.7
	431701	AW935490	Hs.14658	ESTs	11.3	2.6
	429399	AA452244	Hs.16727	ESTs	11.2	2.2
15	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	11.2	27.8
	442671	AI005668	Hs.134779	EST	11.1	11.1
	402524				11.1	11.1
	415558	AA885143	Hs.125719	ESTs	11.1	11.1
	422390	AW450893	Hs.121830	ESTs, Weakly similar to KIAA0924 protein	11.0	8.8
20	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	11.0	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	11.0	5.6
	410297	AA148710	Hs.159441	ESTs	11.0	3.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	11.0	11.0
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	10.9	3.3
25	427194	AA399018	Hs.250835	ESTs	10.8	8.0
	432060	AW971364		gb:EST383453 MAGE resequences, MAGL Homo	10.8	10.0
	453861	AI026838	Hs.30120	ESTs	10.8	10.8
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	10.6	3.3
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	10.6	3.4
30	418049	AA211467	Hs.190488	hypothetical protein FLJ10120	10.6	10.6
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.6	27.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	10.5	2.0
	434408	AI031771	Hs.132586	ESTs	10.5	10.5
	451697	AW449774	Hs.257208	ESTs	10.5	6.2
35	435754	AI061288	Hs.133437	ESTs, Moderately similar to gonadotropin	10.3	10.3
	410298	AI693821	Hs.182185	ESTs	10.3	2.9
	412766	BE544475	Hs.54347	ESTs	10.3	10.3
	450689	AI369275	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G	10.3	10.3
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.3	4.5
40	442007	AA301116	Hs.142838	Homo sapiens cDNA: FLJ23444 fis, clone H	10.3	10.3
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	10.2	2.1
	440684	AI253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NEST1	10.1	10.1
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	10.0	10.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	9.9	15.8
45	419972	AL041465	Hs.294038	ESTs, Moderately similar to ALU2_HUMAN A	9.7	23.2
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	9.6	6.5
	434851	AA806164	Hs.116502	ESTs	9.5	6.5
	436306	AA805939	Hs.117927	ESTs	9.5	4.7
	453331	AI240665	Hs.8895	ESTs	9.2	5.8
50	414429	R51494	Hs.71818	ESTs	9.0	6.2
	424998	U58515	Hs.154138	chitinase 3-like 2	8.9	18.1
	446936	H10207	Hs.47314	ESTs	8.9	3.6
	410276	AI554545	Hs.68301	ESTs	8.8	3.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	8.8	3.8
55	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	8.8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	8.7	3.0
	441079	AW150697	Hs.107418	ESTs	8.7	2.2
	437517	AI927675	Hs.99858	ribosomal protein L7a	8.6	4.5
	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	8.6	12.2
60	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434C0921 (f	8.6	10.4
	409260	AW242407	Hs.18479	ESTs	8.5	11.6
	442343	AA992480	Hs.129874	ESTs	8.4	4.6
	416439	AA180363	Hs.118769	ESTs	8.4	7.2
	428054	AI948688	Hs.266619	ESTs	8.2	9.2
65	421633	AF121860	Hs.106260	sorting nexin 10	8.2	2.6
	433285	AW975944	Hs.237396	ESTs	8.1	3.3
	433226	AW503733	Hs.9414	KIAA1488 protein	8.0	13.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	8.0	2.5
	425681	AB018297	Hs.159183	KIAA0754 protein	7.9	4.8
70	445034	AW293376	Hs.160323	ESTs	7.9	3.7
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	7.6	6.4
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5	7.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.5	3.9
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.5	2.2
75	439864	AI720078	Hs.291997	ESTs	7.4	6.9
	419723	AL120193	Hs.92614	Homo sapiens growth differentiation fact	7.4	3.5
	447896	AI436124	Hs.294069	ESTs, Weakly similar to ORF2 contains a	7.3	22.1
	404210				7.3	40.8
	436671	AW137159	Hs.146151	ESTs	7.2	11.8
	439231	AW581935	Hs.141480	ESTs	7.2	2.5
80	418030	BE207573	Hs.83321	neuromedin B	7.1	6.4
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	7.0	6.7
	423869	BE409301	Hs.134012	C1q-related factor	7.0	4.9
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4

	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	6.9	8.6
	428500	AW863261	Hs.15036	ESTs, Highly similar to AF161358.1 HSPC0	6.9	7.7
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	6.9	3.1
	402604				6.8	7.0
5	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.8	2.5
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	6.8	2.9
	433577	AW007080	Hs.8817	ESTs	6.6	2.6
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	6.6	13.9
	413886	AW958264	Hs.103832	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6	2.2
10	451460	AI797550	Hs.209652	ESTs	6.5	13.7
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	6.5	15.6
	437273	AL137451	Hs.120873	ESTs, Highly similar to hypothetical pro	6.5	2.4
	418365	AW014345	Hs.161690	ESTs	6.4	12.8
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.4	4.3
15	449458	AI805078	Hs.208261	ESTs	6.4	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	6.3	13.2
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	6.3	10.9
	417709	D87434	Hs.82426	KIAA0247 gene product	6.3	23.3
	448499	BE613280	Hs.250655	prothymosin, alpha (gene sequence 28)	6.2	2.9
20	444880	AW118683	Hs.154150	ESTs	6.2	19.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	6.2	12.7
	444864	AW965446	Hs.46637	ESTs, Weakly similar to cDNA EST yk289g5	6.2	4.1
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	6.2	3.4
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	6.1	2.6
25	424232	AB015982	Hs.143460	protein kinase C, nu	6.1	14.6
	436443	AW138211	Hs.128746	ESTs	6.1	2.8
	433647	AA603367	Hs.222294	ESTs	6.1	15.0
	449961	AW265634	Hs.133100	ESTs	6.1	3.4
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	6.1	6.1
30	408393	AW015318	Hs.23165	ESTs	6.1	21.6
	450693	AW450461	Hs.203965	ESTs	6.1	2.2
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	6.0	2.4
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.0	10.9
	440650	R44692	Hs.6640	ESTs	6.0	2.1
35	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	6.0	2.4
	411083	N41340	Hs.68318	hypothetical protein FLJ20344	6.0	3.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.0	6.0
	402855				6.0	2.6
40	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.0	11.6
	418791	AA935633	Hs.194628	ESTs	5.9	6.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	5.9	2.3
	435677	AA694142	Hs.293726	ESTs	5.9	11.8
	430334	AI824719	Hs.47557	ESTs	5.9	7.5
	452834	AI639627	Hs.105685	ESTs	5.9	2.6
45	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	5.8	3.1
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	5.8	2.0
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	5.8	2.5
	417115	AW952792	Hs.1066	small nuclear ribonucleoprotein polypept	5.8	16.0
	436758	AW977167	Hs.155272	ESTs	5.8	3.8
50	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	5.7	5.1
	423943	AF163570	Hs.135756	polymerase (DNA-directed) kappa	5.7	11.1
	428180	AI129767	Hs.182874	Homo sapiens cDNA: FLJ21929 fis, clone H	5.6	7.1
	424343	AW956360	Hs.4748	ESTs, Highly similar to JN0902 pituitary	5.6	2.2
	417318	AW953937	Hs.12891	ESTs	5.6	25.0
55	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	5.6	4.1
	427472	AA522539	Hs.131250	transposon-derived Busler3 transposase-I	5.4	3.5
	434701	AA460479	Hs.4096	KIAA0742 protein	5.4	21.2
	430147	R60704	Hs.234434	hair/enhancer-of-split related with YRP	5.3	2.7
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	5.3	4.1
60	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	5.3	2.4
	424028	AF055084	Hs.153692	KIAA0686 protein	5.3	2.7
	444534	AW271626	Hs.42294	ESTs	5.3	2.1
	426171	AI128606	Hs.301454	ESTs	5.2	3.8
65	431843	AA516420	Hs.183526	ESTs	5.2	6.2
	438204	AI589645	Hs.128690	ESTs	5.2	5.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	5.2	8.4
	436223	AK001884	Hs.23799	ESTs	5.2	2.4
	450649	NM_001429	Hs.297722	Human DNA sequence from clone RP1-85F18	5.2	15.3
70	441689	AI123705	Hs.106932	ESTs	5.2	2.2
	443392	AI055821	Hs.293420	ESTs	5.1	3.3
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	5.1	16.7
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	5.1	18.7
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.0	2.4
75	458435	AI18718	Hs.144121	ESTs, Weakly similar to dJ37E16.2 fLsap	5.0	3.9
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	5.0	2.8
	452040	AW973242	Hs.293690	ESTs	5.0	4.5
	404029				5.0	4.3
	421141	AW117261	Hs.125914	ESTs	5.0	2.1
80	402605				4.9	4.2
	435839	AF249744	Hs.25961	Rho guanine nucleotide exchange factor (4.9	2.5
	416404	AA180138	Hs.107924	ESTs	4.9	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	4.9	7.2
	448425	AI500359	Hs.233401	ESTs	4.9	4.9

	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.9	2.9
	448451	AW015994		gb:U1-H-B10p-abh-g-09-0-U1.s1 NC_CGAP_S	4.9	2.2
	444838	AV651680	Hs.208558	ESTs	4.8	6.7
5	452438	BE514230	Hs.29595	JM4 protein	4.8	2.7
	443898	AW804296	Hs.9950	Sec61 gamma	4.8	7.2
	452776	AA194540	Hs.13522	ESTs	4.8	3.4
	426108	AA622037	Hs.166468	programmed cell death 5	4.8	16.7
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.8	3.2
10	427704	AW971063	Hs.292882	ESTs	4.8	23.8
	433588	AI056872	Hs.133366	ESTs	4.8	12.8
	410108	AA081659	Hs.191098	KIAA1479 protein	4.7	2.1
	433556	W56321	Hs.111460	Homo sapiens cDNA: FLJ21715 fis, clone C	4.7	11.2
	418962	AA714835	Hs.271863	ESTs	4.7	2.2
	404049				4.7	3.0
15	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fs, clone HE	4.7	3.3
	425234	AW152225	Hs.165909	ESTs	4.7	3.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	4.7	9.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	4.7	2.7
20	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.6	6.7
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	4.6	13.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.6	18.4
	422488	AI679968	Hs.152060	ESTs	4.6	7.7
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	4.6	4.6
25	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT	4.5	11.9
	442495	AI184717		gb:qd64b01.x1 Soares_testis_NHT Homo sap	4.5	4.5
	403549				4.5	11.6
	456209	W06033	Hs.297792	ESTs	4.5	5.1
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhotobin-like 1)	4.5	10.6
30	439566	AF086387		gb:Homo sapiens full length insert cDNA	4.4	2.6
	446329	NM_013272	Hs.14805	solute carrier family 21 (organic anion	4.4	17.2
	446488	AB037782	Hs.15119	KIAA1361 protein	4.4	8.4
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	4.4	2.5
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	4.4	14.3
	424340	AA339036	Hs.7033	ESTs	4.4	3.9
35	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.3	31.1
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	4.3	6.1
	434476	AW858520	Hs.271825	ESTs	4.3	4.5
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	4.3	3.6
40	419904	AA974411	Hs.18672	ESTs	4.3	17.1
	407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	4.3	9.0
	425836	AW955696	Hs.94842	ESTs	4.3	3.2
	426304	AA374532	Hs.297985	ESTs	4.3	6.6
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	4.3	2.3
45	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.3	2.5
	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	4.2	4.1
	409509	AL036923	Hs.127006	ESTs	4.2	16.4
	424391	BE550112	Hs.112712	ESTs	4.2	3.8
	425248	AW957442	Hs.252766	ESTs	4.2	11.1
50	418259	AA215404	Hs.137289	ESTs	4.2	19.3
	445525	BE149866	Hs.14831	ESTs	4.2	3.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.2	34.8
	430935	AW072916	Hs.115654	ESTs	4.2	3.0
	442233	AW967149	Hs.28439	ESTs, Weakly similar to ORF2 [M.musculus	4.2	2.4
55	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	4.1	15.3
	437097	N45312	Hs.46506	ESTs	4.1	15.6
	428189	AA424030	Hs.46627	ESTs	4.1	3.6
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.1	12.2
	425500	AB011541	Hs.158200	EGF-like-domain, multiple 4	4.1	2.8
60	435177	AI018174	Hs.42936	ESTs	4.1	2.1
	418357	Z44718	Hs.301010	ESTs, Highly similar to AF159851 1 Rho G	4.1	4.1
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	4.1	4.1
	436557	W15573	Hs.5027	ESTs	4.0	2.1
	425588	F07396	Hs.46751	ESTs	4.0	2.2
65	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.0	3.6
	437095	D14661	Hs.119	Wilms' tumour 1-associated protein	4.0	10.0
	425332	AA633306	Hs.127279	ESTs	4.0	10.9
	431556	AF016028	Hs.260039	sarcospan (Kras oncogene-associated gene	4.0	3.8
	427209	H06509	Hs.92423	KIAA1566 protein	4.0	3.1
70	435468	AW362803	Hs.166271	ESTs	4.0	2.2
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.0	2.6
	440483	AI200836	Hs.150386	ESTs	4.0	2.5
	444821	AA053564	Hs.12040	STE20-like kinase	4.0	10.4
	433873	AW156913	Hs.150478	ESTs, Weakly similar to KIAA0987 protein	4.0	2.3
75	420028	AB014680	Hs.8786	carbohydrate (chondroitin 6/keratan) sul	3.9	2.8
	445706	AW807631	Hs.190488	hypothetical protein FLJ10120	3.9	3.8
	424530	AI632083	Hs.28511	ESTs	3.9	2.2
	446851	AW007332	Hs.16261	Homo sapiens cDNA: FLJ22063 fis, clone H	3.9	16.0
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	3.9	4.5
	409456	U34962	Hs.54473	cardiac-specific homeo box	3.9	8.0
80	420439	AW270041	Hs.193053	eukaryotic translation initiation factor	3.9	7.9
	447340	AW961327	Hs.280833	ESTs	3.9	2.1
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.9	2.5
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.9	4.6

	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.9	4.0
	410079	U94362	Hs.58589	glycogenin 2	3.9	18.3
	426818	AA554827	Hs.124841	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.9	3.0
5	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.8	4.0
	427228	AA115770	Hs.174051	small nuclear ribonucleoprotein 70kD pol	3.8	7.9
	443801	AW206942	Hs.253594	ESTs	3.8	3.4
	450746	D82673	Hs.169921	general transcription factor II, i, pseu	3.8	2.2
	443837	A1984625	Hs.9884	spindle pole body protein	3.8	6.5
10	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	3.8	2.2
	426757	AW205640	Hs.158206	ESTs	3.7	3.1
	443101	A1268936	Hs.129872	sperm surface protein	3.7	2.4
	440118	AB040893	Hs.6968	KIAA1460 protein	3.7	3.5
	410612	AW502698	Hs.118152	ESTs	3.7	22.5
15	435869	AF255910	Hs.54650	vascular endothelial junction-associated	3.7	4.2
	433208	AW002834	Hs.24095	ESTs	3.7	16.0
	432357	AA452506	Hs.274412	similar to yeast Upt3, variant A	3.7	2.6
	413916	N49813	Hs.75615	apolipoprotein C-II	3.7	5.4
	429766	AA612710	Hs.146140	ESTs	3.7	3.2
20	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.7	6.4
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.7	10.7
	420361	N92054	Hs.206910	ESTs	3.7	18.7
	408819	AW163483	Hs.48320	DKFZP566B1346 protein	3.7	8.8
	411960	R77776	Hs.18103	ESTs	3.7	2.3
25	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	3.7	2.2
	440145	AW021433	Hs.250863	ESTs	3.7	3.8
	453740	AL120295		gb:DKFZp761M067_s1 761 (synonym: hamy2)	3.6	3.0
	440975	AW499914	Hs.7579	hypothetical protein FLJ10402	3.6	2.0
	443135	A1376331	Hs.156103	ESTs	3.6	12.4
30	419687	A1638859	Hs.227699	ESTs, Weakly similar to Yhr217cp [S.cere	3.6	2.7
	451029	AA852097	Hs.25829	ras-related protein	3.6	2.9
	414512	AL044336	Hs.6831	golgi resident protein GCP60	3.6	10.5
	410853	H04588	Hs.30469	ESTs	3.6	23.9
	419900	A1469960	Hs.170698	ESTs	3.6	3.6
35	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.6	7.5
	428290	A1932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	3.6	9.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	3.6	4.9
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.6	2.1
	441269	AW015206	Hs.178784	ESTs	3.6	2.8
40	447961	W32791	Hs.170405	ESTs	3.5	4.6
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.5	2.1
	437580	AA761075	Hs.293567	ESTs	3.5	3.5
	447710	A1420523	Hs.161282	ESTs	3.5	3.5
	436446	AW016809	Hs.119021	ESTs	3.5	2.2
45	448412	A1219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.5	4.1
	409712	AA167385	Hs.13583	ESTs	3.5	3.8
	404048				3.5	3.2
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	3.5	10.6
50	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.5	3.8
	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 [fr	3.5	32.2
	436252	A1539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	3.5	4.6
	433954	AA610649		gb:np95c03.s1 NCI_CGAP_Thy1 Homo sapiens	3.5	3.5
	408495	W68796	Hs.237731	ESTs	3.5	6.1
55	418801	AA228366	Hs.115122	ESTs	3.5	5.1
	422493	AW474183	Hs.233816	ESTs	3.5	15.2
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	3.5	2.4
	414591	A1888490	Hs.55902	ESTs	3.5	8.3
60	439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone H	3.5	30.2
	444969	AL203334	Hs.160628	ESTs	3.5	3.1
	435370	A1964074	Hs.225838	ESTs	3.5	3.0
	443228	W24781	Hs.293798	ESTs	3.4	4.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	3.4	5.0
	437410	AW023340	Hs.14880	ESTs	3.4	2.7
65	444172	BE147740	Hs.104558	ESTs	3.4	12.9
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.4	2.8
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.4	4.0
	428776	AW016636	Hs.155647	ESTs, Highly similar to R29144 1 [H.sapi	3.4	2.5
	409493	AA386192	Hs.193482	ESTs	3.4	3.4
70	432559	AW452948	Hs.257631	ESTs	3.4	6.3
	451455	A1937227	Hs.8821	liver-expressed antimicrobial peptide	3.4	6.1
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.4	2.6
	422872	BE326786	Hs.187646	ESTs	3.4	2.2
	414761	AL077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.4	2.6
75	416131	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	3.4	9.5
	408576	NM_003542	Hs.46423	H4 histone family, member G	3.4	3.4
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	3.4	21.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.4	2.1
	422573	AW297985	Hs.28777	H2A histone family, member L	3.4	3.7
80	436865	AW880358	Hs.190488	hypothetical protein FLJ10120	3.4	7.6
	442091	AW770493	Hs.195904	guanine nucleotide binding protein (G pr	3.4	2.9
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.4	5.5
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.4	3.9
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.4	16.8

5	447279	AA325308	Hs.18016	Homo sapiens mRNA; cDNA DKFZp586H0324 (f	3.3	3.0
	410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver,	3.3	5.8
	447272	NM_014827	Hs.17969	KIAA0863 gene product	3.3	13.4
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	3.3	2.3
	435354	AA678267	Hs.117115	ESTs	3.3	5.5
10	443884	N20617	Hs.226527	leptin receptor	3.3	8.6
	444984	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	3.3	2.0
	431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	2.4
	424682	AW604804	Hs.151717	KIAA0437 protein	3.3	13.7
	457972	AI419060	Hs.47448	ESTs	3.3	4.2
15	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	3.3	3.2
	438666	AW014493	Hs.126727	ESTs	3.3	10.8
	447796	AW953622	Hs.223025	RAB31, member RAS oncogene family	3.3	4.2
	426751	W92744	Hs.22664	ESTs	3.3	2.6
	436251	BE515065	Hs.5092	nucleolar protein (KKE/D repeat)	3.3	3.9
20	452688	AA721140	Hs.49930	ESTs, Weakly similar to B34087 hypopheti	3.3	4.9
	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316	3.3	4.2
	424090	X99699	Hs.139262	XIAP associated factor-1	3.3	2.9
	434987	AW975114	Hs.293273	ESTs	3.3	2.2
	428542	NM_014899	Hs.188006	KIAA0878 protein	3.3	5.7
25	420372	AW960049	Hs.293660	ESTs, Weakly similar to A49618 probable	3.3	5.5
	422224	NM_013982	Hs.113264	neuregulin 2	3.2	3.0
	432482	L19267	Hs.275924	dystrophin myotonia-containing WD repea	3.2	2.7
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.2	2.0
	428418	AI368826	Hs.30654	ESTs	3.2	2.4
30	416728	AB024597	Hs.79558	casein kinase 1, epsilon	3.2	2.8
	416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	3.2	2.2
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	3.2	4.3
	431387	AI878854	Hs.252229	v-maf musculoaponeurotic fibrosarcoma (a	3.2	2.8
	404171				3.2	35.8
35	435575	AF213457	Hs.44234	liggering receptor expressed on myeloid	3.2	2.6
	426421	AW367884	Hs.169832	zinc finger protein 42 (myeloid-specific	3.2	3.8
	445070	NM_000677	Hs.258	adenosine A3 receptor	3.2	7.6
	407047	X65965		gb.H.sapiens SOD-2 gene for manganese su	3.2	82.0
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	3.2	2.2
40	430890	X54232	Hs.2699	glypican 1	3.2	4.3
	439807	AA376417	Hs.173501	Homo sapiens mRNA for FLJ00008 protein,	3.2	2.3
	430412	AW341754	Hs.189305	ESTs	3.2	2.0
	442807	AL049274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (fr	3.2	2.7
	420253	AI656055	Hs.96200	neighbor of A-kinase anchoring protein 9	3.2	2.9
45	436042	AF284422	Hs.119178	cation-chloride cotransporter-interactin	3.2	4.6
	423422	AC005175	Hs.128425	NY-REN-24 antigen	3.2	4.0
	413020	R98736		gb:yr31h09.r1 Soares fetal liver spleen	3.2	4.1
	452877	AI250789	Hs.32478	ESTs	3.2	4.0
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.1	9.0
50	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.1	2.0
	450219	AI826999	Hs.224624	ESTs	3.1	23.7
	434256	AI378817	Hs.191847	ESTs	3.1	3.4
	421407	T82331	Hs.127453	ESTs	3.1	3.9
	451198	AW964541	Hs.11500	Homo sapiens cDNA: FLJ21127 fis, clone C	3.1	3.9
55	445664	AW968638	Hs.237691	ESTs	3.1	7.9
	411089	AA456454	Hs.118637	Homo sapiens cDNA FLJ13365 fis, clone PL	3.1	6.0
	458050	AA834708		gb:od99d04.s1 NCI_CGAP_Ov2 Homo sapiens	3.1	4.4
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	3.1	2.7
	417270	AA429615	Hs.98593	Homo sapiens cDNA: FLJ23233 fis, clone C	3.1	2.4
60	427951	AI826125	Hs.43546	ESTs	3.1	2.3
	443693	AI344782	Hs.9683	protein-kinase, interferon-inducible dou	3.1	7.2
	413367	NM_006517	Hs.75317	solute carrier family 16 (monocarboxylic	3.1	2.6
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	3.1	6.5
	447752	M73700	Hs.347	lactotransferrin	3.1	19.4
65	408949	AF189011	Hs.49163	putative ribonuclease III	3.1	3.7
	418039	R06859	Hs.193172	ESTs	3.1	3.8
	447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	3.1	2.2
	424441	X14850	Hs.147097	H2A histone family, member X	3.1	3.2
	435163	AA668884	Hs.19155	ESTs	3.1	2.1
70	428712	AW085131	Hs.190452	KIAA0365 gene product	3.1	2.7
	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	3.1	14.3
	428147	AW629985	Hs.234983	ESTs	3.1	2.7
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	3.1	2.5
	422170	AI791949	Hs.112432	anti-Mullerian hormone	3.1	8.1
75	448801	N57423	Hs.179898	HSPC055 protein	3.0	2.0
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	3.0	18.3
	431562	AI884334	Hs.11637	ESTs	3.0	3.9
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.0	3.0
	458962	NM_005859	Hs.25180	purine-rich element binding protein A	3.0	3.0
80	436277	R86520	Hs.120917	ESTs	3.0	2.7
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.0	3.0
	447471	AF039843	Hs.18576	sprouty (Drosophila) homolog 2	3.0	4.1
	442554	AW467376	Hs.129640	ESTs	3.0	4.7
	441466	AW673081	Hs.54828	ESTs	3.0	3.0
	420297	AI628272	Hs.88323	ESTs	3.0	8.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.0	18.7
	453405	AI567972	Hs.49919	ESTs	3.0	9.6

	434521	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)		
	447948	AI620923	Hs.46579	ESTs	3.0	9.3
	445756	AA290690	Hs.288493	ESTs	3.0	10.1
5	413243	AA769266	Hs.193657	ESTs	3.0	3.5
	422845	AA317841	Hs.301838	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0	5.9
	419409	AW237831	Hs.143792	ESTs	3.0	2.2
	446441	AK001782	Hs.15093	hypothetical protein	3.0	2.1
	427150	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate	3.0	2.1
10	421043	BE379455	Hs.89072	ESTs	3.0	4.1
	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.0	3.0
	433312	AI241331	Hs.131765	ESTs	3.0	4.1
	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.0	11.0
	414702	L22005	Hs.76932	cell division cycle 34	3.0	6.0
15	428673	AW601325	Hs.274472	high-mobility group (nonhistone chromoso	3.0	3.3
	422676	D28481	Hs.1570	histamine receptor H1	3.0	15.8
	451693	BE220445	Hs.279635	ESTs	3.0	2.1
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.0	2.3
	424005	AB033041	Hs.137507	KIAA1215 protein	3.0	10.5
20	440769	BE561793		gb:601346842F1 NIH_MGC_8 Homo sapiens cD	3.0	3.9
	428832	AA578229		gb:ml22b12s1 NCI_CGAP_HSC1 Homo sapiens	3.0	5.1
	430293	AI416988	Hs.238272	inositol 1,4,5-triphosphate receptor, ty	3.0	2.3
	450883	NM_001348	Hs.25619	death-associated protein kinase 3	3.0	6.3
	407879	AA045464	Hs.6557	ESTs	3.0	5.6
25	426167	AF039023	Hs.167496	Homo sapiens cDNA FLJ11120 fis, clone PL	2.9	7.0
	435281	AB020699	Hs.4864	KIAA0892 protein	2.9	2.6
	432339	AW411259	Hs.25945	ESTs	2.9	3.9
	440524	R71264	Hs.16798	ESTs	2.9	2.9
	408083	BE383668	Hs.42484	hypothetical protein FLJ10618	2.9	9.7
30	427729	AB033100	Hs.300646	Homo sapiens cDNA FLJ11744 fis, clone HE	2.9	4.4
	422072	AB018255	Hs.111138	KIAA0712 gene product	2.9	3.1
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.9	2.9
	440100	BE382685	Hs.158549	ESTs	2.9	3.6
35	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	2.9	3.6
	428005	AW302245	Hs.181390	casein kinase 1, gamma 2	2.9	13.9
	403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	2.9	3.7
	419175	AW270037	Hs.179507	KIAA0779 protein	2.9	5.8
	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog)	2.9	2.3
40	413922	AI535895	Hs.221024	ESTs	2.9	2.3
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	2.9	2.8
	441789	D52059	Hs.7972	KIAA0871 protein	2.9	3.3
	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	2.9	2.1
	448560	BE613183	Hs.23213	ESTs	2.9	2.8
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9	3.0
45	434946	AW295389	Hs.119768	ESTs	2.9	3.3
	408146	R45821	Hs.81057	ESTs, Moderately similar to CL3BC [R,nor	2.9	5.1
	446644	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (up	2.9	2.8
	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	2.9	8.5
	433017	Y15067	Hs.279914	zinc finger protein 232	2.9	2.2
50	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	2.9	4.5
	444706	AK000398	Hs.11747	hypothetical protein FLJ20391	2.9	3.6
	407925	BE002320	Hs.287864	Homo sapiens cDNA FLJ14030 fis, clone HE	2.9	2.1
	431730	AF208856	Hs.268122	hypothetical protein	2.9	2.5
	447118	AB014599	Hs.17411	KIAA0699 protein	2.8	2.1
55	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.8	7.4
	425227	H84455	Hs.40639	ESTs	2.8	2.3
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.8	76.2
	421465	AK001020	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	2.8	6.1
60	409095	AW337272	Hs.293656	ESTs	2.8	34.0
	424066	Z98348	Hs.112461	ESTs	2.8	2.1
	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	2.8	11.9
	414079	H19184	Hs.205230	ESTs	2.8	2.1
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.8	3.9
	438890	AA827756	Hs.135049	ESTs	2.8	4.9
65	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble	2.8	5.2
	458367	AA088470	Hs.83135	p53-responsive gene 6	2.8	4.4
	412014	AI620650	Hs.43761	ESTs	2.8	4.8
	428727	AF078847	Hs.191356	general transcription factor IIIH, polype	2.8	6.7
	447942	F12628	Hs.155470	zinc finger protein 38 (KOX 25)	2.8	2.2
70	426432	AF001601	Hs.169857	paraoxonase 2	2.8	3.5
	439189	AI951185	Hs.144630	nuclear receptor subfamily 2, group F, m	2.8	2.5
	446756	AW028485	Hs.26136	ESTs	2.8	4.1
	432148	AW504912	Hs.81907	ESTs, Moderately similar to ALU4_HUMAN A	2.8	2.6
	405649				2.8	3.8
75	414473	BE302693		gb:ba74c02.y1 NIH_MGC_20 Homo sapiens cD	2.8	2.4
	443839	AW139834	Hs.143321	ESTs	2.8	2.1
	448804	AW512213	Hs.42500	ADP-ribosylation factor-like 5	2.8	2.7
	426825	AL133415	Hs.2064	vimentin	2.8	25.0
	417528	H47315	Hs.27519	ESTs	2.8	11.6
80	453657	W23237	Hs.296162	ESTs	2.8	3.2
	432714	Y12059	Hs.278675	bromodomain-containing 4	2.8	6.7
	441072	AW275480	Hs.39504	ESTs	2.7	2.7
	441297	AW403084	Hs.7765	ubiquitin-conjugating enzyme E2E 1 (homo	2.7	2.2
	443849	BE566066	Hs.9893	ASB-3 protein	2.7	3.0

	406243	Y00787	Hs.624	interleukin 8	2.7	3.8
	446243	BE296396	Hs.14512	Homo sapiens cDNA FLJ11761 fis, clone HE	2.7	3.3
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	2.7	3.0
5	433944	AL117518	Hs.3586	KIAA0978 protein	2.7	3.1
	411400	AA311919	Hs.69851	GAR1 protein	2.7	16.0
	436840	AW450376	Hs.130803	ESTs, Highly similar to T00367 hypotheti	2.7	4.1
	428281	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	2.7	3.2
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.7	2.0
10	408320	AI125867	Hs.20734	ESTs	2.7	4.7
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.7	2.2
	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	2.7	4.7
	408912	AB011084	Hs.48924	KIAA0512 gene product	2.7	2.1
	419304	AI271326	Hs.146101	ESTs	2.7	3.4
15	415045	AA321559	Hs.38270	Homo sapiens cDNA: FLJ20984 fis, clone C	2.7	2.3
	441872	BE567100	Hs.154938	hypothetical protein MDS025	2.7	2.3
	422343	AI628633		gb:U77005.x1 NCL CGAP_Kid11 Homo sapien	2.7	2.5
	415539	AI733881	Hs.72472	ESTs	2.7	2.7
	443823	BE089782	Hs.9877	hypothetical protein	2.7	4.7
	419881	AA329340	Hs.44649	ESTs	2.7	3.3
20	429155	BE242291	Hs.197540	hypoxia-inducible factor 1, alpha subuni	2.7	5.5
	431319	AA873350		gb:oh64h02.s1 NCL CGAP_Kid5 Homo sapiens	2.7	65.9
	430219	X99209	Hs.235887	HMT1 (hnRNP methyltransferase, S. cerevi	2.7	3.1
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.7	5.2
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.7	10.7
25	431747	AW979134	Hs.10700	hypothetical protein	2.7	2.9
	408085	N25929	Hs.42500	ADP-ribosylation factor-like 5	2.7	7.8
	426218	AF119043	Hs.168005	transcriptional intermediary factor 1 ga	2.7	4.5
	434845	BE267057	Hs.4200	hypothetical protein R32184_1	2.7	4.6
	451644	N23235	Hs.30567	ESTs	2.7	2.3
30	428408	W74437	Hs.188757	Homo sapiens mRNA; cDNA DKFZp564M113 (fr	2.7	5.7
	446627	AI973016	Hs.15725	hypothetical protein SBB148	2.7	2.9
	450167	AA446404	Hs.24563	NTF2-related export protein 1	2.7	9.9
	408821	AL050385	Hs.48332	NIMA (never in mitosis gene a)-related k	2.7	2.1
	452068	W76412	Hs.57877	ESTs	2.7	2.1
35	431129	AL137751	Hs.263571	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	2.7	6.2
	429025	AI399910	Hs.4842	ESTs	2.7	2.9
	421114	AW975051	Hs.293156	ESTs	2.7	8.8
	428755	D87454	Hs.192966	KIAA0265 protein	2.7	3.0
40	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.7	5.7
	414283	AW960011	Hs.154993	ESTs	2.7	5.9
	425262	D87119	Hs.155418	GS3955 protein	2.7	3.7
	447726	AL137638	Hs.19368	Homo sapiens mRNA; cDNA DKFZp434J065 (fr	2.7	14.3
	424623	AW963062	Hs.165809	ESTs	2.7	5.6
45	444772	AW450800	Hs.176859	ESTs	2.7	2.7
	428419	U49436	Hs.286236	eukaryotic translation initiation factor	2.7	4.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.7	4.5
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3	2.6	5.1
	447720	AL038765	Hs.161304	ESTs	2.6	3.2
50	419708	AK000753	Hs.92374	hypothetical protein	2.6	3.0
	445502	AW379160	Hs.12813	DKFZP434J214 protein	2.6	5.0
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.6	2.9
	444147	AB002306	Hs.10351	KIAA0308 protein	2.6	6.8
	433193	AB040881	Hs.32580	Homo sapiens cDNA FLJ13122 fis, clone NT	2.6	3.2
55	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	2.6	3.9
	450309	W61348	Hs.4864	KIAA0892 protein	2.6	3.8
	422092	AB007883	Hs.111373	KIAA0423 protein	2.6	2.3
	424118	BE269041	Hs.140452	cargo selection protein (mannose 6 phosp	2.6	5.5
	407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.6	2.9
60	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	2.6	3.2
	442878	AI868648	Hs.22315	ESTs	2.6	4.7
	448771	BE315511	Hs.296244	SNARE protein	2.6	5.0
	416611	AA568308	Hs.192789	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6	7.7
	409348	AI401535	Hs.146090	ESTs	2.6	3.5
	439349	AI660898	Hs.195602	ESTs	2.6	3.2
65	428433	AA521410	Hs.41371	ESTs	2.6	7.9
	436565	BE547674	Hs.204169	ESTs	2.6	3.0
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.6	2.6
	429362	T25833	Hs.200478	ubiquitin-conjugating enzyme E2M (homolo	2.6	2.3
70	459035	AW291109	Hs.208787	ESTs	2.6	2.6
	451814	AA847992	Hs.137003	ESTs	2.6	19.1
	452331	AA598509	Hs.29117	H.sapiens mRNA for pur alpha extended 3'	2.6	2.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	2.6	2.1
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (f	2.6	4.9
75	423699	H41850	Hs.131846	PCAF associated factor 65 alpha	2.6	3.7
	441226	BE563042	Hs.118820	ESTs	2.6	2.5
	444940	AK002148	Hs.12151	hypothetical protein FLJ11286	2.6	3.4
	448731	AI522273	Hs.42640	ESTs	2.6	3.2
	424250	AF073310	Hs.143648	insulin receptor substrate 2	2.6	2.5
80	433468	AA832055	Hs.232217	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6	3.3
	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	2.6	4.6
	441364	AW450466	Hs.126830	ESTs	2.6	2.6
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	2.5	2.7
	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	2.5	2.5

	408392	U28831	Hs.44566	KIAA1641 protein	2.5	25.4
	432426	AW973152	Hs.31050	ESTs	2.5	10.0
	436623	AI417073	Hs.107265	ESTs	2.5	2.1
5	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.5	2.6
	410582	AW867197	Hs.14562	Homo sapiens cDNA: FLJ21616 fis, clone C	2.5	3.7
	441328	AI982794	Hs.159473	ESTs	2.5	9.2
	453983	H94997	Hs.16450	ESTs	2.5	26.1
	438826	R26709	Hs.10095	hypothetical protein from EUROIMAGE 1669	2.5	2.3
10	427899	AA829286	Hs.181062	serum amyloid A1	2.5	20.3
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	2.5	3.5
	458933	AI638429	Hs.24763	RAN binding protein 1	2.5	3.5
	444871	U46386	Hs.12102	sorting nexin 3	2.5	2.3
	411329	AL360265	Hs.69554	hypothetical protein FLJ20552	2.5	2.9
15	424074	AI902456	Hs.210761	ESTs	2.5	4.0
	438988	H30039	Hs.107674	ESTs	2.5	2.7
	412836	AA121384	Hs.191446	ESTs	2.5	5.7
	430189	AI298841	Hs.135133	ESTs, Weakly similar to ORF YNL310c [S.c	2.5	3.0
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.5	13.4
20	416926	H03109	Hs.108920	HT018 protein	2.5	2.8
	451429	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5	3.9
	416388	AI417358	Hs.73677	ESTs	2.5	4.2
	421561	Z45399	Hs.105779	protein inhibitor of activated STAT prot	2.5	7.5
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	2.5	2.6
25	416273	AW575691	Hs.79123	KIAA0084 protein	2.5	2.6
	427149	H94688	Hs.173737	ras-related C3 botulinum toxin substrate	2.5	2.6
	453041	AI680737	Hs.289068	transcription factor 4	2.5	2.2
	446899	NM_005397	Hs.16426	podocalyxin-like	2.5	4.7
	447301	AW958124	Hs.142442	HP1-BP74	2.5	3.2
30	447769	AW873704	Hs.48764	ESTs	2.5	2.4
	447754	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 fis, clone MA	2.5	2.5
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.5	23.6
	440903	AI468079	Hs.126623	ESTs	2.5	2.3
	432353	NM_016558	Hs.274411	SCAN domain-containing 1	2.5	4.1
35	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.5	2.5
	411373	BE326276	Hs.8861	ESTs	2.5	3.9
	452402	AI138530	Hs.22216	peroxisome proliferative activated recep	2.5	2.4
	429998	AI458063	Hs.57841	ESTs	2.5	2.6
	421772	Z24958	Hs.108139	zinc finger protein 212	2.5	3.7
40	442573	H93366	Hs.7557	Homo sapiens cDNA: FLJ21962 fis, clone H	2.5	2.1
	444677	AL110212	Hs.9242	purine-rich element binding protein B	2.5	3.4
	441887	AW967865	Hs.92145	ESTs	2.5	3.3
	451031	AI360187	Hs.4254	ESTs	2.5	4.8
	432450	AI990739	Hs.77868	ORF	2.5	2.4
45	415860	D56051	Hs.78888	diazepam binding inhibitor (GABA recepto	2.5	4.8
	439630	AA313607	Hs.58633	Homo sapiens cDNA: FLJ22145 fis, clone H	2.4	2.3
	428607	AB002353	Hs.186840	KIAA0355 gene product	2.4	4.0
	415402	AA164687	Hs.297889	ESTs	2.4	2.5
	446888	AL030996	Hs.16411	hypothetical protein LOC57187	2.4	2.2
50	439208	AK000299	Hs.180952	dynactin p62 subunit	2.4	2.4
	452900	AA626794	Hs.250655	prothymosin, alpha (gene sequence 28)	2.4	3.4
	408657	AA782601	Hs.173328	protein phosphatase 2, regulatory subuni	2.4	3.6
	439143	AI359214	Hs.179260	ESTs	2.4	2.5
	439867	AA847510	Hs.161292	ESTs	2.4	9.3
55	408138	AA535740	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	2.4	5.6
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	2.4	4.2
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.4	2.2
	405268				2.4	3.1
60	439734	AC005013	Hs.149	cAMP response element-binding protein CR	2.4	3.6
	445378	AV653564	Hs.226946	ESTs	2.4	2.4
	454085	D82418	Hs.29626	ESTs, Weakly similar to unknown [D.melan	2.4	22.0
	427354	T57896	Hs.191095	ESTs	2.4	3.6
	452906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibito	2.4	2.2
	450065	AL050107	Hs.301558	DKFZP586I1419 protein	2.4	3.6
65	451091	AA810932	Hs.131899	ESTs, Weakly similar to coded for by C.	2.4	2.7
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	2.4	2.6
	420303	AA258282	Hs.278436	KIAA1474 protein	2.4	2.0
	437068	AA743643	Hs.291427	ESTs	2.4	2.6
	417446	AL118671	Hs.82163	monoamine oxidase B	2.4	4.4
70	421454	AI660389	Hs.286108	chorionic somatomammotropin hormone 1 (p	2.4	3.5
	434943	AI929819	Hs.320	xeroderma pigmentosum, complementation g	2.4	6.4
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	2.4	3.0
	452847	AK000857	Hs.30783	hypothetical protein FLJ20850	2.4	2.1
	422506	R20909	Hs.117816	sorcin	2.4	2.2
75	405204				2.4	4.3
	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (f	2.4	11.7
	442293	AW292634	Hs.150358	ESTs	2.4	2.1
	451484	AV648896	Hs.26461	hypothetical protein	2.4	2.0
	438545	AB032977	Hs.6298	KIAA1151 protein	2.4	2.1
80	442724	AA355525	Hs.159604	cysteinyt-IRNA synthetase	2.4	2.8
	405517				2.4	6.6
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	3.8
	445679	AI343868	Hs.58800	Homo sapiens cDNA FLJ12488 fis, clone NT	2.4	2.3
	408636	BE294925	Hs.46680	CGI-12 protein	2.4	8.1

5	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	2.4	2.4
	422043	AL133649	Hs.110953	Homo sapiens mRNA; cDNA DKFZp434A139 (tr	2.4	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.4	2.6
	442560	AA355042	Hs.228598	ESTs	2.4	4.9
	418126	T91451	Hs.86538	ESTs	2.4	11.7
10	413313	NM_002047	Hs.75280	glycyl-tRNA synthetase	2.4	2.1
	415167	AA160784	Hs.26410	ESTs	2.4	4.4
	440040	BE219431	Hs.300713	ESTs	2.4	3.4
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	2.4	10.7
	438977	AA482026	Hs.298625	ESTs	2.4	2.8
15	452066	AA772149	Hs.16979	ESTs	2.4	5.4
	428500	AI815395	Hs.184641	delta-6 fatty acid desaturase	2.4	2.2
	408503	AW119059	Hs.63163	ESTs, Weakly similar to UDP-GalNAc:polyp	2.4	2.7
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	2.4	4.8
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.4	2.2
20	453753	BE252983	Hs.35086	ubiquitin specific protease 1	2.4	2.8
	424050	AA211218	Hs.138381	farnesyltransferase, CAAX box, alpha	2.4	3.9
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfam	2.4	76.7
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	2.4	12.3
	415156	X84908	Hs.78060	phosphorylase kinase, beta	2.4	10.4
25	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	2.4	7.7
	429831	AA564489	Hs.137526	ESTs	2.4	4.1
	407373	AA031576	Hs.143812	Homo sapiens cDNA FLJ12956 fis, clone NT	2.4	3.3
	422221	AA306649	Hs.168213	gb:EST177656 Jurkat T-cells VI Homo sapi	2.4	3.8
	451351	AW058261	Hs.158311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	3.3
30	410082	AA081594	Hs.238927	Musashi (Drosophila) homolog 1	2.4	2.5
	430304	AL122071	Hs.25566	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	2.4	6.5
	418863	AL135743	Hs.21145	ESTs	2.4	5.2
	448414	BE391820	Hs.183779	Homo sapiens cDNA: FLJ22489 fis, clone H	2.4	3.7
	428351	AK001701	Hs.159455	Homo sapiens cDNA FLJ10590 fis, clone NT	2.4	6.2
35	425750	AL050276	Hs.75839	zinc finger protein 288	2.4	5.1
	426295	AW367283	Hs.254562	zinc finger protein 6 (CMPX1)	2.4	113.6
	408772	W88532	Hs.294084	ESTs	2.4	12.3
	426307	F24978	Hs.252748	ESTs	2.4	4.0
	405203		Hs.156089	ESTs	2.4	2.5
40	453537	AA036755	Hs.283681	ESTs	2.4	3.6
	431427	AK000401	Hs.143851	Homo sapiens cDNA FLJ20394 fis, clone KA	2.4	6.2
	458021	AI885190	Hs.87627	ESTs, Weakly similar to KIAA1339 protein	2.4	4.3
	453928	BE222198	Hs.111911	ESTs	2.4	2.6
	446853	AV660630	Hs.13999	disrupter of silencing 10	2.3	9.7
45	441626	AA281167	Hs.104557	ESTs	2.3	23.0
	446138	AW504182	Hs.3337	KIAA0700 protein	2.3	2.2
	452568	AA805634	Hs.22862	transmembrane 4 superfamily member 1	2.3	22.2
	417665	AW852858	Hs.298033	ESTs	2.3	8.0
	420088	AC006486	Hs.14947	Homo sapiens cDNA: FLJ22286 fis, clone H	2.3	5.1
50	421456	AW579842	Hs.182828	hypothetical protein FLJ10697	2.3	2.5
	412093	BE242691	Hs.25010	ESTs	2.3	31.4
	428172	U09367	Hs.173840	zinc finger protein 136 (clone pHZ-20)	2.3	4.9
	450447	AF212223	Hs.249889	hypothetical protein P15-2	2.3	2.3
	436001	AW903849	Hs.34401	HUEL (C4orf1)-interacting protein	2.3	4.1
55	414786	AI246482	Hs.30332	ESTs	2.3	2.1
	459284	AF155660	Hs.14791	mitochondrial solute carrier	2.3	2.9
	452701	NM_005110	Hs.29468	glutamine-fructose-6-phosphate transamin	2.3	2.6
	446320	AF126245	Hs.239720	acyl-Coenzyme A dehydrogenase family, me	2.3	3.9
	446669	AW972832	Hs.301805	ESTs	2.3	3.8
60	434616	D79338	Hs.16542	CCR4-NOT transcription complex, subunit	2.3	3.6
	452135	AI492175	Hs.184013	ESTs	2.3	2.3
	408696	AW958157	Hs.92381	ESTs, Highly similar to unnamed protein	2.3	2.8
	436176	AL121422	Hs.55501	ESTs	2.3	3.2
	419713	AW968058	Hs.54982	nudix (nucleoside diphosphate linked moi	2.3	17.0
65	414197	W44877	Hs.73793	ESTs	2.3	11.8
	445270	AI762154	Hs.170098	Homo sapiens cDNA FLJ14014 fis, clone HE	2.3	4.2
	412247	AF022375		vascular endothelial growth factor	2.3	5.1
	426494	AL119528		KIAA0372 gene product	2.3	4.4
	405687				2.3	2.2
70	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	2.3	2.0
	450747	AI064821	Hs.48306	ESTs, Highly similar to EWS_HUMAN RNA-BI	2.3	3.8
	433680	AI805366	Hs.199945	ESTs	2.3	6.7
	420025	AF184939	Hs.94392	LDL induced EC protein	2.3	2.4
	413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.3	3.1
75	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	2.3	3.0
	424414	AI361002	Hs.94814	Homo sapiens cDNA FLJ12168 fis, clone MA	2.3	2.0
	435791	AA243086	Hs.25204	chondroitin 4-O-sulfotransferase 2	2.3	2.4
	457635	AV660976	Hs.3569	hypothetical protein	2.3	6.9
	427985	AI770170	Hs.65583	ESTs	2.3	2.3
80	445498	AV654019	Hs.180402	Homo sapiens cDNA: FLJ23506 fis, clone L	2.3	2.3
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.3	4.1
	450368	AU077158	Hs.24930	tubulin-specific chaperone a	2.3	3.5
	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	2.3	2.6
	448607	AL042506	Hs.21599	Homo sapiens cDNA FLJ10107 fis, clone HE	2.3	2.8
	447975	BE378418	Hs.127240	ESTs	2.3	2.2
	429767	AW793022	Hs.218329	hypothetical protein	2.3	11.5
	408877	AA479033	Hs.130315	ESTs	2.3	2.3

448481	W15284	Hs.74832	ESTs		
452833	BE559681	Hs.30736	KIAA0124 protein	2.3	3.3
421057	T58283	Hs.42679	ESTs	2.3	2.8
408885	C02741	Hs.48712	hypothetical protein FLJ20736	2.3	11.0
427615	BE410107	Hs.179817	CGI-82 protein	2.3	4.6
448861	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	2.3	2.3
430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	2.3	6.3
428494	AA233439	Hs.184634	hypothetical protein FLJ20005	2.3	34.6
422987	AW407887	Hs.301772	serine/threonine kinase 11 (Peutz-Jegher	2.3	10.2
408216	AA741038	Hs.6670	ESTs	2.3	3.2
407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV	2.3	3.3
432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.3	5.7
410086	AI268405	Hs.13467	Homo sapiens BAC clone RP11-121A8 from 7	2.3	2.1
444853	AW576245	Hs.149740	Homo sapiens mRNA for FLJ00028 protein,	2.3	2.2
413284	AU077055	Hs.289107	baculoviral IAP repeat-containing 2	2.3	4.5
445547	D86181	Hs.273	galactosylceramidase (Krabbe disease)	2.3	4.8
420258	AA477514	Hs.96247	translin-associated factor X	2.3	2.5
437223	C15105	Hs.107884	ESTs	2.3	3.5
437353	AA749195	Hs.143746	ESTs	2.3	2.7
426224	BE085860	Hs.168075	karyopherin (importin) beta 2	2.3	2.6
402575	Z23024	Hs.138860	Rho GTPase activating protein 1	2.3	36.1
430712	AW044647	Hs.196284	ESTs	2.3	3.1
452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat	2.3	2.4
425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.3	2.4
441648	H05734	Hs.30559	ESTs	2.3	4.3
424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (f	2.3	2.1
414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	2.3	2.9
423814	AF105020	Hs.132999	putative protein O-mannosyltransferase	2.3	12.2
421641	AI638184	Hs.106334	Homo sapiens clone Z3836 mRNA sequence	2.3	3.7
427882	AA640987	Hs.193767	ESTs	2.3	2.3
442159	AW163390	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	2.3	10.2
412541	BE009398	Hs.74002	nuclear receptor coactivator 1	2.3	4.4
447217	BE465754	Hs.17778	neuropilin 2	2.3	2.4
452336	AA960961	Hs.29147	hypothetical protein FLJ11015	2.3	3.0
423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	2.3	4.1
411737	AW160339	Hs.71791	hypothetical protein	2.3	3.4
412276	BE262621	Hs.73798	macrophage migration inhibitory factor (2.2	2.0
456974	M12529	Hs.169401	apolipoprotein E	2.2	2.4
416033	NM_012201	Hs.78979	Golgi apparatus protein 1	2.2	2.6
406739	AI566709	Hs.182426	ribosomal protein S2	2.2	10.4
448646	AU077149	Hs.21704	transcription factor 12 (HTF4, helix-loo	2.2	115.3
437371	AK000868	Hs.5570	hypothetical protein FLJ10006	2.2	4.2
451413	AA448974	Hs.26367	PC3-96 protein	2.2	3.6
408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2	6.2
437548	AI701596	Hs.121592	ESTs	2.2	3.2
452053	AI750575	Hs.173933	nuclear factor IIA	2.2	3.0
428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.2	3.3
441376	H94227	Hs.6592	ESTs, Weakly similar to salivary proline	2.2	3.4
413399	BE091833	Hs.22564	gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.2	2.5
448913	AA194422	Hs.6456	myosin VI	2.2	2.1
439053	BE244588	Hs.157313	chaperonin-containing TCP1, subunit 2 (b	2.2	2.4
428065	AI634046	Hs.159629	ESTs	2.2	3.1
425846	AA102174	Hs.273138	myosin IXB	2.2	3.5
426404	AA377607	Hs.128856	ESTs	2.2	7.1
423464	NM_016240	Hs.5057	CSR1 protein	2.2	3.3
436135	D85390	Hs.246849	carboxypeptidase D	2.2	2.1
450476	AL045285	Hs.99936	ESTs, Moderately similar to ALU6_HUMAN A	2.2	9.1
420798	W93774	Hs.281789	keratin 10 (epidermolytic hyperkeratosis	2.2	2.5
433530	BE349534	Hs.5105	ESTs	2.2	2.8
436297	AI084582	Hs.280666	hypothetical protein FLJ10569	2.2	2.1
433058	H86865	Hs.191952	Homo sapiens chromosome 19, cosmid R3218	2.2	2.4
435924	AW029203	Hs.81248	ESTs	2.2	2.3
417125	AW181998	Hs.394	CUG triplet repeat, RNA-binding protein	2.2	3.2
449338	H73444	Hs.6949	adrenomedullin	2.2	2.3
446065	AA085191	Hs.65403	ESTs, Weakly similar to T2D3_HUMAN TRANS	2.2	18.3
410668	BE379794	Hs.96918	hypothetical protein	2.2	3.1
424992	AW290893	Hs.5848	Homo sapiens cDNA: FLJ21561 fis, clone C	2.2	2.6
437801	AA613866	Hs.73957	Homo sapiens mRNA; cDNA DKFZp564L222 (f	2.2	10.8
412491	W31589	Hs.15020	RAB5A, member RAS oncogene family	2.2	2.5
446392	AF142419	Hs.25042	homolog of mouse quaking QKI (KH domain	2.2	2.4
450503	R35917	Hs.143696	Homo sapiens mRNA full length insert cDN	2.2	3.4
432476	T94344	Hs.107153	gb:ye31h10.s1 Stratagene lung (937210) H	2.2	2.8
424251	AA677466	Hs.49994	coactivator-associated arginine methyltr	2.2	2.6
456619	AV647917	Hs.208334	inhibitor of growth family, member 1-Rk	2.2	5.0
433411	AI658666	Hs.79219	ESTs	2.2	2.6
424714	AI114630	Hs.76549	Homo sapiens cDNA: FLJ21874 fis, clone H	2.2	2.1
416326	AF186780	Hs.141003	RaiGDS-like gene; KIAA0959 protein	2.2	2.7
407696	AI697340	Hs.77269	ATPase, Na+K+ transporting, alpha 1 pol	2.2	2.2
445939	BE018658	Hs.287420	Homo sapiens cDNA: FLJ21691 fis, clone C	2.2	6.5
414765	X07854	Hs.181165	guanine nucleotide binding protein (G pr	2.2	4.4
407136	T64896	Hs.164485	Homo sapiens cDNA FLJ11533 fis, clone HE	2.2	6.2
453665	AA626250		eukaryotic translation elongation factor	2.2	2.8
433608	AW340005		ESTs	2.2	2.3
				2.2	2.1

5	447646	BE619752	Hs.66053	ESTs, Weakly similar to S22126 finger pr	2.2	4.1
	433139	AB029826	Hs.47649	3-methylcrotonyl-CoA carboxylase biotin-	2.2	11.7
	413433	NM_003199	Hs.289068	transcription factor 4	2.2	2.2
	421535	AB002359	Hs.105478	phosphonobosylformylglycinamide synthase	2.2	2.2
	428591	BE313029	Hs.185807	Homo sapiens clone 24758 mRNA sequence	2.2	4.8
10	417248	AA329449	Hs.247302	twisted gastrulation	2.2	2.5
	403966				2.2	5.2
	437112	AA744692	Hs.166539	ESTs	2.2	3.0
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	2.2	4.9
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	2.2	4.4
15	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	2.2	2.5
	426543	AV650198	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.2	2.4
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	2.2	4.2
	443804	AL135352	Hs.255883	ESTs	2.2	2.2
	435080	AI831760	Hs.155111	ESTs	2.2	2.5
20	452808	AF244135	Hs.30670	hepatocellular carcinoma-associated anti	2.2	7.1
	433934	AW273261	Hs.216292	ESTs	2.2	2.1
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.2	4.4
	452518	AA280722	Hs.24758	ESTs	2.2	3.0
	409600	AJ011679	Hs.55099	Homo sapiens mRNA; cDNA DKFZp586D2123 (f	2.2	2.3
25	448965	AF092134	Hs.22679	CGI-24 protein	2.2	4.0
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	2.2	5.3
	458894	AW292171	Hs.23978	scaffold attachment factor B	2.2	2.5
	402269				2.2	2.2
	423798	AF047033	Hs.301617	Homo sapiens mRNA full length insert cDN	2.2	4.0
30	413836	W92003	Hs.70614	ESTs	2.2	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	2.1	2.1
	412204	AI125507	Hs.130829	ESTs	2.1	3.0
	438807	AA848011	Hs.124570	ESTs, Weakly similar to reverse transcri	2.1	2.2
	404170				2.1	41.6
35	434858	AW979012	Hs.134462	ESTs	2.1	2.2
	426882	AA149707	Hs.173091	ubiquitin-like 3	2.1	2.1
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.1	26.5
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.1	3.7
	424950	AA602917	Hs.156974	ESTs	2.1	19.9
40	418123	AA669830	Hs.83530	hypothetical protein	2.1	4.6
	440467	AK001519	Hs.7194	CGI-74 protein	2.1	5.3
	437092	AA744292	Hs.181244	major histocompatibility complex, class	2.1	3.0
	421579	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	2.1	3.3
	428953	AA306610	Hs.194676	DKFZP434C013 protein	2.1	5.0
45	457313	AF047002	Hs.241520	transcriptional coactivator	2.1	3.5
	420570	AI453665	Hs.290870	ESTs, Weakly similar to S23650 retroviru	2.1	2.1
	446918	AL135125	Hs.13913	KIAA1577 protein	2.1	2.3
	427567	N24236	Hs.179662	nucleosome assembly protein 1-like 1	2.1	2.8
	446363	AL117440	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	2.1	4.0
50	428482	AI290352	Hs.184592	KIAA0344 gene product	2.1	2.8
	456559	AI336273	Hs.102548	glucocorticoid receptor DNA binding fact	2.1	2.3
	442819	BE622721	Hs.301766	ESTs, Weakly similar to hypothetical pro	2.1	27.1
	428808	AA436007	Hs.188780	ESTs	2.1	5.0
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	2.1	15.9
55	447023	AA356764	Hs.17109	integral membrane protein 2A	2.1	3.0
	402250	AV655272	Hs.20252	novel Ras family protein	2.1	4.2
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	2.1	7.9
	420006	H14429	Hs.94300	serologically defined colon cancer antig	2.1	5.6
	407316	AA031663	Hs.28802	centaurin-alpha 2 protein	2.1	4.4
60	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.1	103.2
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.1	29.9
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	2.1	2.1
	428680	U69199	Hs.90259	ESTs, Weakly similar to alpha 1 [H.sapie	2.1	2.5
	448501	AA332316	Hs.4273	hypothetical protein FLJ13159	2.1	2.0
65	422552	N39729	Hs.118243	deoxyribonuclease II, lysosomal	2.1	2.9
	419476	AW953030	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	2.1	3.1
	408681	AW953853	Hs.292833	ESTs	2.1	3.9
	417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	2.1	4.1
	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.1	4.9
70	442711	AF151073	Hs.8645	hypothetical protein	2.1	2.2
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	2.1	7.4
	452897	BE066058	Hs.269233	ESTs	2.1	4.2
	409147	AI889208	Hs.17283	hypothetical protein FLJ10890	2.1	4.5
	433028	AI199144	Hs.283737	AD-017 protein	2.1	2.6
75	407831	BE613377	Hs.15580	Homo sapiens cDNA: FLJ22276 fis, clone H	2.1	8.5
	417871	AA521368	Hs.24252	ESTs	2.1	2.9
	428754	AI521102	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	2.1	5.3
	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit,	2.1	4.3
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	2.1	8.5
80	414242	AA749230	Hs.22666	ESTs	2.1	2.8
	433323	AA805132	Hs.30701	ESTs	2.1	5.0
	439022	AA356599	Hs.173904	ESTs	2.1	6.4
	443357	AW016773	Hs.75615	apolipoprotein C-II	2.1	2.0
	449103	T24968	Hs.23038	HSPC071 protein	2.1	2.7
	427512	AB018322	Hs.179507	KIAA0779 protein	2.1	2.0
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.1	2.9
	440112	AA099014	Hs.231029	ESTs	2.1	2.3

5	446920	BE397649	Hs.31257	Homo sapiens cDNA FLJ13634 fis, clone PL	2.1	4.8
	428459	D44650	Hs.184411	gene with multiple splice variants near	2.1	2.9
	432842	AW674093	Hs.279525	hypothetical protein PRO2605	2.1	2.3
	438829	AA826926	Hs.204214	ESTs	2.1	2.7
	411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.1	2.2
10	409423	AI969783	Hs.43071	ESTs, Weakly similar to AF151900 1 CGI-1	2.1	2.2
	456804	AI421645	Hs.139851	caveolin 2	2.1	15.2
	434536	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho	2.1	2.8
	447126	AW150632	Hs.62954	ferritin, heavy polypeptide 1	2.1	25.0
	442328	AI952430	Hs.265237	ESTs	2.1	2.1
15	444488	AW192879	Hs.184796	ESTs, Weakly similar to PET2_HUMAN OLIGO	2.1	2.9
	438874	H02780		gb:yy41a11.1 Soares placenta Nb2HP Homo	2.1	10.6
	412805	AW954569	Hs.296287	ESTs	2.1	4.6
	446334	U52427	Hs.14839	polymerase (RNA) II (DNA directed) polyp	2.1	2.3
	427201	AB037860	Hs.173933	nuclear factor IIA	2.1	5.1
20	436997	AA741151	Hs.137323	ESTs	2.1	3.0
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	2.1	2.3
	453613	F05838	Hs.14763	ESTs	2.1	2.4
	413276	Z24725	Hs.75260	mitogen inducible 2	2.1	5.5
	422050	AA302741	Hs.25786	ESTs	2.1	4.0
25	424797	AA622394	Hs.153177	ribosomal protein S28	2.1	2.1
	437365	AW965771	Hs.91065	hypothetical protein DKFZp761B2423	2.1	3.0
	412482	AI499930	Hs.181043	KIAA0788 protein	2.1	2.7
	418662	AI801098	Hs.151500	ESTs	2.1	2.1
	404030				2.1	2.1
30	437802	AI475995	Hs.122910	ESTs	2.1	3.8
	441130	AI160734	Hs.283429	SMC (mouse) homolog, X chromosome	2.1	3.5
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	2.1	7.4
	409944	BE297925	Hs.57687	four and a half LIM domains 3	2.1	6.3
	425421	L11669	Hs.157145	tetracycline transporter-like protein	2.1	7.1
35	428399	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	2.1	2.7
	421313	NM_014923	Hs.103329	KIAA0970 protein	2.1	2.6
	445229	BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.1	4.7
	401001				2.1	14.7
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.1	7.2
40	438855	AW946276	Hs.6441	tissue inhibitor of metalloproteinase 2	2.1	4.9
	433369	Z49254	Hs.3254	mitochondrial ribosomal protein L23	2.1	25.0
	433228	F28212	Hs.284247	KIAA1491 protein	2.1	5.1
	445392	AA057478	Hs.23272	ESTs	2.0	2.3
	433891	AA613792		gb:nc097h03.s1 NCI_CGAP_Pr2 Homo sapiens	2.0	2.5
45	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!	2.0	2.9
	448474	AI792014	Hs.13809	ESTs	2.0	12.1
	427045	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	2.0	2.9
	444916	AB028956	Hs.12144	KIAA1033 protein	2.0	4.2
	439177	AW820275	Hs.76611	ESTs	2.0	3.3
50	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.0	5.0
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	2.0	2.3
	424429	U63830	Hs.146847	TRAF family member-associated NFkB activ	2.0	12.7
	428385	AF112213	Hs.184062	putative Rab5-interacting protein	2.0	4.6
	458946	AA009716	Hs.42311	ESTs	2.0	16.4
55	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	2.0	4.9
	426829	AI761241	Hs.301719	ESTs	2.0	2.4
	433619	AW965275	Hs.284288	hqp0256 protein	2.0	4.4
	421985	AK001779	Hs.110445	CGI-97 protein	2.0	3.8
	439895	AB037773	Hs.6762	hypothetical protein FLJ10595	2.0	2.2
60	449188	AW072939	Hs.23200	myotubularin related protein 1	2.0	2.2
	404820				2.0	2.7
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.0	2.5
	422163	AF027208	Hs.297332	Homo sapiens cDNA: FLJ21471 fis, clone C	2.0	3.7
	431172	AI125639	Hs.250666	hairy (Drosophila)-homolog	2.0	10.2
65	415200	AL040328	Hs.301912	Homo sapiens cDNA: FLJ22920 fis, clone K	2.0	2.1
	458176	AI961519	Hs.140309	ESTs, Weakly similar to KIAA0681 protein	2.0	5.0
	407895	R44203	Hs.265540	HSPC042 protein	2.0	4.6
	449816	AI701457	Hs.38694	ESTs	2.0	2.0
	422976	AU076657	Hs.1600	sec61 homolog	2.0	5.7
70	430220	BE378277	Hs.152230	ESTs	2.0	11.7
	435446	AA682305	Hs.133268	ESTs	2.0	4.2
	431031	AA830335	Hs.105273	ESTs	2.0	14.1
	425233	Z17861	Hs.155218	E1B-55kDa-associated protein 5	2.0	5.6
	426458	D83032	Hs.169984	nuclear protein	2.0	5.9
75	421965	AA301100		gb:EST14128 Testis tumor Homo sapiens cD	2.0	2.1
	427128	AW301984	Hs.173685	Homo sapiens cDNA FLJ12619 fis, clone NT	2.0	6.3
	449722	BE280074	Hs.23960	cyclin B1	2.0	2.1
	450816	BE271927	Hs.87385	ESTs	2.0	2.4
	453507	AF083217	Hs.33085	WD repeat domain 3	2.0	13.1
80	422801	AF125672	Hs.287994	nuclear receptor co-repressor 2	2.0	3.5
	418178	AA043951	Hs.83715	Sjogren syndrome antigen B (autoantigen	2.0	3.9
	417819	AI253112	Hs.133540	ESTs	2.0	4.0
	414787	AL049332	Hs.77311	BTG family, member 3	2.0	4.0
	447032	AK000310	Hs.17138	hypothetical protein FLJ20303	2.0	7.0
	431742	NM_016652	Hs.268281	CGI-201 protein	2.0	2.5
	448431	BE613061	Hs.300697	ESTs, Weakly similar to CA13_HUMAN COLLA	2.0	6.5
	456444	AA884517	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.0	2.5

5	419178	NM_006284	Hs.89657	TATA box binding protein (TBP)-associate	2.0	6.0
	446437	AW014360	Hs.202119	ESTs, Weakly similar to A46010 X-linked	2.0	2.2
	449910	AI074585	Hs.58440	ESTs	2.0	2.1
	435963	AF271212	Hs.87627	disrupter of silencing 10	2.0	2.1
	421283	AI760018	Hs.205071	ESTs	2.0	2.6
	414482	S57498	Hs.76252	endothelin receptor type A	2.0	2.4
	450960	AB013897	Hs.25722	Homo sapiens mRNA for HKR1, partial cds	2.0	2.1
	438644	AI126162	Hs.129037	ESTs	2.0	2.1
10	458343	AI004775	Hs.205091	ESTs, Weakly similar to WW domain bindin	2.0	6.5
	412574	BE410731	Hs.74050	follicular lymphoma variant translocatio	2.0	12.4
	458079	AI796870	Hs.54277	ESTs	2.0	3.8
	450582	AI339732	Hs.13144	HSPC160 protein	2.0	2.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	2.0	3.1
15	426865	D63476	Hs.172813	PAK-interacting exchange factor beta	2.0	3.3
	446430	AA346837	Hs.15075	hypothetical protein DKFZp434E2216	2.0	2.0

Table 4B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

20	Pkey	CAT Number	Accession
	447197	2176805_1	R36075 R36167 AI366546
25	407192	2200202_1	AA602964 AA609200
	429007	327976_1	AA443145 BF958169 AW904500 AL119015 D80642
	429163	1238297_1	AW974271 AA592975 AA447312 AA884766
	439579	24302_1	AF086400 W73990 W79232
	432060	1235850_1	AA525021 AW971364 AA570759
30	416913	924456_1	AW934714 AW749864 AW749902 BE162498 BE161005 BE162499 BE161006 AA190449 AW513465 BE162500 BE161007
	426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
	433586	32908_1	BC011194 AW517087 AA601054 T85512
	448451	7632_32	AW000978 R39988 AW015994 AI598202 BF821479 AI521706
	442495	928718_1	AI184717 AW518883 AF121173
35	439566	23928_1	AF086387 W72711 W77884
	407939	600387_1	AW118352 AW196215 W05608
	453740	612139_1	AL120295 BG291384 T88779
	433854	899720_1	BG675161 H59558 AI699484 AA610649 AI937812
	413020	1485885_1	BE048113 R98736 Z42904
40	458050	61684_1	AK057874 AW901381 AW901380 AV730240 T50211 AA828756 AA834708
	440769	21430_5	BG419454 BF924037 R13764 AW793200 BE561793 BG698295 BE270077
	428832	1137866_1	BI008687 AA481363 AA436432 BI008686 AA578229 AA481375
	414473	35761_3	BG392866 BE302693
	422343	786037_1	AW961833 AA309282 AA551780 AI628633 AA551995 AW378461
45	431319	122030_1	BG435498 BG924768 AV718536 AA873350 T82428 T82429 AU185416 AA658442
	422221	319_18	BG910399 BE826714 BF905312 AA305649 Z40822 N76633
	413399	1511159_1	BE091833 BE091874 BE091871
	432476	1237465_1	AW973269 AA548913 T94344 AA834800 AA857492
	438874	52147_1	AF075017 R66779 R22463 H02780
50	433891	647290_1	AW182329 AA613792 T05304 AW858385
	421965	1883_13	BC022394 AI742351 BE676249 AI742341 AW572776 AI566256 AI538553 BI837905 AA301100 AA620903 AI142397 AW082310 AI147387 BF509145
			AW968207 AA468415 AU185163 AW450843 AI568752 AW137191

TABLE 4C:

55	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position:	Indicates nucleotide positions of predicted exons.

60	Pkey	Ref	Strand	NI_position
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	405238	7249119	Minus	51728-51836
	400992	8096828	Plus	140390-140822
65	400860	9757499	Minus	151830-152104,152649-152744
	402524	9798518	Minus	20529-21096
	404210	5006246	Plus	169926-170121
	402604	9909420	Plus	20393-20767
	402855	9662953	Minus	59763-59909
70	404029	7671252	Plus	108716-111112
	402605	9909420	Minus	47680-47973
	404049	3688074	Minus	75765-78155
	403549	8081591	Minus	137150-137362
	404048	3688074	Minus	54421-56808
75	404171	9930793	Plus	173667-173783,176876-177055
	405649	4926908	Minus	50032-50132,50624-50764
	405268	4156151	Minus	24404-24521
	405204	7230116	Plus	126569-126754
	405517	9454624	Plus	114757-114877
80	405203	7230116	Plus	125295-125463
	405687	6249668	Minus	54787-54891,55844-55917
	403966	8568861	Plus	158193-158277,160116-160290
	402269	3128156	Minus	1168-1324,5492-5611,23445-23851
	404170	9930793	Plus	168836-169248

404030 7671252 Plus 149362-151749
 401001 7229886 Minus 113631-113762
 404820 4678240 Plus 20475-21085

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TABLE 5A: ABOUT 43 GENES UPREGULATED IN GLIOBLASTOMA THAT ENCODE PREDICTED MEMBRANE PROTEINS

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
R1:	Ratio of brain tumor to body atlas				
R2:	Ratio of brain tumor to normal brain				
Pkey	ExAccn	UnigeneID	Unigene title	R1	R2
415817	U88967	Hs.78857	protein tyrosine phosphatase, receptor-1	72.0	11.3
447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	54.2	7.1
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	22.0	7.6
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	21.2	3.0
412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	18.6	18.6
417355	D13168	Hs.82002	endothelin receptor type B	16.4	16.4
419721	NM_001650	Hs.288550	aquaporin 4	16.2	4.4
452355	N54926	Hs.29202	G protein-coupled receptor 34	13.9	13.9
410227	AB009284	Hs.61152	exostosins (multiple)-like 2	11.9	2.9
419723	AL120193	Hs.92614	Homo sapiens growth differentiation factor	7.4	3.5
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4
443898	AW804296	Hs.9950	Sec61 gamma	6.8	7.2
422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	4.3	6.1
414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.2	34.8
431555	AF016028	Hs.260039	sarcomin (Kras oncogene-associated gene	4.0	3.8
435869	AF255910	Hs.54550	vascular endothelial junction-associated	3.7	4.2
440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	3.5	2.4
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.4	2.8
431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	2.4
445070	NM_000677	Hs.258	adenosine A3 receptor	3.2	7.6
430890	X54232	Hs.2699	glypican 1	3.2	4.3
423422	AC005175	Hs.128425	NY-REN-24 antigen	3.1	2.6
413367	NM_006517	Hs.75317	solute carrier family 16 (monocarboxylic	3.0	4.1
447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.0	4.1
427150	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate	3.0	2.1
422676	D28481	Hs.1570	histamine receptor H1	3.0	6.3
430293	AI416988	Hs.238272	inositol 1,4,5-trisphosphate receptor, ty	2.8	7.4
453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.7	3.2
428281	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	2.4	4.4
417446	AL118671	Hs.82163	monoamine oxidase B	2.4	2.2
412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.4	76.7
440225	BE295782	Hs.159	tumor necrosis factor receptor superfam	2.3	2.3
450447	AF212223	Hs.25010	hypothetical protein P15-2	2.3	4.1
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.3	2.4
452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat	2.3	3.0
447217	BE465754	Hs.17778	neuropilin 2	2.1	3.0
447023	AA356764	Hs.17109	integral membrane protein 2A	2.1	4.9
422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.1	15.2
456804	AI421645	Hs.139851	caveolin 2	2.1	2.3
430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	2.0	3.7
422163	AF027208	Hs.297332	Homo sapiens cDNA: FLJ21471 fls, clone C	2.0	2.4
414482	S57498	Hs.76252	endothelin receptor type A		

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TABLE 6A: ABOUT 397 GENES DOWNREGULATED IN GLIOBLASTOMA

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
R1:	Ratio of normal brain to body atlas				
R2:	Ratio of normal brain to brain tumor				

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Pkey	Ex Accn	UnigeneID	Title	R1	R2
439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.47	77.82
424846	AU077324	Hs.1832	neuropeptide Y	4.49	55.32
428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	7.06	45.64
416836	D54745	Hs.80247	cholecystokinin	9.45	44.59
401412	c14p3_2958		exon	3.20	32.56
451835	T63643	Hs.209715	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.21	28.93
412768	AW996044	Hs.26239	ESTs	3.16	28.12
415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.27	27.04
411305	BE241596	Hs.69547	myelin basic protein	13.80	25.92
438054	AA776626	Hs.62183	ESTs	3.59	25.06
410837	BE145698		gb:LL0-HT0205-231199-145-a07 HT0205 Homo	3.05	24.43
425121	AI797511	Hs.154679	synaptotagmin 1	6.92	23.67
456763	AJ271351	Hs.128180	B-cell translocation gene 4	3.29	23.32
429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	8.03	22.56
451892	AI821302	Hs.167834	ESTs	4.12	21.82

5	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	4.41	21.28
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	5.27	21.20
	432247	AA531287	Hs.105805	ESTs	3.25	21.14
	436812	AW298067		gb:UL-H-BWD-ajp-g-09-0-UL.s1 NCI_CGAP_Su	3.02	21.12
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.38	20.50
10	435708	AI362949	Hs.75169	ESTs	8.79	20.45
	423135	N67655	Hs.26411	ESTs	6.82	20.28
	440600	AI807691	Hs.126351	ESTs	3.56	20.09
	405230	cNp1_7656		exon	3.31	19.95
	456915	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.14	19.40
15	425130	AA448208	Hs.99163	ESTs	3.53	19.20
	416812	H91010	Hs.44940	ESTs	3.54	19.08
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.78	19.04
	457463	AW877031	Hs.272321	Homo sapiens cDNA FLJ12571 fis, clone NT	3.13	18.91
	454589	AW809699		gb:MR4-ST0124-241199-026-e12 ST0124 Homo	4.10	18.60
20	418104	T05726	Hs.177130	ESTs	3.17	18.41
	416357	T82050	Hs.268907	ESTs	3.11	18.13
	414683	S78296	Hs.76888	interneuron neuronal intermediate filamen	5.55	18.13
	447694	AI420083	Hs.170303	ESTs	3.56	17.79
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	4.63	17.65
25	428010	AA806554	Hs.185375	ESTs	3.03	17.40
	417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	3.23	17.38
	436788	AA766908	Hs.259047	ESTs	3.16	17.21
	459349	AW749381		gb:QV3-BT0381-170100-060-c02 BT0381 Homo	3.26	17.10
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	3.86	17.04
30	438068	AI927209	Hs.283089	HMT1 (hnRNP methyltransferase, S. cerevi	3.54	16.48
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.63	16.32
	435315	AA700240	Hs.165402	ESTs	4.06	16.12
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.69	15.92
	412446	AI768015	Hs.92127	ESTs	5.44	15.75
35	449714	AB033015	Hs.23941	KIAA1189 protein	4.59	15.43
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	4.63	14.97
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	5.93	14.81
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl	3.29	14.61
	414187	BE312141		gb:G01145962F1 NIH_MGC_19 Homo sapiens c	3.37	14.46
40	417868	AI078534	Hs.122592	ESTs	7.57	14.22
	428536	AI143139	Hs.2288	visinin-like 1	5.16	13.98
	402125	c18p3_155		exon	3.11	13.94
	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	3.49	13.92
	419090	T85201	Hs.188468	ESTs	3.25	13.79
45	437665	AA765417	Hs.292053	ESTs	3.07	13.79
	457113	AI734016	Hs.270508	ESTs	3.50	13.69
	424933	AW999974	Hs.5181	proliferation-associated 2G4, 38kD	3.59	13.48
	443489	AI073512	Hs.133916	ESTs	3.24	13.20
	404289	c6p3_5821		exon	3.99	13.12
50	406534	ph2_4616		exon	3.89	13.10
	423280	AA324037		gb:EST26901 Cerebellum II Homo sapiens c	3.38	13.03
	455421	AW937661	Hs.288324	Homo sapiens cDNA FLJ13283 fis, clone OV	3.04	12.93
	433725	AF063559	Hs.283919	Homo sapiens clone HQ0117 PRO0117 mRNA,	3.71	12.85
	416660	R98905	Hs.35992	ESTs	3.92	12.74
55	407593	AW044083	Hs.237008	ESTs	3.85	12.67
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	7.41	12.59
	410366	AI267589	Hs.25214	hypothetical protein	7.89	12.50
	405348	cNp3_13716		exon	3.45	12.42
	442338	AI761976	Hs.156080	ESTs	3.69	12.35
60	424458	M29273	Hs.1780	myelin associated glycoprotein	4.72	12.31
	431400	AA504607		gb:aa63a02.s1 NCI_CGAP_GCB1 Homo sapiens	3.42	12.29
	417754	R13027	Hs.268703	ESTs	3.35	12.18
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	6.15	12.11
	431339	AA506294	Hs.257266	ESTs	3.50	11.97
65	452265	BE501516	Hs.114772	ESTs	3.82	11.96
	419297	AA446040	Hs.98640	Homo sapiens cDNA: FLJ21069 fis, clone C	3.16	11.86
	424991	AA775471	Hs.241467	ESTs	3.03	11.64
	431988	AC002302	Hs.77202	protein kinase C, beta 1	3.78	11.62
	450987	AA017202	Hs.32794	ESTs	3.28	11.61
70	440607	AA894559	Hs.192097	ESTs	3.11	11.60
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	3.26	11.54
	442000	H38671	Hs.8071	KIAA0735 gene product; synaptic vesicle	3.44	11.51
	437948	AA772920		gb:ae73c09.s1 Stratagene schizo brain S1	3.16	11.46
	401081	c11p3_921		exon	3.18	11.35
75	438919	AW979114		gb:EST391224 MAGE resequences, MAGP Homo	4.16	11.35
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	3.02	11.27
	422279	H69644	Hs.114231	C-type lectin-like receptor-2	3.35	11.13
	453101	AW952776	Hs.94943	ESTs	3.21	11.07
	455836	BE145795		gb:MR0-HT0208-101299-103-a12 HT0208 Homo	3.61	10.83
80	413324	V00571	Hs.75294	corticotropin releasing hormone	3.72	10.71
	412266	N59006	Hs.26133	ESTs	3.80	10.60
	436887	AW953157	Hs.193235	ESTs	7.24	10.56
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	3.05	10.53
	418162	T11958		gb:A802R Heart Homo sapiens cDNA clone A	3.07	10.50
	425537	AB007913	Hs.158291	KIAA0444 protein	3.07	10.46
	436230	AI248723	Hs.17711	ESTs	3.09	10.45
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.02	10.43

	447359	NM_012093	Hs.18268	adenylate kinase 5	5.91	10.40
	457187	AA443927	Hs.144360	EST	3.30	10.39
	407539	X91103		gb:H.sapiens mRNA for Hs44 protein.	3.02	10.35
5	452855	R17746	Hs.84469	ESTs	3.02	10.26
	440352	AI692322	Hs.65373	ESTs	3.03	10.20
	456116	Z28528	Hs.172004	titin	3.11	10.17
	458172	BE007237		gb:PMO-BN0139-050500-003-g09 BN0139 Homo	3.32	10.14
	445881	AI263029	Hs.210689	ESTs	3.04	10.11
10	454059	NM_003154	Hs.37048	statherin	3.27	9.97
	402624	c1p1_2660		exon	3.05	9.94
	441539	AA937200	Hs.192939	ESTs	3.27	9.82
	412172	N76794		gb:yv45g07.r1 Soares fetal liver spleen	3.03	9.78
	427942	AA417856		gb:zv01d05.r1 NCI_CGAP_GCB1 Homo sapiens	4.09	9.73
15	438867	BE041837	Hs.120316	ESTs	3.25	9.73
	454688	AW814472		gb:MR3-ST0203-010200-109-b06 ST0203 Homo	3.41	9.73
	446122	AI362790	Hs.181801	ESTs	3.40	9.71
	420480	AL137361	Hs.98173	hypothetical protein	3.03	9.56
	433447	U29195	Hs.3281	neuronal pentraxin II	3.72	9.54
20	407178	AA195651	Hs.104106	ESTs	3.89	9.47
	415614	F12926	Hs.165998	DKFZP564M2423 protein	3.06	9.45
	450518	BE245175	Hs.270893	ESTs	3.99	9.39
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	3.46	9.32
	458459	AA253074	Hs.146261	ESTs	4.08	9.30
25	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	5.18	9.23
	455644	BE064521		gb:RC4-BT0311-250200-014-d02 BT0311 Homo	3.02	9.20
	419800	AA282392	Hs.191525	ESTs	3.28	9.16
	430964	Y10929	Hs.248167	zinc finger protein 186 (Kruppel type)	3.04	9.00
	409716	AL117454	Hs.56027	Homo sapiens mRNA; cDNA DKFZp586J1717 (f	3.02	9.00
30	412962	AW839578	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	3.33	8.99
	445040	AW444934	Hs.195929	ESTs, Weakly similar to pre-serum amyloid	3.50	8.96
	451496	AW503407		gb:UL-HF-BN0-akw-d-11-0-UL.r1 NIH_MGC_50	3.17	8.94
	424617	AA344151		gb:EST50059 Gall bladder I Homo sapiens	3.25	8.91
	441914	AA971496	Hs.128465	ESTs	3.42	8.88
35	405320	cNp3_12168		exon	3.30	8.84
	449179	AI633785	Hs.196561	ESTs	3.43	8.84
	400335	Y13187	Hs.248066	Homo sapiens dmd gene, intron 11	3.13	8.78
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	4.16	8.74
	407803	AW081681	Hs.269064	ESTs	3.09	8.73
40	455260	AW878317		gb:MR3-OT0007-260300-206-e09 OT0007 Homo	3.78	8.70
	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clones TN62 and	4.01	8.67
	424481	R19453	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	8.12	8.63
	407616	AW054849	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	3.08	8.53
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.26	8.51
45	439239	AI031540	Hs.235331	ESTs	5.78	8.48
	410926	AW810708		gb:MR2-ST0129-051099-007-g07 ST0129 Homo	3.34	8.47
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	4.26	8.45
	409623	AW449185		gb:UL-H-BI3-akg-e-05-0-UL.s1 NCI_CGAP_Su	3.32	8.43
	420156	AW449258	Hs.6187	ESTs	3.40	8.38
50	411555	AF113537	Hs.70669	HMP19 protein	5.85	8.34
	408509	AA497035	Hs.110502	ESTs	3.17	8.34
	442368	AI698577	Hs.202481	ESTs	3.02	8.33
	457870	AA732217	Hs.294054	ESTs	3.04	8.32
	437254	AA831258		gb:oc73f04.s1 NCI_CGAP_GCB1 Homo sapiens	3.35	8.24
55	415508	R39236		gb:yc91d03.s1 Soares infant brain 1NIB H	3.07	8.22
	409483	U49379	Hs.54506	diacylglycerol kinase, epsilon (64kD)	3.31	8.20
	435229	AA676556	Hs.269515	ESTs, Moderately similar to ALUB_HUMAN !	3.21	8.19
	458120	W21398	Hs.54523	ESTs, Weakly similar to cytochrome P-450	3.22	8.17
	444613	H29627	Hs.79092	ESTs	3.78	8.16
60	417050	N39540	Hs.108029	ESTs	4.06	8.14
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	3.68	8.06
	413263	BE075131		gb:PM1-BT0585-110200-003-g03 BT0585 Homo	3.40	8.04
	424549	AI873205	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	3.27	8.03
	452689	F33868	Hs.284176	transferrin	3.03	8.01
65	405476	cNp3_19940		exon	3.28	8.00
	403932	cSp1_533		exon	3.58	7.99
	407095	AF011757	Hs.105937	RAGE binding protein	3.32	7.96
	415967	H11124		gb:ym14h07.s1 Soares infant brain 1NIB H	3.10	7.96
	417555	H65366		gb:yr67c10.r1 Soares fetal liver spleen	3.05	7.95
70	448985	AA324885	Hs.22777	carbonic anhydrase XI	5.30	7.79
	428689	NM_014351	Hs.189810	sulfotransferase-related protein	3.87	7.74
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	4.68	7.74
	441099	AW339393	Hs.126573	ESTs	3.08	7.74
	448589	AF017090	Hs.21554	KIAA1107 protein	3.10	7.73
75	406112	ph0_24243		exon	3.22	7.70
	458439	AV647220	Hs.282889	ESTs, Weakly similar to strong similarit	3.22	7.69
	429859	NM_007050	Hs.225352	protein tyrosine phosphatase, receptor I	3.15	7.68
	412090	AW955826	Hs.12396	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.01	7.67
	413547	BE147440		gb:RC1-HT0229-080100-015-f09 HT0229 Homo	3.01	7.66
80	447772	AI924558	Hs.161399	ESTs	3.04	7.63
	411132	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.72	7.61
	425490	NM_002248	Hs.158173	potassium intermediate/small conductance	3.15	7.60
	454568	BE141434		gb:MRO-HT0079-051099-002-d01 HT0079 Homo	3.16	7.59
	439099	AB037800	Hs.6462	KIAA1379 protein	3.40	7.57

	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	5.71	7.57
	428175	AJ810774	Hs.98376	ESTs	3.04	7.55
	413162	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo	3.43	7.54
5	451361	AA053854	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	3.11	7.53
	442527	AF150289	Hs.205436	ESTs	3.31	7.53
	450407	NM_000810	Hs.24959	gamma-aminobutyric acid (GABA) A recepto	5.24	7.53
	456966	AI589569	Hs.190082	ESTs	3.13	7.47
	441799	AW292276	Hs.127872	ESTs	3.38	7.41
10	424185	AA279752	Hs.142570	Homo sapiens clone 24629 mRNA sequence	3.16	7.40
	429783	AA811987	Hs.125779	ESTs	3.13	7.38
	429268	AA205386	Hs.198481	RAR-related orphan receptor B	3.48	7.38
	400708	c11p1_1292		exon	3.33	7.35
	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	3.04	7.33
15	455377	AW905347		gb:QV2-NN1073-220400-159-f06 NN1073 Homo	3.03	7.33
	435070	AI821270	Hs.116930	ESTs	3.03	7.33
	405427	cNp3_17682		exon	3.03	7.25
	455149	AW861879		gb:CM0-CT0341-260100-160-h12 CT0341 Homo	3.56	7.24
	402816	c1p3_2531		exon	3.13	7.21
20	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	3.40	7.15
	422297	AW961290	Hs.155615	ESTs	3.44	7.10
	412686	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	3.91	7.09
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	3.09	7.09
	412290	BE069037		gb:QV3-BT0379-161299-040-e12 BT0379 Homo	3.04	7.08
25	415486	H12214	Hs.13284	ESTs	4.22	7.07
	407728	AW071502	Hs.175931	ESTs	3.05	7.06
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	5.93	7.05
	417275	X63578	Hs.81849	parvalbumin	4.08	7.04
	418425	AI871247	Hs.6262	ESTs	4.10	7.04
30	440558	AA889574	Hs.177511	ESTs	3.28	7.04
	411427	AW846080		gb:MR3-CT0176-081099-002-b09 CT0176 Homo	3.11	7.03
	422272	AI452421	Hs.77965	Clk-associating RS-cyclophilin	3.39	7.03
	410816	AW806175		gb:MR1-UM0108-130400-003-a06 UM0108 Homo	3.30	7.02
	418375	NM_003081	Hs.84389	synaposomal-associated protein, 25kD	9.93	7.01
35	421627	AI138551	Hs.97318	ESTs	3.10	7.01
	447258	BE047911		gb:zb44a05.y1 NCL_CGAP_Bm52 Homo sapien	3.09	6.99
	455547	AW994078		gb:RC3-BN0036-090200-011-h02 BN0036 Homo	3.35	6.98
	432209	AW971278		gb:EST383367 MAGE resequences, MAGL Homo	3.49	6.92
	404541	c8p1_6409		exon	4.62	6.89
40	451539	AA059467	Hs.218933	ESTs	3.01	6.88
	429954	AI918130	Hs.21374	ESTs	3.82	6.87
	411138	AW819500		gb:RC5-ST0293-180100-012-c07 ST0293 Homo	3.08	6.87
	447464	AW444957	Hs.201897	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.33	6.85
	454713	AW815111		gb:QV4-ST0212-091199-023-c09 ST0212 Homo	3.16	6.84
45	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.00	6.84
	429667	AA456275	Hs.44841	ESTs	3.09	6.80
	403008	c21p3_2374		exon	3.04	6.78
	446079	T56522	Hs.154030	ESTs	3.11	6.75
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.49	6.75
50	437804	AA828257	Hs.124324	ESTs	3.42	6.73
	436454	AA757615	Hs.291509	ESTs	3.01	6.72
	416334	H53139	Hs.36271	ESTs	3.12	6.70
	455955	BE167014		gb:CM2-HT0502-140200-088-d08 HT0502 Homo	3.05	6.68
	445085	AI569295	Hs.179285	ESTs	3.19	6.68
55	445611	AW418497	Hs.145583	ESTs	3.61	6.68
	437762	T78028	Hs.154679	synaptotagmin 1	7.21	6.68
	416268	H49111		gb:yo21c07.r1 Soares adult brain N2b5HB5	3.02	6.67
	449766	AI668690	Hs.54773	ESTs	3.25	6.64
	443100	AI033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	3.07	6.64
60	408070	AW148852		gb:zf05d05.x1 NCL_CGAP_Bm35 Homo sapien	3.12	6.60
	451602	AW008846	Hs.60857	ESTs	3.05	6.59
	441447	AA934077	Hs.126980	ESTs	4.06	6.59
	445078	AI869975	Hs.4775	junctional protein 3	4.25	6.59
	434501	AF143878	Hs.194152	Homo sapiens clone IMAGE:115304 mRNA seq	3.25	6.58
65	415960	R49020	Hs.24974	ESTs	3.34	6.58
	403395	c3p1_11541		exon	3.59	6.57
	403061	c2p1_10450		exon	3.06	6.56
	419232	AI382037	Hs.87421	ESTs	3.28	6.56
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	6.50	6.56
70	403717	c4p1_3133		exon	3.52	6.53
	452178	AW043576	Hs.171929	ESTs	3.38	6.53
	455758	R15709	Hs.284231	Novel human gene mapping to chromosome 22	4.42	6.52
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fs, clone NT	3.58	6.52
	425440	AA357518		gb:EST66256 LNCAP cells 1 Homo sapiens c	3.15	6.49
75	419412	AW161058	Hs.90297	synuclein, beta	5.60	6.47
	423678	AW963357	Hs.7847	ESTs	3.47	6.47
	416625	R97839	Hs.35758	ESTs	3.10	6.46
	451854	T92536	Hs.194096	ESTs	3.28	6.46
	406732	AA487229	Hs.2064	vimentin	3.71	6.44
	434619	H43163	Hs.32810	ESTs	3.05	6.44
80	413797	BE167274	Hs.5996	ESTs	3.23	6.44
	438612	AW977980	Hs.292129	ESTs	3.39	6.42
	412317	AW991979		gb:RC1-BN0014-210100-012-f05 BN0014 Homo	3.46	6.42
	422159	N76767	Hs.153406	ESTs	3.03	6.41

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.46	6.35
	427334	R44789	Hs.119486	ESTs, Weakly similar to transmembrane re	3.93	6.35
	453839	AL138417		gb:DKFZp434B1729_r1 434 (synonym: htes3)	3.06	6.34
5	429096	AB011106	Hs.196012	KIAA0534 protein	3.12	6.33
	444609	AW571659	Hs.278081	ESTs	3.30	6.33
	419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A recepto	3.11	6.33
	418900	BE207357	Hs.301709	ESTs	3.14	6.30
	437979	AA774318	Hs.121708	ESTs	3.25	6.29
10	410359	R38624	Hs.105313	ESTs	4.74	6.28
	415990	R76929	Hs.29633	ESTs	3.39	6.28
	419392	W28573		gb:51110 Human retina cDNA randomly prim	3.00	6.28
	424312	AB013452	Hs.144931	ATPase, aminophospholipid transporter (A	3.06	6.26
	444762	AI733700	Hs.143883	ESTs	3.09	6.25
	447785	AL041765	Hs.161423	ESTs	3.05	6.22
15	418199	AA884555	Hs.86603	ESTs	3.55	6.22
	440582	AA993337	Hs.129082	ESTs	3.73	6.21
	457766	AL119470	Hs.145631	ESTs	3.69	6.21
	426814	AF036943	Hs.172619	KIAA1106 protein	4.71	6.21
20	412018	BE148152		gb:RC4-HT0231-041199-012-b04 HT0231 Homo	3.36	6.21
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.68	6.19
	420127	AA360399	Hs.44811	ESTs	3.54	6.18
	418833	AW974899	Hs.292776	ESTs	3.08	6.18
	441265	AA927180	Hs.153261	ESTs	3.21	6.17
25	413408	R51793	Hs.21745	ESTs	3.56	6.15
	434512	AW139932	Hs.188941	ESTs	3.56	6.15
	422253	W81526	Hs.118329	ESTs	5.04	6.10
	439950	AW937417	Hs.293561	ESTs	3.24	6.10
	417210	N99228	Hs.49162	ESTs	3.54	6.10
30	414306	BE272198	Hs.283869	Human DNA sequence from clone RPS-1013A2	3.35	6.10
	411265	AW834695		gb:RC0-LT0001-261199-031-D05 LT0001 Homo	3.07	6.10
	412734	AW993498		gb:RC2-BN0033-170300-019-b08 BN0033 Homo	3.36	6.09
	425172	AA447729	Hs.12714	ESTs	5.40	6.06
	451759	W23161	Hs.32886	ESTs	3.21	6.02
35	432154	AI701523	Hs.112577	ESTs	3.50	6.02
	401313	c13p1_435		exon	3.92	5.96
	446951	AI350575	Hs.156730	ESTs	3.20	5.95
	440917	AA909651	Hs.160025	ESTs	3.06	5.94
	405961	ph0_14521		exon	3.12	5.91
40	428737	AA984728	Hs.192760	kinesin family member 5A	3.05	5.90
	417292	N69197	Hs.191361	ESTs	3.62	5.89
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	3.52	5.88
	452524	AW136499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	3.07	5.88
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	4.08	5.87
45	423641	AL137256	Hs.130489	Homo sapiens mRNA; cDNA DKFZp761K0912 (f	3.28	5.87
	420755	AI699437	Hs.165268	ESTs	3.17	5.86
	448116	AW352276	Hs.170700	ESTs	3.28	5.86
	412694	AW984373		gb:PM3-HN0011-200300-001-f01 HN0011 Homo	3.00	5.83
	437612	AA827715	Hs.105153	Homo sapiens cDNA FLJ14230 fis, clone NT	3.09	5.82
50	411522	AW850286		gb:IL3-CT0219-161199-031-H11 CT0219 Homo	3.26	5.81
	456910	BE185921	Hs.98073	ESTs	3.20	5.80
	439915	AI521791	Hs.252358	ESTs	3.55	5.80
	404403	c8p1_1094		exon	3.23	5.80
	405332	cNp3_13017		exon	3.51	5.78
55	411167	AW820204		gb:QV2-ST0296-190100-029-c11 ST0296 Homo	3.04	5.78
	416139	H21109	Hs.172853	ESTs	3.63	5.77
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.65	5.77
	415247	F02431	Hs.6581	ESTs	3.08	5.75
	446037	AI076806	Hs.282965	ESTs	3.42	5.75
60	450478	AW451709	Hs.271200	ESTs	3.80	5.72
	446588	AV659343	Hs.282954	ESTs	3.29	5.72
	413118	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	3.03	5.72
	416946	NM_012324	Hs.80545	mitogen-activated protein kinase 8 inter	3.91	5.72
	454751	AW819132		gb:RC3-ST0281-240400-015-c10 ST0281 Homo	3.06	5.72
65	457194	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.54	5.71
	438601	AA811713	Hs.163222	ESTs	3.26	5.71
	439032	AA829487	Hs.274412	similar to yeast Upf3, variant A	3.10	5.67
	408940	M58583	Hs.662	cerebellin 1 precursor	3.32	5.67
	437700	AA766060	Hs.122848	ESTs	3.23	5.66
70	416061	R45516	Hs.26119	ESTs	3.85	5.65
	452851	BE177663		gb:RC1-HT0598-020300-011-h11 HT0598 Homo	3.04	5.64
	430330	AA476583	Hs.132981	ESTs	3.51	5.63
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	5.67	5.62
	400710	c11p1_1297		exon	3.04	5.61
75	457130	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.31	5.60
	434513	AF143888	Hs.18213	Homo sapiens clone IMAGE:121736 mRNA seq	3.93	5.60
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	3.67	5.58
	440854	AW444900	Hs.246715	ESTs	3.30	5.58
	457086	AA412591	Hs.204685	ESTs	3.37	5.57
80	431883	AA731404	Hs.105510	ESTs	3.67	5.56
	400758	AA158742	Hs.225084	Homo sapiens cDNA FLJ14280 fis, clone PL	3.43	5.55
	455374	AW904039		gb:CM3-NN1040-200400-156-d03 NN1040 Homo	3.36	5.52
	440750	AW105131	Hs.245405	ESTs	3.10	5.50
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.38	5.50

5	453100	AW806871	Hs.224786	ESTs	3.30	5.49
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	3.24	5.49
	454935	AW846075		gb:MR3-CT0176-081099-002-b02 CT0176 Homo	3.26	5.48
	435447	A1872932	Hs.142442	HP1-BP74	3.89	5.47
	402953	c20p3_3451		exon	3.28	5.47
	456233	AA203339		gb:zx56a01.r1 Soares_fetal_liver_spleen_	3.02	5.47
	407718	AW070784	Hs.243243	EST	3.30	5.45
	417429	A1950529	Hs.286237	Homo sapiens cDNA FLJ111841 fis, clone HE	3.31	5.38
10	446408	A1797169	Hs.208486	ESTs	3.07	5.37
	441792	AW873635	Hs.143962	ESTs	3.19	5.35
	450661	AW952160	Hs.32916	ESTs	3.70	5.35
	433932	AW954599	Hs.169330	neuronal protein	6.78	5.33
	427002	AA524093	Hs.23158	ESTs	4.00	5.32
15	428741	AA461386		gb:zx70h06.r1 Soares_tatal_fetus_Nb2HFB_	3.10	5.32
	446383	T05816	Hs.92511	EST	3.39	5.30
	442988	A1026130	Hs.131683	ESTs	3.07	5.29
	426713	A1655299	Hs.130055	ESTs	3.33	5.29
	421294	AA713486	Hs.180291	ESTs	3.44	5.28
20	406452	ph2_21981		exon	3.20	5.28
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.26	5.27
	442114	BE217975	Hs.157021	ESTs	3.32	5.26
	432508	A1808915	Hs.190201	ESTs	3.46	5.26
	425604	U94320	Hs.158330	neuropeptide Y receptor Y5	3.26	5.23
25	417925	R26789	Hs.23995	ESTs	3.08	5.23
	444448	H66317	Hs.143660	ESTs	3.81	5.22
	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	3.71	5.22
	437911	AA848010	Hs.124250	ESTs	3.11	5.18
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin	4.95	5.17
30	407131	R98679		gb:yr31c03.s1 Soares fetal liver spleen	3.30	5.16
	435776	A1537162	Hs.263988	ESTs	3.14	5.13
	455532	AW984828		gb:RC1-HN0015-120400-021-h11 HN0015 Homo	3.14	5.13
	457352	AA489099		gb:aa56h09.s1 NCI_CGAP_GCB1 Homo sapiens	3.48	5.12
35	428670	AA431682	Hs.134832	ESTs	3.17	5.12
	445962	A1268410	Hs.201386	ESTs	3.14	5.12
	418153	R13696	Hs.112830	ESTs	3.16	5.10
	440565	AW103823	Hs.131586	ESTs	3.08	5.10
	431446	AW294929	Hs.255369	Homo sapiens cDNA FLJ10265 fis, clone HE	3.42	5.09
40	456036	BE536554	Hs.75839	zinc finger protein 6 (CMPX1)	3.21	5.09
	420883	A1735488	Hs.111436	ESTs	3.17	5.08
	455528	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.35	5.08
	408442	R59608	Hs.21435	ESTs	3.10	5.07
	446093	A1346849	Hs.145896	ESTs	3.30	5.06
45	403489	c3p1_2255		exon	3.43	5.05
	405278	clp3_1070		exon	3.05	5.03
	412804	H18857	Hs.22547	ESTs	3.63	5.03
	458407	W90022	Hs.185809	ESTs, Highly similar to LECT2 precursor	3.52	5.03
	407367	AA130773		gb:zo13d01.r1 Stratagene colon (937204)	3.51	5.02
50	439108	AW163034	Hs.6467	synaptogyrin 3	5.63	5.01
	445335	A1220339	Hs.166775	ESTs	3.21	5.01
	435404	A1240661	Hs.124995	ESTs	3.99	5.00

TABLE 6B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

55	Pkey	CAT Number	Accession
	410837	282574_1	AW806917 AW866469 BF898475 BF898476 AW866540 AW866614 BE145698 AW866575
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
60	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454589	28039_6	BG574750 BF374578 AW810080 AW810106 AW810084 BF374755 AW809621 BF374734 BF374590 BF374594 AW809699 BF374588 AW810437
			AW810161 AW809662 AW810151
	417159	2075888_1	R01760 N49787 R01761
65	459349	1027822_1	AW749381 H93337
	414187	315279_1	BE259777 BE312141 BF942980
	423280	881045_1	AW955178 H86636 AA324037
	431400	1233916_1	AW969094 AA504607 AA504705
	454566	154604_1	AW807605 AW807690 AW807677 AW807752 AW807673 AW807900 AW807955 AW807679 AW807615 AW807917 AW807849 AW807832 AW807821
70			AW807842 AW807827 AW807754 AW807830 AW807829 AW807825 AW807819 AW807769 AW807685 AW807603 AW807763 AW807612 AW807840
			AW807908 AW807684 AW807609 AW807596 AW807595 AW807593 AW807907 AW807902 AW807846 AW807756 AW807687 AW807836 AW807835
			AW807770 AW807753 AW807669 AW807678 AW807696 AW807680 AW807688 AW807847 AW807957 AW807674 AW807602 AW807617 AW807921
			AW807667 AW807952 AW807918 AW807670 AW807760 AW807956 AW807608 AW807683 AW807839 AW807601 AW807822 AW807898
	437948	330397_1	AA772920 D59870 D61151 AI591331 BF960996
75	438919	1242618_1	AW979114 AA828060 AA837606 AA829203
	454578	1670_3	BE150647 AW971143 AW809224 AW809221 BF753820 AW809220 AW809178 AW809150 AW809195 AW809175
	455836	1518824_1	BE145800 BE145921 BE145873 BE145871 BE145930 BE145797 BE145795
	454968	1085677_1	AW848279 AW849039 AW847956 AW847957 AW849046 AW848698 AW849034 AW849033
	418162	2189291_1	T11756 T20135 T19729 T11958 T11816 R45874
80	431169	1235760_1	AW971240 AA493723 AA493843
	458172	363900_1	BE007237 BE546311 AA984819 BI256810 W19919 BE007263 BG000322 BF327011 AA890198 BE007496
	412172	709034_1	W04156 AW897535 N94221
	427942	465847_1	BE543651 AA417856 AV756446 BG505084 BI460307 BI460993 BG613293
	454688	1066481_1	BF375123 AW814472 AW814474 AW813343 AW816161 AW813380 AW813300

5	455675	1490763_1	BE065984 BE066085 BE065942 BE065955
	455644	1489581_1	BE064521 BE064441 BE064426 BE064285 BE064286
	451496	85420_1	AA046879 BF327988 AW503407 AA018131
	424617	895912_1	AW963059 AA344151 AA344472
	454962	323094_1	AW853945 AW854083 BF962818 AW847791 BI035483 AW847645 BF961514 BF963484 BF952264 BF963521
	455260	231032_1	BE161805 AW878317 BE161759 BF870032 BF869588
	434589	14676_1	AF147363 T47219 T47218
	410926	1064369_1	AW810708 AW810808 AW810771 AW810924
10	409623	830636_1	AW449665 BE220971 AW449185
	437254	1239876_1	AW976161 AA831258 AA765857 AA747712 AI784019
	415508	1874742_1	R45579 F10822 R39236
	413263	1497122_1	BE075132 BE075131 BE075130 D60395 BF688035
	415967	1899490_1	H49130 H11230 BF363165 H49061 H11124
	417555	1978200_1	AA203678 AL597143 H65366
15	413547	1520005_1	BE147456 BE147563 BE147708 BE147440
	411132	1070974_1	AW819177 AW819242 AW819191 AW819175 AW819252 AW819244 AW819265 AW819269 AW819190 AW819268 AW819183 AW819246 AW819194
			AW819249 AW819186 AW819180 AW819188 BE158470 AW819251 BE152602 AW819263
20	454568	1061859_1	AW807909 AW807824 AW807826 AW807903 AW807766 AW807750 AW807911 BE141434 AW807611 AW807837 AW807899 BF374481
	413162	1492355_1	BE068104 BE068096 BE068198 BE068115 BE068102 BE068154 BE068103
	455377	154707_1	BF947516 AW905291 BF947512 BF952606 BF952706 BF952525 BF952524 BF952619 BF947500 BF952608 BF952523 BF952532 BF952344
			BF746516 BF947614 BF746511 BF952358 AW905400 AW905300 BF947617 AW905349 BF952531 AW905403 BF952528 BE081655 BF746513
			AW905286 BF952868 BF947513 BF947510 BF947618 BF947619 AW905347
			AW861879 AW861948 AW868447 AW861873 AW858418 AW861871
25	455149	1099453_1	AW984068 AW984077 AW984072
	412686	1243154_1	AJ227879 BE065178 BE065329
	436383	46767_1	BE069037 BE069178 AW936034 AW936025
	412290	1163352_1	AW846080 AW846074 AW846118 AW846130
	411427	1083097_1	AW806175 AW806176 AW806170 AW806156
	410816	1060611_1	BE617316 BE047911 AA984167
30	447258	1485710_1	AW994078 BE176183
	455547	1245954_1	AW971278 AA528270 AA553447 AW971281
	432209	1235790_1	AW819500 AW819503 AW819481 AW819459 BF375618
	411138	1071173_1	AW815111 AW815094 AW815218
	454713	1067889_1	BE167014 BE167058 BE167062
35	455965	1555935_1	H41854 H49111 H46317
	416268	1959926_1	BE004743 AW804074 BE089437 BE089439 BE089378 BE089438 BE004795 W02375 AI033188 BF332422 BF332418 BE178660
	443100	416959_1	AW148852 BG994152
	408070	632273_1	AW962960 AA357518 AA360531
40	425440	1228191_1	AW991979 AW991981 AW991983 AW936856 AW991977 AW991971 AW936852
	412317	1164038_1	AL138417 AL138418
	453839	3209657_1	W28573 W27418
	419392	215562_2	BE148133 BE148132 BF736564 BE148152 BE148159 BF893700
	412018	147109_1	AW834695 AW834717 AW834714
	411265	1074383_1	AW993498 AW993484 AW993490 BF512974
45	412734	1245451_1	AW984388 AW984392 AW984379 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984373 AW984372 AW984353 AW984362
	412694	1243393_1	BE143505 BF374194 BF374190 AW850286
	411522	1089092_1	AW820323 AW820314 AW820321
	411167	1071740_1	BE066079 BE065939 BE065956
	413118	1490760_1	AW819132 AW819122 AW819018 AW819135 AW819126 AW819024 AW819012 AW819141
50	454751	1070838_1	BE177663 AW994738 AI923735 BF948431 BF948329
	452861	319757_1	AW904029 AW904030 AW904039 AW904031 AW904032 AW904046
	455374	1161013_1	AW846075 AW846103 BF333976 AW846077 AW846122 AW846129 AW846095 AW846076 BF333979 BF333978 AW846092
	454935	1083098_1	AA203339 AA906160 AA929005
	456233	2635744_1	AA461386 AA433841 AA433845
55	428741	1384399_1	AW984828 AW984787 AW984806 AW984817 AW984826 AW984822 AW984773 AW984786 AW984803 AW984796
	455532	1243692_1	AW968968 AA489099 N72933 AA489184
	457352	1233795_1	AW984734 AW984757 AW984797 AW984745
	455528	1243660_1	AF085963 H72550 H72951 AA130773
	407367	4907_1	
60	TABLE 6C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
65	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand NL_position
70	401412	7940103	Minus 43347-45776
	405230	7249032	Minus 97493-97682
	402125	4033680	Plus 172732-172868
	404289	2769644	Plus 15049-15286,30267-30457
	406534	7711477	Plus 40463-40586,41191-41336,41856-41986,4300
	406348	2914717	Minus 43310-43462
75	401081	3478647	Plus 105163-105305
	402624	7885063	Minus 31308-31439
	405320	3478667	Minus 118511-118926,119175-119331
	405476	2121229	Plus 69890-70883
	403932	7454203	Minus 8142-8753
80	406112	9133145	Plus 61863-62028
	400708	7249204	Plus 118115-119445
	405427	7243901	Minus 6509-6729
	402816	6723302	Minus 25104-25291
	404541	8318559	Plus 103456-103664

403008	6070396	Plus	94608-94785,95096-95233
403395	9438353	Minus	144947-145075
403061	8954192	Plus	142875-143008
403717	7259747	Minus	79168-79758
401313	9212516	Minus	190842-191090
405961	8190197	Plus	45132-45254
404403	7272157	Minus	72053-72238
405332	3169141	Minus	70483-71207
400710	7249204	Plus	156753-157120
402953	9408724	Minus	122603-122743
406452	9588380	Minus	76322-76427
403489	7331314	Minus	38897-39212
405278	6139075	Minus	3863-3965,4823-4891,5439-5529,6043-6170

TABLE 7A: EXTENDED GLIOBLASTOMA SEQUENCES: This table includes sequence information for 21 DNA and protein sequences

DNA sequence 1

Gene name: Protein tyrosine phosphatase, receptor-type, Z polypeptide 1

Unigene number: Hs.78867

Probeset Accession #: M93426

Nucleic Acid Accession #: NM_002851

Coding sequence: 148-7092

1	11	21	31	41	51	
5						
10						
15						
20						
25	CACACATACG	CACGCACGAT	CTCAGCTTGA	TCTATACACT	GGAGGATTAA	AACAAACAAA 60
	CAAAAAAATC	ATTTCCTTGG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA 120
	CGCGCAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCTTAA	AGCGTTTCCT	CGCTTGCATT 180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA 240
30	CTTGTGTAAG	AGATTGGCTG	GTCTTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAG 300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA 360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA 420
	AACACATTCA	TTCATAAAC	TGGGAAAAAC	GTGGAAATTA	ATCTCACTAA	TGACTACCGT 480
	GTGAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACCTGGGA 540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT 600
35	GAGATGCAAA	TCTACTGCTT	TGATGCCGAC	CGATTTTCAA	GTTTGGAGGA	AGCAGTCAAA 660
	GGAAAAAGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TGGGACAGA	AGAAAAITTTG 720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	GCAGGCTGCT 780
	TTAGATCCAAT	TCATCTGTTT	GAACCTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTAC 840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT 900
40	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCCTAC	AATGCAACAA 960
	TCGTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACCAAT	TTGGAGAGCA	ACAGTACAAG 1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACT	GGAAAGGAAG	AGATTTCATGA	AGCAGTTTGT 1080
	AGTTCAGAAC	CAGAAATATG	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTATCA 1140
45	TGGGAAGAGC	CTCAGTCTGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG 1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG 1260
	GGTGCTATTTC	TCATTAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA 1320
	TGCACTAATG	GCCTATATGG	AAAATACAGC	GACCAACTGA	TTGTGCAGAT	GCCTACTGAT 1380
	AATCTGCAAT	TTGATCTTTT	CCCTGAATTA	ATTGGAAGTG	AAGAAATAAT	CAAGGAGGAG 1440
50	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA 1500
	AACCAATACA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG 1560
	ACGAAATACA	ATGAGGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA 1620
	AAGGGTATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTAC	TAAATAGGCC 1680
	ACAGAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AAGTCCACCC	TCACATGTG 1740
55	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG 1800
	AACTTGTGCG	GGACTGCGAG	ATCCTTAAAT	ACAGTTTCTA	TAAACAGAATA	TGAGGAGGAG 1860
	AGTTTATTTCA	GCTTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	CTCCAGTCCC 1920
	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTCC 1980
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	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT 2520
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	CCCAACATGT	ATGTAATATG	AAATAAGTTG	AATGGGTCTT	TACAAGAAAC	CTCTGTTTCC 3420
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 5 CCAAGAGTTG ATAAAGTGT TCTTCCAGCT GTGCCCACTG ATCCAATATT GGTGAAACC 3840
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 40 ACCTTTGTGA GAAAGGCAGC CTATGCCAAG CGCCATGCGT TGGGGCTGT TGTGCTCCAC 5940
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 70 ATAATTGTAG ATTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTTCTG TGTAAITGTT 7680
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 GGTTTTATC CAAGGAATTG CAAAAATAA TATAAATATT GCCATTAATA AAAAAAATA 7920
 AAAAAAAAAA AAAAAAAAAA A

Protein sequence 1

Gene name: Protein tyrosine phosphatase, receptor-type, 2 polypeptide 1

Unigene number: Hs.78867

Protein Accession #: NP_002842

Signal sequence: 1-20

Pfam domain: carb anhydrase [38-300]

Transmembrane domains: 1639-1661

Cellular Localization: plasma membrane

1 11 21 31 41 51

MRILKRFAC IQLLCVCRID WANGYYRQR KLVEEIGWSY TGALEQKNG KKYPTCNPK 60
 QSPINDEEDL TQVNVNKKL KFGQWDKISL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFHW GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSEFEAV KGKGLRLALS 180
 ILFEVGTEDN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSY 300
 TGKEEIHFAV CSSEPEVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPDLDFPE 420
 LIGTEELIKE EEBGKIDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHPT VEGTSASLND 540
 GSKTVLRSEPH MNLSGTAESL NTVSITIEYEE ESLLTSFKLD TGAEDSSGSS PATSAIFPIS 600
 ENISQGYIFS SENPETITYD VLIPEASRNA SEDSTSSGSE ESKLDPMSMEG NVWFPSSTDI 660
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 ILPQVTSATE SDKVPLHSL PVAGDLLLL PSQAQYSDVL STTHAASETL EFGSESGVLY 900
 KTLMSQVSEP PSSDAMMHAR SSGPEPSYAL SDNEGSHQIF TVSYSSAIPV HDSVGVTYQG 960
 SLFSGPSHIP IPKSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020
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 AVPSDPILVE TPXVDKISS MLHLIVNSA SSNMLHSTS VPVFDVSPTS HMHSASLQGL 1260
 TISYASEKYE PVLLKSESH QVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320
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 PGKSPSANGL SQKHNDGKEE NDIQTGSALL PLSPEKANA VLTSDEESGS QGQTSDSLNE 1560
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 ESRIGLAEGL ESEKKAVIPL VIVSALTFIC LVVLVLGILI WRKCFQTAHF YLEDSTSPRV 1680
 ISTPTPTIFP ISDDVGAIFI KHFPKHVADL HASSGFTEEF ETLKEFYQEV QSCTVDLGIT 1740
 ADSNHPNPK HKNRYINIVA YDHSRVKLAQ LAEKDGKLD YINANYVDGY NRPKAYIAAQ 1800
 GPLKSTAEDE WRNIWEHNV VIVMITNLVE KGRKCDQYW PADGSEEYGN FLVTQKSVQV 1860
 LAYYTVRNF LNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVPYSLPV LTFVRKAAYA 1920
 KRHAVGPVVV HCSAGVGRGT TYIVLDSMLQ QIQHEGTVNI FGFLKHIRSQ RNYLVQTEEQ 1980
 YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGT KLEKQFQLS QSNIQQSDYS 2040
 AALKQCNREK NRTSSIIPE RSRVGISSLS GEGTDYINAS YIMGYQSNB FIITQHPLLH 2100
 TKDFWRMIW DHNAQLVVM PDGQNMMAEDE FVYWPKNDEP INCESFKVIL MAEBHKCLSN 2160
 EEKLIQDFI LEATQDDYVL EVRHFPQPKW PNPDPISKT FELISVKEE AANRDGPMIV 2220
 HDEHGGVTAG TFCALTLLMH QLEKENSVDV YQVAKMINLM RGVVFADIEQ YQFLYKVLIS 2280
 LVSTRQENP STSLDSNGAA LPDGNIAESL ESLV

DNA SEQUENCE 2

Gene name: tyrosylprotein sulfotransferase 1

Unigene number: Hs.110903

Probeset Accession #: D61594

Nucleic Acid Accession #: NM_003596

Coding sequence: 82-1194

1 11 21 31 41 51
 | | | | |
 GTAGACTGTC CATGGCCTGA ACATTTTCCG AAAATCATT TGAGCAAAAT ATCTGTTTAA 60
 TAACAAGATA ACCACATCAA GATGGTTGGA AAGCTGAAGC AGAACTTACT ATTGGCATGT 120
 CTGGTGATTA GTTCTGTGAC TGTGTTTAC CTGGGCCAGC ATGCCATGGA ATGCCATCAC 180
 CGGATAGAGG AACGTAGCCA GCCAGTCAA TTGGAGAGCA CAAGGACCAC TGTGAGAACT 240
 GGCTGGAC TCAGAACCAA CAAACCTTT GCCTATCACA AAGATATGCC TTTAATATTT 300
 ATTGGRGTG TGCCCTCGAG TGAACACCA CTCATGAGG CCATGCTGGA CGCACATCCT 360
 GACATTGCT GTGGAGAGGA AACGAGGTC ATTCCCGAA TCCTGGCCCT GAAGCAGATG 420
 TGGTCACGGT CAAGTAAAGA GAAGATCCGC CTGGATGAGG CTGGTGTAC TGATGAAGTG 480
 CTGGATTCTG CCATGCAAGC CTCTTACTA GAAATTATCG TTAAGCATGG GGAGCCAGCC 540
 CTTATTAT GTAAATAAGA TCCTTTGCC CTGAAATCTT TAACTTACCT TTCTAGGTTA 600
 TTCCCAATG CCAAAATTTCT CCGATGGTC CGAGATGGCC GGCATCAGT ACATTCAATG 660
 ATTTCTCGAA AAGTTACTAT AGCTGGATT GATCTGAACA GCTATAGGGA CTGTTTGACA 720
 AAGTGAATC GTGCTATAGA GACCATGTAT AACCATGTAT TGGAGGTTGG TTATAAAAG 780
 TGCAATGTTG TTCATATGA ACAACTGTG TTACATCTCG AACGGTGGAT GAGAACACTC 840
 TTAAAGTTCC TCCAGATTCC ATGGAACCAC TCAGTATTGC ACCATGAAGA GATGATTGGG 900
 AAAGCTGGGG GAGTGTCTCT GTCAAAAGTG GAGAGATCTA CAGACCAAGT AATCAAGCCA 960
 GTCAATGTAG GAGCTCTATC AAAATGGGTT GGAAGATAC CGCCAGATGT TTTACAAGAC 1020
 ATGGCAGTGA TTGCTCCTAT GCTTGCCAAG CTGGATATG ACCCATATGC CAACCCACCT 1080
 AACTACGGAA AACCTGATCC CAAATATTAT GAAACACTC GAAGGGTCTA TAAGGGAGAA 1140
 TTCCAATCTC CTGACTTTCT TAAAGAAAA CCACAGACTG AGCAAGTGGA GTAGCAGAAC 1200
 CAGGAGCCTC TTCCATACAT GAGGAAAGAT TGCTGCCTTT TCAGCAGAA GGAATTCCT 1260
 AGGATTGGCT GTCCCTGCC AAGCTTGGTG GAGCGTCTGC ACCTTGGCTG CGCCGCTGT 1320
 GCATTGCCA GTTCTCTCC ACTGAGAGGA TGGAGGTGTC CGCACAGCTT TGGGCTCGT 1380
 GAGGATCTG CCTCTGAGC AAGAGCTCT TGATCCCGAT TTATGCACA GCCTGCGAT 1440
 AAGGAGCCCA GAAGGAACAT GTGTTCTCTG TTAAGTCTC TCTGTCTC TTTTCTTACA 1500
 TTATGAGCTT TGTTTTCAAG GAGAGGGTTT AAAATGGGA TCCTGTAAAG AGACTTGGGC 1560
 AGTCTCTCTT TGAATAGGT TGTCTGTACA TGTTCTAATG TTTGTAGTAA CACGTGTGCC 1620
 TGTTTAAGTG TATTGATGTG AATAATATTA AATATCTTAA TTATTTAATT CATGTATTG 1680
 TTTCTGAGAA GTTGGGAAAT TACCATTATA CATTACAC CTAATGACTT TTGTATTTA 1740
 TTTTCAAAA TAAAGCTTT CAATGTGA

Protein sequence 2

Gene name: tyrosylprotein sulfotransferase 1

Unigene number: Hs.110903

Protein Accession #: NP_003587

Signal sequence: 1-21

Transmembrane domains: none found
Cellular Localization: plasma membrane

1 11 21 31 41 51
| | | | |
5 MVGKLKQNL LACLVISSVT VFYLGQHAME CHRIEERSQ PVKLESTRTT VRTGLDLKAN 60
KTFAYEKDMP LIFIGGVPRS GTTLMRAMLD AHPDIRCGEE TRVIPRILAL KQMSRSRSKE 120
KIRLDEAGVT DEVLDSAMQA FLLEIIIVKHG EPAPYLCKND PFALKSLTYL SRLFPNAKFL 180
LMVRDGRASV HSMISRKVTI AGFDLNSYRD CLTKWNRAT TMYNQCMVEG YKKCMVLVHYE 240
10 QLVLHPRWMM RTLLKFLQIP WNHSLVHHEE MIGKAGGVSL SKVERSTDQV IKPVNVGALS 300
KHWGKIPDPV LQDMAVIAPM LAKLGYPYA NPPNYGKPDF KIIENTRRVY KGEFQLPDFL 360
KEKFPQTEQVE

DNA sequence 3

Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Nucleic Acid Accession #: NM_000640
Coding sequence: 94-1236

1 11 21 31 41 51
| | | | |
20 CGGATGAAGG CTATTGAAG TCGCCATAAC CTGGTCAGAA GTGTGCGCTGT CGGCGGGGAG 60
AGAGGCAATA TCAAGGTTT AAATCTCGGA GAAATGGCTT TCGTTTGCTT GGCTATCGGA 120
TGCTTATATA CTTTCTGAT AAGCACAACT TTTGGCTGTA CTTTCATCTC AGACACCGAG 180
25 ATAAAAGTTA ACCCTCCCTCA GGATTTTGAG ATAGTGGATC CCGGATACTT AGGTTATCTC 240
TATTTGCAAT GGCACACCCC ACTGCTCTG GATCATTTTA AGGAATGCAC AGTGGAAATAT 300
GAACATAAAT ACCGAAACAT TGGTAGTGAA ACATGGAAGA CCATCATTAC TAAGAATCTA 360
CATTACAAAG ATGGGTTTGA TCTTAACAAG GGCATTGAAG CGAAGATACT CACGCTTTTA 420
CCATGGCAAT GCACAAATGG ATCAGAAGTT CAAAGTTCCT GGGCAGAAAC TACTTATTGG 480
30 ATATCACCAC AAGGAATTC AGAACTAAA GTTCAGGATA TGGATTGCGT ATATTACAAT 540
TGSCAATATT TACTCTGTTT TTGGAAACCT GGCATAGGTG TACTTCTTGA TACCAATTAC 600
AACTGTGTTT ACTGTATGTA GGGCTTGGAT CATGCATTAC AGTGTGTTGA TTATCATCAAG 660
GCTGATGGAC AAAATATAGG ATGCAGATT CCCTATTGG AGGCATCAGA CTATAAAGAT 720
TTCTATATTG GTGTTAATGG ATCATCAGAG AACAGCCTA TCAGATCCAG TTATTTCACT 780
35 TTTCACTTC AAAATATAGT TAAACCTTTG CCGCCAGTCT ATCTTACTTT TACTCGGGAG 840
AGTTTCATGT AAATTAAGCT GAAATGGAGC ATACCTTTGG GACCTATTCC AGCAAGGTGT 900
TTTGATTATG AAATTGAGAT CAGAGAAGAT GATACTACCT TGGTGACTGC TACAGTTGAA 960
AATGAAACAT ACACCTTGAA AACACAAAT GAAACCGAC AATTATGCTT TGTAGTAAGA 1020
AGCAAAAGTA ATATTATATG CTCAGATGAC GGAATTTGGA GTGAGTGGAG TGATAAAACAA 1080
40 TGCTGGGAAG GTGAAGACCT ATCGAAGAAA ACTTGTCTAC GTTCTGGCT ACCATTGGT 1140
TTCATCTTAA TATTAGTTAT ATTGTAAACC GGTCTGCTTT TCGTAAGCC AACACCTAC 1200
CCAAAATGA TTCAGAAAT TTTCTGTGAT ACATGAAGAC TTTCCATATC AAGAGACATG 1260
GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA TATGAGTCTC AATAAACTGA 1320
ATTTTCTCTG CGAAAAA AAAA AAAA AAAA AAAA AAAA AAAA 1380
AA

Protein sequence 3

Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Protein Accession # NP_000631
Signal sequence: 1-23
FN3 domain: 155-322

Transmembrane domains: 340-362
Cellular Localization: plasma membrane

1 11 21 31 41 51
| | | | |
55 MAFVCLAIGC LYTFLLSTTF GCTSSSDTEI KVNPPQDFEI VDPGYLGVLV LQWQPFLSLD 60
HFKECTVEYE LKYNIGSET WKTIIITKNLH YKDGFDLNGK IEAKIHTLLP WQCTNGSEVQ 120
60 SSWAETTYWI SPQIPETKV QDMDCVYVNW QYLLCSWKPG IGVLLDTNIN LFYWYEGLDH 180
ALQCVDYIKA DQONIGCRFP YLEASDYKDF YICVNGSSEN KPIRSSYTF QLQNIIVKPLP 240
FVYLTFTRFS SCEIKLWISI PLGPPIPARCF DYEIEIREDD TTLVTATVEN ETYTLKTTNE 300
TRQLCFVVRV KVMICYSDDG IWSEWSDKQC WEGEDLSKKT LLRFWLPFGF ILILVIFVTG 360
LLLRKENTYP KMIPEFFCDT

DNA sequence 4

Gene name: chemokine (C-X3-C) receptor 1
Unigene number: Hs.78913
Probeset Accession #: U20350
Nucleic Acid Accession #: NM_001337
Coding sequence: 46-1113

1 11 21 31 41 51
| | | | |
75 GGGGAGATC CAGATTCCTT TTGCAGTCCA CGCCAGGCCT TCACCATGGA TCAGTTCCCT 60
GAATCAGTGA CAGAAAACCT TGAGTACGAT GATTGGCTG AGGCCTGTTA TATTGGGGAC 120
ATCGTGGTCT TGGGACTGT GTTCTGTGCC ATATTCTACT CCGTCATCTT TGCCATTGGC 180
CTGGTGGGAA ATTGTTGGT AGTGTGTTGCC CTCACCAACA GCAAGAGACC CAAGAGTGTC 240
ACCGACATTT ACCTCCTGAA CCTGGCCTTG TCTGATCTGC TGTGTTGAGC CACTTTGCC 300
78 TTCTGGAGTC ACTATTGAT AAATGAAAAG GGCCTCCACA ATGCCATGTG CAAATTCAT 360
ACCGCTTCT TCTTCATCGG CTTTCTTGGG AGCATATTCT TCATCACCGT CATCAGCATT 420
80 GATAGGTACC TGGCCATCGT CCTGGCGGCC AACTCCATGA ACAACCGGAC CGTGACGAT 480
GGCGTCACCA TCAGCCTAG CGTCTGGGCA CGAGCCATT TGGTGGCAGC ACCCCAGTTC 540
ATGTTCAACA AGCAGAAAGA AAATGAATGC CTGGTGACT ACCCCAGGAT CTTTCAGGAA 600
ATCTGGCCCG TGCTCCGCAA TGTGGAACA AATTTCTTG GCTTCTCTAC CCCCCTGCTC 660
ATTATGAGTT ATTGCTACT CAGATCATC CAGAGCTGT TTTCTGCAAG GAACCAAG 720

AAAGCCAAAG CCATTAAACT GATCCTTCTG GTGGTCATCG TGTITTTCTT CTCTGGACA 780
CCCTACAACG TTTATGATTTT CCTGGAGACG CTTAAGCTCT ATGACTTCTT TCCCAGTTGT 840
GACATGAGGA AGGATCTGAG GCTGGCCCTC AGTGTGACTG AGACGGTTGC ATTTAGCCAT 900
TGTTCCTGTA ATCCTCTCAT CTATGCATTG GCTGGGGAGA AGTTCAGAAG ATACCTTTTAC 960
CACCTGTATG GGAATGCCTT GGCTGTCTCT TGTGGGCGCT CAGTCCACGT TGATTTCTCC 1020
TCATCTGAAT CACAAGGAG CAGGCATGGA AGTGTCTCTG GCAGCAATT TACTTACCAC 1080
ACGAGTGATG GAGATGCATT GCTCCTTCTC TGAAGGGAAT CCCAAAGCCT TGTGTCTACA 1140
GAGAACCTGG AGTTCCTGAA CCTGATGCTG ACTAGTGAGG AAGATTTTGT TTGTTATTTT 1200
TTACAGGCAC AAAATGATGG ACCCAATGCA CACAAAACAA CCTTAGAGTG TTGTTGAGAA 1260
TTGTGCTCAA AATTTGAAGA ATGAACAAAT TGAACCTCTT GAATGACAAA GAGTAGACAT 1320
TTCTCTTACT GCAAAATGTA TCAGAACTTT TTGGTTTGCA GATGACAAA ATTCAACTCA 1380
GACTAGTTTA GTTAAATGAG GGTGGTGAAT ATTGTTTATA TTGTGGCACA AGCAAAAAGG 1440
GTGTCGAGC CCTCAAAGTG AGGGGAACCA GGGCCTGAGC CAAGCTA

Protein sequence 4

Gene name: chemokine (C-X3-C) receptor 1

Unigene number: Hs.78913

Protein Accession #: NP_001328

Signal sequence: 1-44

Pfam domain: 7tm_1 [48-293]

Cellular Localization: plasma membrane

1 11 21 31 41 51
MDQPPESVTE NFEYDDLAEA CYIGDIVVFG TVFLSIFYSV IFAIGLVGNL LVVFALTNK 60
KPKSVTDIYL LNLALSDLLE VATLPFWTHY LINEKGLHNA MCKFTTAPFF IGFFGSIPFI 120
TVISIDRYLA IVLAANSMMN RTVQHGVTIS LGVWAAAILV AAPQFMFTKQ KENECLGDYP 180
EVLQEIWVPL RNVETNPLGF LLPLLIMSYC YFRIIQTLS CKNHKAKAI KLILLVVIVF 240
FLFWTPYNVM IFLETLKLYD FFPSCDMRKD LRLALSVTET VAFSHCLNLP LIYAFAGEKF 300
RRYLHYLYGK CLAVLCGRSV HVDFSSSESQ RSRHGSVLSS NFTYHTSDGD ALILL

DNA sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

Probeset Accession #: 412986

Nucleic Acid Accession #: NM_001840

Coding sequence: 92-1510

1 11 21 31 41 51
TCGGCTTATT TGTITTTCCCT CCTCTTAGGA TTGCCCCCTG TGGGTCACCT TCTCAGTCAT 60
TTTGAGCTCA GCTAATCAA AGACTGAGGT TATGAAGTCG ATCTAGATG GCCTTGACAG 120
TACCACCTTC CGCACCATCA CCACTGACCT CTTGTACGTG GGCTCAAATG ACATTGAGTA 180
CGAAGACATC AAAGGTGACA TGGCATCCAA ATTAGGGTAC TTCCCACAGA AATTCCCTTT 240
AACTTCCTTT AGGGGAAGTC CCTTCCAAGA GAAGATGACT GGGGAGACA ACCCCAGCT 300
AGTCCACGCA GACCAGGTGA ACATTACAGA ATTTTACAAC AAGTCTCTCT CGTCCCTCAA 360
GGAGAAATGAG GAGAACATCC AGTGTGGGGA GAACTTCATG GACATAGAGT GTTTCATGCT 420
CCTGAACCCC AGCCAGCAGC TGGCCATTGC AGTCTGTGCC CTCACGCTGG GCACCTTCAG 480
GGTCTCTGAG AACCTCCTGG TGCTGTGCGT CATCTCCAC TCCCGCAGCC TCCGCTGACG 540
GCCTTCCTAC GACTTCATCG GCAGCCTGGC GGTGGCAGAC CTCCTGGGGA GTGTCAATTT 600
TGCTACAGC TTCAATGACT TCCACGTGTT CCACGCAAA GATAGCCGCA ACGTGTCTCT 660
GTTCAAACCTG GGTGGGGTCA CGCCTCCTT CACTGCCTCC GTGGGCAGCC TGTTCCTCAC 720
AGCCATCGAC AGGTACATAT CCATTACAGG GCCCTGGGCC TATAAGAGGA TTGTACACCA 780
GCCCAAGGCC GTGGTGGCGT TTTGCCGTAT GTGGACATA GCCATTGTGA TCGCCGTGCT 840
GCCTCTCCTG GCGCTGAACT GCGAGAAACT GCAATCTGTT TGCTCAGACA TTTTCCACAG 900
CATTGATGAA ACCTACCTGA TGTCTGGAT CGGGGTCAAC AGCGTACTGC TTCTGTTTCT 960
CGTGTATGCG TACATGTATA TTCTCTGGA GGTCTCAGC CACGCCGTCC GCATGATTCA 1020
GCGTGGCACC CAGAAGAGCA TCATCATCCA CAGCTGTAG GATGGGAAGG TACAGGTGAC 1080
CCGGCCAGCA CAAGCCCGCA TGGACATTAG GTTAGCCAAG ACCCTGGTCC TGATCCTGGT 1140
GGTGTGTATC ATCTGCTGGG GCCCTCTGCT TGCAATCATG GTGTATGATG TCTTTGGGAA 1200
GATGAACAGC CTCATTAAGA CGGTGTTTGC ATTCTGCAGT ATGCTCTGCC TGCTGAACTC 1260
CACCGTGAAC CACATCATCT ATGCTCTGAG GAGTAAGGAC CTGCGACAGC CTTTCCGGAG 1320
CATGTTTCCC TCTTGTGAAG GCACTGCGCA GCCTCTGGAT AACAGCATGG GGGACTCGGA 1380
CTGCCTGCAC AAACAGCGAA ACAATGCAGC CAGTGTTCAC AGGGCCGCGA AAAGCTGCAT 1440
CAAGAGCACA GTCAAGATTG CCAAGGTAAC CATGCTGTG TCCACAGACA CGTCTGCGGA 1500
GGCTCTGTGA GCCTGATGCC TCCCTGGCAG CACAGGAAAA GAATTTTTTT TTTTAAGCTC 1560
AAAATCTAGA AGAGTCTATT GTCTCCTTGG TTATATTTTT TTAACCTTAC CATGCTCAAT 1620
GAAAAGGTGA TTGTCACCAT GATCATTAT CAGTTTGCTA ATGTTTCCAT AGTTTAGGTA 1680
CTCAAACTCC ATTCTCCAGG GGTTTACAGT GAAGAAAGCC TGTGTGTTAA GTGACTGAAC 1740
GATCCTTCAA AGTCTCAATG AAATAGGAGG GAAACCTTTG GCTACACAAT TGGAAAGTCTA 1800
AGAACCCATG GAAAAATGCC ATCAAATGAA TAATGCCTTT GTAACCAAA CTTTCACTAT 1860
AATGTGAAT GTAACGTGCC GTAGATACAG AGATGTCCAT TTTTACAAGT TATAGTACTA 1920
GAGATATTT GTAAAATGTA TTATGTCCTG TGAGATGTGT ATCAGTGTGT ATGTGCTATT 1980
AATATTTGTT TAGTTCAGCC AAACGTGAAAG GTAGACTTTT ATGAGAACAA TGGACAAGCA 2040
GTGGATACGT GTCAATGTGT GCACCTTTTT TCTATATTAT TGCCCATGAT ATAACCTTAG 2100
AAATAAACCT TAATATTTCT TCCCAAAAAA AAAAA

Protein sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

Protein Accession #: NP_001831

Signal sequence: none found

Pfam domain: 7tm_1 [133-397]

Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400

Cellular Localization: plasma membrane

1 11 21 31 41 51

	MKSILDGLAD	TFTRITITDL	LYVGSNDIOY	EDIKGDMSK	LGYPFQKFPPL	TSFRGSPFQPE	60
	KMTAGDNPOL	VPADQVNITE	FYNKSLSSFK	ENEENIQCGE	NFMDIECFMV	LNPSQQLAIA	120
5	VLSLTLTGFT	VLNLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIF	VYSFIDFHVF	180
	HRKDSRNVFL	FKLGGVTASF	TASVGSFLT	AIDRYISIRH	PLAYKRIVTR	PKAVVAFCLM	240
	WTIAIVIAVL	PLLGMNCEKL	QSVCSDFIPE	IDETYLFWFI	GVTSVLLLF	VYAYMYILWK	300
	AHSHAVRMIO	RGTQKSIIH	TSDEGKVQVT	RPDQARMDIR	LAKTLVLILV	VLIICWGPLL	360
	AIMVYDVFGK	MNKLKTVFA	FCSMLCLINS	TVPNIIYALR	SKDLRHAFRS	MFPSCGTAQ	420
10	PLDNSMGDS	CLHKHANNA	SVHRAAESC	KSTVKIAKVT	MSVSTDTSAE	AL	
	DNA sequence 6						
	Gene name: endothelin receptor type B						
	Unigene number: Hs.82002						
15	Probeset Accession #: D13168						
	Nucleic Acid Accession #: NM_000115						
	Coding sequence: 238-1566						
	1	11	21	31	41	51	
20	GAGACATTCC	GGTGGGGGAC	TCTGGCCAGC	CCGAGCAACG	TGGATCCTGA	GAGCACTCCC	60
	AGGTAGGCAT	TGCCCCGGT	GGGACGCCCT	GCCAGAGCAG	TGTGTGGCAG	GCCCCCGTGG	120
	AGGATCAACA	CAGTGCTCGA	ACACTGGGAA	GGAACTGGTA	CTTGGAGTCT	GGACATCTGA	180
	AACCTGGCTC	TGAAACTGGG	CAGCGGCCAC	CGGACGCCCT	CTGGAGCAGG	TAGCAGCATG	240
	CAGCCGCCCT	CAGTCTGTG	CGGACGCCCC	CTGTTGCCGC	TGGTCTTTCG	CTGCGGCTTG	300
25	TGCGGATCT	GGGAGAGGA	GAGAGGCTTC	CGCGCTGACA	GGGCCACTCC	GCTTTTGCAA	360
	ACCCGACAGA	TAATGACGCC	ACCCACTAAG	ACCTTATGGC	CCAAGGTTTC	CAACGCCAGT	420
	CTGGCGCGGT	CGTTGGCACC	TGCGGAGGTG	CCTAAGGAGG	ACAGGACGGC	AGGATCTCCG	480
	CCACGCACCA	TCTCCCTCC	CCCGTGCCAA	GGACCCATCG	AGATCAAGGA	GACTTTCAAA	540
	TACATCAACA	CGGTTGTGTC	CTGCCTTGTG	TCTGTCTGCG	GGATCATCGG	GAACCTCCAA	600
30	CTTCTGAGAA	TTATCTACAA	GAACAAGTGC	ATGCGAAACG	GTCCCAATAT	CTTGATCGCC	660
	AGCTTGGCTC	TGGGAGACCT	GCTGCACATC	GTCAATTGACA	TCCCTATCAA	TGTCTACAAG	720
	CTGCTGGGAG	AGGACTGGCC	ATTGAGAGCT	GAGATGTGTA	AGCTGGTGCC	TTTCATACAG	780
	AAAGCCTCCG	TGGGAATCAC	TGTGCTGAGT	CTATGTGCTC	TGAGTATTGA	CAGATATCGA	840
	GCTGTGTCTT	CTTGGAGTAG	AATTAAAGGA	ATTGGGGTTC	CAAAATGGAC	AGCAGTAGAA	900
35	ATTGTTTTGA	TTTGGGTGGT	CTCTGTGGTT	CTGGCTGTCC	CTGAAGCCAT	AGGTTTGTAT	960
	ATAATTACGA	TGGACTACAA	AGGAAGTTAT	CTGCGAATCT	GCTTGCTTCA	TCCGTTTCAG	1020
	AAGACAGCTT	TCATGCAGTT	TTACAAGACA	GCAAAAGATT	GGTGGCTGTT	CAGTTTCTAT	1080
	TTCTGCTTGC	CATTGGCCAT	CACCTGCATT	TTTTATACAC	TAATGACCTG	TGAAATGTTG	1140
	AGAAAGAAAA	GTGGCATGCA	GATTGCTTTA	AATGATCACC	TAAAGCAGAG	ACGGGAAGTG	1200
40	GCCAAAACCG	TCITTTGCCCT	GCTCCTTGTG	TTTGGCCCTCT	GCTGGCTTCC	CCTTCACTCC	1260
	AGCAGGATTC	TGAAGCTCAC	TCITTTATAAT	CAGAATGATC	CCAATAGATG	TGAACCTTTG	1320
	AGCTTCTCTG	TGATATTGGA	CTATATTGGT	ATCAACATGG	CTTCACTGAA	TTCTCTGATT	1380
	AACCCAAATG	CTCTGTATTT	GCTGAGCAAA	AGATTCAAAA	ACTGCTTTAA	GTCAATGCTTA	1440
	TGCTGCTGGT	GCCAGTCATT	TGAAGAAAAA	CAGTCTCTGG	AGGAAAGACA	GTCGTGCTTA	1500
45	AAGTTCAAAG	CTAATGATCA	CGGATATGAC	AACCTCCGTT	CCAGTAATAA	ATACAGCTCA	1560
	TCTTGAAAGA	AGAACTATTC	ACTGTATTTC	ATTTTCTTTA	TATTGGACCG	AAGTCATTAA	1620
	ARCAAAATGA	AACATTGTCC	AAAAACAAC	AAAAAATAT	GTATTGTGAC	AGCACTACTA	1680
	TAAATATTTA	AGTGAATTTA	TTTTAACACT	CACAGCTACA	TATGACATTT	TATGAGCTGT	1740
	TTACGGCATG	GAAAGAAAAA	CAGTGGGAAT	TAAGAAAGCC	TGCTCGTGAA	AGCACTTAAT	1800
50	TTTTTACAGT	TAGCACTTCA	ACATAGCTCT	TAACAACCTC	CAGGATATTG	ACACAACACT	1860
	TAGGCTTAAA	AATGAGCTCA	CTCAGAATTT	CTATTCTTTT	TAAAGAGAGA	TTTATTTTTA	1920
	AATCAATGGG	ACTCTGATAT	AAAGGAAGAA	TAAGTCACTG	TAAACAGAAA	CTTTTAAATG	1980
	AAGCTTAAAT	TACTCAATTT	AAAATTTTAA	AATCCTTTAA	AACAACCTTT	CAATTAATAT	2040
	TATCACACTA	TTATCAGATT	GTAATTAGAT	GCAATGAGA	GAGCAGTTTA	GTGTGTCAT	2100
55	TTTTGGGACA	CTGGAACAT	TTAAATGATC	AGGAGGGAGT	AACAGAAAGA	GCAAGGCTGT	2160
	TTTTGAAAT	CATTACACTT	TCACTAGAAG	CCCAACCTTC	AGCATTCTGC	AATATGTAAC	2220
	CAACATGTCA	CAACAAGACA	GCATGTAACA	GACTGGCACA	TGTGCCAGCT	GAATTTAAAC	2280
	TATAATACCT	TTAAAGAGAA	AATTATTACA	TCCTTTACAT	TCAGTTAAGA	TCAAACCTCA	2340
	CAAAGAGAAA	TAGAAATGTT	GAAAGGCTAT	CCCAAGAGAC	TTTTTTGAAT	CTGTCAATTC	2400
60	CATACCCTGT	GAAGACAATA	CTATCTACAA	TTTTTTTCAG	ATTATTAATA	TCTTCTTTTT	2460
	TCACTATGCT	AGCTTAAACT	CTGTTTGGTT	TTGTCACTCG	TAAATACTTA	CCTACATACA	2520
	CTGCATGTAG	ATGATTAAAT	GAGGGCAGGC	CCTGTGCTCA	TAGCTTTACG	ATGGAGAGAT	2580
	GCCAGTGACC	TCATAATAAA	GACTGTGAAC	TGCCTGGTGC	AGTGCCACA	TGACAAAGGG	2640
	GCAGGTAGCA	CCCTCTCTCA	CCCATGCTGT	GGTTAAATG	GTTTCTAGCA	TATGTATAAT	2700
65	GCTATAGTTA	AAATACTATT	TTTCAAAATC	ATACAGATTA	GTACATTTAA	CAGCTACCTG	2760
	TAAAGCTTAT	TACTAATTTT	TGTATTATTT	TTGTAAATAG	CCAATAGAAA	AGTTTGCTTG	2820
	ACATGGTGCT	TTTCTTTTAT	CTAGAGGCAA	AACCTGCTTT	TGAGACCGTA	AGAACCTCTT	2880
	AGCTTTGTGC	GTTCCTGCCT	AATTTTATA	TCTTCTAAGC	AAAGTGCTTT	AGGATAGCTT	2940
	GGGATGAGAT	GTGTGTGAAA	GTATGTACAA	GAGAAAACGG	AAGAGAGAGG	AAATGAGGTG	3000
70	GGTTGGAGG	AAACCCATGG	GGACAGATT	CCATTCTTAG	CCTAACGTTT	GTCAATGCTT	3060
	CGTCACATCA	ATGCAAAAGG	TCCTGATTTT	GTTCACAGCA	AACACAGTGC	AATGTTCTCA	3120
	GAGTGACTTT	CGAAATAAAT	TGGGCCCAAG	AGCTTTAACT	CGGTCTTAAA	ATATGCCCAA	3180
	ATTTTACTTT	TGTTTTTCTT	TTAATAGGCT	GGGCCACATG	TTGGAAATAA	GCTAGTAATG	3240
	TGTGTTTCTG	TCAATATTGA	ATGTGATGGT	ACAGTAAACC	AAACCCCAAC	AATGTGGCCA	3300
75	GAAAGAAAGA	GCAATAATAA	TTAATTCACA	CACCATATGG	ATTCTATTTA	TAAATCACCC	3360
	ACAAACTTGT	TCTTTAATTT	CATCCCAATC	ACTTTTTTCAG	AGGCCTGTTA	TCATAGAAGT	3420
	CATTITAGAC	TCTCAATTTT	AAATTAATTT	TGAATCACTA	ATATTTTTCAC	AGTTTATTAA	3480
	TATATTTAAT	TCTTATTAAA	ATTTTAGATT	ATTTTATTA	CCATGTACTG	AATTTTACA	3540
	TCCTGATACC	CTTTCCTTCT	CCATGTGAGT	ATCATGTTCT	CTAATTATCT	TGCCAAATTT	3600
80	TGAAACTACA	CACAAAAGC	ATACCTGCAT	TATTTATAAT	AAAATTGTCAT	TCAGTGGCTT	3660
	TTTAAAAAAA	ATGTTTGATT	CAAAACCTTA	ACATACTGAT	AAGTAAGAAA	CAATTATAAT	3720
	TTCTTTACAT	ACTCAAAACC	AAGATAGAAA	AAGGTGCTAT	CGTTCAACTT	CAAAACATGT	3780
	TTCTTAGTAT	TAAGGACTTT	AATATAGCAA	CAGACAAAAT	TATGTGTAAC	ATGGATGTTA	3840
	CAGCTCAAAA	GATTTATATA	AGATTTTAAC	CTATTTTCTC	CCTTATTATC	CAGTGCTAAT	3900
	GTGGATGTAT	GTTCAAAAC	CTTTTAGTAT	TGATAGCTTA	CATATGCCCA	AAGGAATACA	3960

5
 GTTTATAGCA AACATGGGT ATGCTGTAGC TAACCTTTATA AAAGTGAAT ATAACAATGT 4020
 AAAAAATTAT ATATCTGGGA GGATTTTITG GTTGCCTAAA GTGGCTATAG TTACTGATT 4080
 TTATTATGT AAGCAAAACC AATAAAAAAT TAAGTTTTTT TAACCACTAC CTTATTTTTC 4140
 ACTGTACAGA CACTAATTCA TTAATACTA ATTGATTGTT TAAAAGAAAT ATAAATGTGA 4200
 CAAGTGGACA TTATTTATGT TAAATATACA ATTATCAAGC AAGTATGAAG TTATCAATT 4260
 AAAATGCCAC ATTTCTGGTC TCTGGG

Protein sequence 6

Gene name: endothelin receptor type B

Unigene number: Hs.82002

Protein Accession #: NP_000106

Signal sequence: 1-27

Pfam domain: 7tm_1 [118-386]

Transmembrane domains: 100-122, 138-160, 173-195, 221-243, 277-299, 325-347, 358-380

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MQPPPSLCGR ALVALVLACG LSRINGEERG FPPDRATPLL QTAEIMTPPT KTLWPKGSNA 60
 SLARSLAPAE VPKGDRTAGS PPRTISPPPC QGPIEIKETF KYINTVVSCL VFVLGIIGNS 120
 20 TLLRIIYKXK CMRNGPNILI ASLALGDLH IVIDIPINIV KLLAEDWPFQ AEMCKLVFFI 180
 QKASVGTIVL SLCAISIDRY RAVASWSRIK GIGVPKWTAV EIVLIWVSV VLAAPPAIGF 240
 DIITMDYKGS YLRICLLHPV QKTFMQFYK TAKDWLFSF YFCLPLAITA PFYTLMTCEM 300
 LRKKSQMQLA LNDHLKORRE VAKTVFCLVL VFALCWLPLH LSRILKLTLY NQNDPNRCEL 360
 25 LSFLVLVDYI GNMASLNSC INPIALYLVS KRKNCPKSC LCCWCQSFEK QKSLEEKQSC 420
 LKFKANDHGY DNFRSSNKYS SS

DNA sequence 7

Gene name: G protein-coupled receptor 34

Unigene number: Hs.29202

Probeset Accession #: N54926

Nucleic Acid Accession #: AF039686

Coding sequence: 79-1224

1 11 21 31 41 51
 | | | | |
 35 AAAAACTGA AGACATAAGA ACTACACATG AGGAATATGT CATTTAGCAC TTTCACITTT 60
 TGATCTCCAC AGAAGACAAT GAGAAGTCAT ACCATAACAA TGACGACAAC TTCAGTCAAGC 120
 AGCTGGCCTT ACTCCTCCCA CAGAATGCGC TTTATAACCA ATCATAGCGA CCAACCGCCA 180
 CAAAACITCT CAGCAACACC AAATGTTACT ACCTGTCCCA TGGATGAAAA ATTGCTATCT 240
 40 ACTGTGTTAA CCACATCCTA CTCGTATT TTCTCGTGG GACTGGTGG GAACATAATC 300
 GCCCTCTATG TATTCTCTGG TATTCAACCGT AAAAGAAATT CCATTCAAAT TTATCTACTT 360
 AACGTAGCCA TTGCAGACCT CCTACTCATC TTCTGCCTCC CTTCCGAAT CATGTATCAT 420
 ATTAACCAAA ACAAGTGGAC ACTAGGTGTG ATTCTGTGCA AGGTGTGGG AACACTGTTT 480
 TATATGAACA TGTACATTAG CATTATTTTG CTGGATTCA TCAGTTTGA TCGCTATATA 540
 45 AAAATTAATC GGTCTATACA GCAACGGAAG GCAATAACAA CCAACAAAG TATTTATGTC 600
 TGTGTATAG TATGGATGGT TGCTCTGGT GGATTCCTAA CTATGATTAT TTTAACACTT 660
 AAGAAAGGAG GGCATAATTC CACAATGTGT TTCCATTACA GAGATAAGCA TAACGCAAAA 720
 GGAGAAGCCA TTTTAACTT CATTCTGTGT GATATGTTCT GGCTAATTTT CTACTAATA 780
 ATCCTTCAT ATATTAAGAT TGGGAAGAAT CTATTGAGGA TTTCTAAAAG GAGGTCAAAA 840
 50 TTTCCTAAT CTGTAATAA TGCCACTACA GCTCGTAACCT CCTTATTGT ACTTATCATT 900
 TTTACTATAT GTTTTGTTC CTATCATGCC TTTCGATTCA TCTACATTTC TTCACAGCTA 960
 AATGTATCAT CTGCTACTG GAAAGAAATT GTTCACAAA CCAATGAGAT CATGCTGGTT 1020
 CTCTCATCT TCAATAGTGT CTTAGATCCA GTCATGTATT TCCTGATGTC CAGTAACATT 1080
 CGCAAAATAA TGTGCCAAT TCTTTTAGA CGATTTCAG GTGAACCAAG TAGGAGTGAA 1140
 55 AGCACTTCAG AATTAAACC AGGATACTCC CTGCATGATA CATCTGTGGC AGTGAATAA 1200
 CAGTCTAGT CTAAAAGTAC TTGAGGTAAA CATACTAAAA TGAATTATAT AATGCAGCCT 1260
 CTTAATCTCT TGAAGAATA AAAAATTAGG AAACAAAGTT CTAGCATTTA CAAAACCTAG 1320
 ATCTCAAGC TCTGCTGTGA TTTGTGATAT TTCAATTGCT TAACGTGAAA CCAT

Protein sequence 7

Gene name: G protein-coupled receptor 34

Unigene number: Hs.29202

Protein Accession #: AAD50531

Signal sequence: none found

Pfam domain: 7tm_1 [71-327]

Transmembrane domains: 90-112, 126-148, 171-193, 217-239, 263-285

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 70 MRSHTITMT TSVSSWPYSS HRMRFITNHS DQPPQNFSA PNVITCPMDE KLLSTVLTS 60
 YSVIFIVGLV GNIIALYVFL GIHRKRNSIQ IYLLNVAIAD LLLIFCLPFR IMYHINQKNH 120
 TLGVILCKVV GTLFYMMYI SIILLGFISL DRYIKINRSI QQRKAITTKQ SIYVCIVVM 180
 VALGGELTMI ILTLKGGHN STMCFYHRDK HNAKGEAIFN FILVVMFWLI FLLIILSYIK 240
 IGKNNLRISK RRSKFPNSGK YATTARNFSI VLIIFTICFV PYHAFRFIYI SSQNLVSSCY 300
 75 WKEIVHKINE IMLVLSFNS CLDPVMYFLM SSNIRKIMCQ LLFRRFQGEF SRSESTSEPK 360
 PGYSLHDTSV AVKIQSSKS T

DNA SEQUENCE 8

Gene name: exostoses (multiple)-like 2

Unigene number: Hs.61152

Nucleic Acid Accession #: NM_001439

Coding sequence: 288-1280

1 11 21 31 41 51
 | | | | |
 80 CACTTTGCGG GCGGCACCTT TTCCAGGTG TTAATCCAGC TAATGGAGAA GGATAGATGC 60

5
 10
 15
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 25
 30
 35
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ACGCTACTTG GTTTAGAAAA AAAACAAAA ATGAGCAAAC GAGACGCCCC TTCOGTTTTA 120
TGATAACTAA GCTGCAGGGA AATAAATCGG CTGGCCCTAC TGCAATCTAC TGCACTCGAG 180
AAACATCACA GAAATTTCTT TGATTTATCT TAATAGTGAC AAGTGAGCCT GCTTCTGTCA 240
ATTACTGAAG CTATAAGGAG ATTTTTTAAA AATTAAACTT CAACACAATG AGGTGTGTGC 300
ACATCTGCAA ACTTCTCTGG AGAGTAATGG GGATTGAGT GCTTCGATTA TCTTTGGTGG 360
TCATCTCGT ATTTATCTAG GTAGCTGGTG CTTTGACTGC CTACTTCCC AGTGTTAAG 420
AAGACAAGAT GCTCATGTTG CGTAGGGAAA TAAATCCCA GGGCAAGTCC ACCATGGACT 480
CCTTACTCT CATATGCGAG ACGTACAACA GAACAGATCT CTTATTGAAA CTTTAAATC 540
ATTATCAGSC TGTACCAAAAT CTGCACAAAG TGATTGTGGT ATGGAACAAT ATTGAGAGA 600
AGGCACCGA TGAATTATGG AATTCTCTAG GGGCCCAACC TATCCCTGTG ATCTTCAAC 660
AACAGACAGC AAACAGGATG AGAATCGAC TCCAGGTCTT TCCTGAATG GAAACCAATG 720
CAGTGTGTGAT GGTAGATGAT GACACACTCA TCAGCACCCC AGAAGTGTG TTTGCTTCT 780
CAGTTTGGCA GCAATTTCTT GATCAAAATG TAGGATTGTG TCCTAGAAAG CACGTCTCTA 840
CTTCATCAGG TATCTACAGT TATGGAAGTT TTGAAATGCA AGCACCAGGG TCTGAAATG 900
GTGACCAGTA CTCTATGGTG CTGATTGGAG CCTCATTCTT CAATAGCAAA TATCTGAAT 960
TATTTCTAGG GCAACCTGCA GCTGTCCATG CTTTGATAGA TGATACCTAA AACTGTGATG 1020
ATATTGCCAT GAATTTTATC ATTGCCAAGC ATATTGGCAA GACTTCAGGG ATATTGTGA 1080
AGCCTGTAAA CGAGGACAAAT TTGAAAAAAG AAACCAACAG TGGCTATTCT GGAATGTGGC 1140
ATCGAGCTGA CGACGCTCTG CAGAGGTCTT ATTGTATAAA TAAGCTTGTT AATATCTATG 1200
ATAGCATGCC CTTAAGATAC TCCAACATTA TGATTCCCA GTTTGGTTT CCATATGCCA 1260
ACTACAAAG AAAAATATAA AAGTAAAAA AACAATAA AACTGAAA CTGCTTGCA 1320
TTTGAGTAGC TTCTCCATGC TATGTATTT TTAAGCAAC ATCATGAAT TTATCTACTC 1380
CAGAAGTCTC TACAATAGAA AAAAAGTGC AGTCTTCTA GGATATAAAA TTCACATTAC 1440
TTTTGAAGC CAAGAGGAAA ATTTGCAGCT GCTTATCCA GTTAGGTTCT CTTATGAAGA GTTTTCATCC 1500
AGGATATATA CTCCTGGTG AGTGATTITA TTGTTTACAT CCTGAGACTG TTCTACAGTT 1560
TCTTTGACTC CTGGCATTGG CCTTAAGGAC CTATAGCAAG CTGTTCTAG GATCAGAAAC 1620
TCAAGAGAGG CATTTCTCTG CTTTTCACT AAAGGTCACT TGTTTTAATT TGAACCTGA 1680
AATGCCTCTT TAGCAAGGCC TGTGGTATGG GGTAAAGCCA TGTAAGAAGA GAATAGTCTC 1740
AGTCACATAT GAAGAGGAAA ATTTGCAGCT GCGAGTCTT TCCTGTGGC CCTGCCAAC 1800
AGCTCTTCCA GGACGAAGCT AGTCCAGCAT GGTTTGATG TAACCATCCA TGCTTTTATT 1860
TTTGTTAAGT CTTTGTGAC TGGGACAGT AATTTTAGTA GCTGAAGAAC GTCTAGTTGT 1920
TTGCTTGATA TTTGTGAACA TTACTGCAT GGATCAGAAA ACAATATACC CTGTATTCT 1980
TACAGCCAC TTATATGCG CAAGGAGTAA ATGTGTACT AGATTGGGT AGTGCAATT 2040
GTCACTGAAT CTGACCTTGA GAATGTACAT TAATCTTAT ATTTTACATA ATGTATGTG 2100
TGTTTAAAG AAATGATAAAA AACCTGAAA AAATGAGTAA GAACCTGGC AAGTTAAAC 2160
CCTTTGTATC AAAAGATCTT TATGTGTAGA GCACTGGTTA TCTTCTGGAT ACTAAAAAT 2220
TGTATTACAA AGCCAAACAC TTGCATTAC AACTTTAAA AAAGATCCAA GGAATATT 2280
ATAATGATGA AATTTCAACT ACATACAAGG AGGAGAAAAT AAGAACCAG TCATAACAGA 2340
GGAATCTAT AGGAGTCTG ATCAATTCAT TCTAAGGTT GCCTACTCTC TGTTATGTGA 2400
ATTAGCGTCT GTGTTTCACC CATGTCTGT GTTTAGTCTT TGTTCAACAC TAAGGCAAG 2460
AATCTTAACT TAGGCTCTG TTTACCAACT TCTCTTCTC CTCTTCTCC TCTTATTCT 2520
CCTTCTCTC TTCTTCTTA TATAATGCTA GTATATTCTC AAAATTGCAA AGCTGTGAGA 2580
ATATTAATAA AATCATGGCT AATGTTCCA TAATGAGGTC TTTGTGCAT TAGTTCGCA 2640
TATGATGGTT TTTTCTTAC ATTAAGAGT ATATGTGCT TAATGCAGTC AGATTGTAAA 2700
AAACAAAC AAAGAACTA AGAATCTTAC TAAAAATCGA TAATGTCAGT TATCTGTTT 2760
GTCCAATATT GGTAGTACTT TTTTGCCTCT TATGATTCT CTAGCAGATA AATAAAGAA 2820
ACTTTTGCCA TCC
  
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 60
 65
 70

Protein sequence 8
 Gene name: exostoses (multiple)-like 2
 Unigene number: Hs.61152
 Protein Accession #: NP_001430
 Signal sequence: 1-38
 Transmembrane domains: none found
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MRCCHICKLP GRVMGIRVLR LSLVVLVLL LVAGALTALL PSVKEDKMLM LRREIKSQGK 60
STMDSFLLIM QTYNRTDLLL KLNHYQAVP NLHKVIVVWN NIGEKAPDEL WNSLGPPIPI 120
VIFKQQTANR MRNRLQVFPE LETNAVLMD DDTLISTPDL VFAPSVWQQF PDQIVGFVPR 180
KHVSTSSGIY SYGSFEMQAP GSGNGDQYSM VLIGASFFNS KYLELFQRQP AAVHALIDDT 240
QNCDIAMNF IIAKHIGKTS GIFVKPVNMO NLEKETNSGY SGMWHERAHA LQSYCINKL 300
VNIYDSMPLR YSNIMISQFG FPYANYKRKI
  
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75
 80

DNA SEQUENCE 9
 Gene name: Homo sapiens growth differentiation factor 1 (GDF1)
 Unigene number: Hs.92614
 Probeset Accession #: AL120193
 Nucleic Acid Accession #: NM_021267
 Coding sequence: 73-1125

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1 11 21 31 41 51
| | | | |
ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGCGGGGCG CAGGCGACGG GCACGGCGGG 60
CGAGCGGGCG GTATGGCGGC GCGGGGCCCC GCGCGGGGCG CGACGGGGCC CGAGCCCATG 120
CGAGGCTAGC CGCAGCTAGT GCAGCGCGCG TGGGGCAGCG CGCTGGCGGC GCGCGGGGCG 180
TGACGCGACT GCGGCTGGGG GCTGGCGCGT GCGCGCCTGG CTGAGCACGC GCACCTGGCG 240
CGCGCCGAGC TGCTGCTGCT GCGGCTCGCG GCGCTGGGCT GGACCGCGCT GCGCTCCGCG 300
GCCACTGCGC GCGCTTTTCG GCGGCTGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360
GCCAAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCGAGTG GAGCTACAGT 420
GCCTACTCTG TGTGTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGCTTCTTAC 480
GACTGGACGC CGGGCATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA 540
AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600
GTGGTCTATG TGCTCCACCA CGTGGTCACT CTCATCCTCA TCGTCTCTTC CTACGCTTTC 660
CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCTGCAGG ATATCAGTGA CGTGCAGCTT 720
  
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5 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCGCGGGCG GCTCCTACCA TCGGCTGCAT 780
 GCCTTGGCAG CAGACTTGGG CTGCTCAGC TTGCGCTTCA GCTGGTTCTG GTTCCGCTC 840
 TACTGGTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT 900
 GACATCCCCT TCTACTTCTT CTTCATATCG CTCTGTCTGC TGCTCAACCT TATGAACCTC 960
 TACTGGTTCC TGTACATCGT GCGTTTGA GCGAAGGTGT TGACAGGCCA GGTGACAGAG 1020
 CTGAAGGACC TGGCGGAGTA TGACACAGCC GAGGCCAGAG GCCTGAAGCC CAGCAAAGCC 1080
 GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCCGC 1140
 CCCCCGTGAC CCGGCCCCAC CCCGAATACC CCGGCCACGC TCCCCGTCTT TGGCCGCCCC 1200
 10 TCCACCCCCC CCAACTCTGC TCCTCTAGGG CCGCCGCCAC CTCCCCCTGG ACCCCGCCCC 1260
 CTCACTCTGC CTGCACTTCC CGGCCACGCC CCCAGGACC CCTGCCCTCT CGGGGACACC 1320
 GGCCCCGCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCAT 1380
 CGCCTGGGAG GAAGATGCCA CCGCCGAGC AAGTCCCTG CGGCCACCAC CTCCTCTCTC 1440
 TCCTGGCCTC GCTGCTGCC TCCTGCCCC TGACCCGCGC CCCCCTGCC CCAGGCCAG 1500
 15 CGCCCGCCCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGCC CCCAGGCTCC 1560
 GGCCCGTCTT TGGCGCTGT TCGCGCTGT TCGACGCGG GAGACCCAG GAGACCAAGT 1620
 CTGGCTCGCG CGGAGCTCC CCAGGGTCA CCTGCAACC GTGCCACGTG GAGGAGCTGG 1680
 GGGTCCGCG AAACATCTGT CGCCACATCC CGGACCGCG TGCGCCACC CGGGCTCTCG 1740
 AGCCTGTCTC GGCCTGGGG CATGCCCCG AGTGGACAGT CGTCTTGCAC CTGTGCGCTG 1800
 20 TGGAAACCCG TGAGCGCCCG AGCCGGGCC GCCTGGAGCT GCGTTCTCGG CGCGCGCGCG 1860
 CGGACGCCCC GAGGGCGCG TGGAAGCTGA GCGTGGCGCA AGCGGGCCAG GCGCGGGCG 1920
 CGGACCCCGG GCGGTGCTGT CTCGCCAGT TGGTCCCGC CCTGGGCGCG CCAGTGCGCG 1980
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG CGCCGCGAGC CTCGCGCTGG 2040
 CGCTGGCCTC ACGCCCGCG GCGCCTGCCG CCTGCGCGCG CTGGCCGAG GCCTCGCTGC 2100
 25 TGCTGTGAC CCTGACCCG CGCCTGTGCC ACCCCTGGC CGCGCGCGCG CGCGAGCCCG 2160
 AACCCGTGTT GCGCGCGCG CCGGGGGCG CTTGTGCGC GCGCGGGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGTCA TCGCGCCCG CGGCTTCTCT GCCAACTACT 2280
 GCGAGGGTCA GTGCGCGCTG CCCGTGCGC TGTGCGGGTC CGGGGGGCGG CCGCGCTCA 2340
 ACCAGCTGTG GCTGCGCGCG CTGATGCAAG CGCGCGCCCG GAGAGCGGCC GACCTGCGCT 2400
 30 GCTGCGTCC CGCGCGCTG TCGCCATCT CCGTGTCTT CTTTGACAAC AGCGACAACG 2460
 TGTGTCTGCG CAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCG TAACCGGGG

Protein sequence 9

Gene name: Homo sapiens growth differentiation factor 1 (GDF1)

Unigene number: Hs.92614

Protein Accession #: NP_067090

Signal sequence: none found

Transmembrane domains: 106-128, 148-169, 184-206, 244-266, 285-307

Cellular Localization: plasma membrane

40 1 11 21 31 41 51
 | | | | |
 MAAAGPAAAG TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESANKFLFYL GSWSYSAAYL 120
 FGTDYPPFFD PPSVYFDWTP GMVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180
 45 LHHVTLILI VSSYAFRYHN VGILVLFLED ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240
 DLGLSFGFS WFWRLYWFPL LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNLYWFL 300
 YIVAFPAKVL TGQVHELKDL REYDTAEASQ LKPSKAEKPL RNLVVKDKRF

DNA SEQUENCE 10

Gene name: epidermal growth factor receptor (avian erythroblastic leukemia

Unigene number: Hs.77432

Nucleic Acid Accession #: NM_005228

Coding sequence: 187-3819

55 1 11 21 31 41 51
 | | | | |
 GCGCGCTGC GCCGAGTCC CGAGCTAGCC CCGCGCGCGC CGCCGCCAG ACCGACGAC 60
 AGGCCACCTC GTCGCGTCC GCGCGAGTCC CCGCTCGCC GCCAACGCCA CAACCACCGC 120
 GCACGCGCCC CTGACTCCGT CCAGTATTGA TCGGGAGAGC CGGAGCGAGC TCTTCGGGGA 180
 GCAGCGATCG GACCTCCCG GACGCGCGG GCAGCGCTCC TGGCGCTGCT GGCTGCGCTC 240
 60 TGCCCGCGCA GTCGGGCTCT GGAGGAAAAG AAGTTTGCC AAGGCACGAG TAACAAGCTC 300
 AGGCACTTGG GCACTTTTGA AGATCATTTT CTCAGCCTCC AGAGGATGTT CAATAACTGT 360
 GAGGTGGTCC TTGGGAATTT GGAAATTACC TATGTGCAGA GSAATTATGA TCTTTCCTTC 420
 TTAAGACCA TCCAGGAGGT GGCTGGTTAT GTCTCATTG CCCTCAACAC AGTGGAGCGA 480
 ATTCTTTGG AAAACCTGCA GATCATCAGA GGAATATGT ACTACGAAAA TTCTATGCC 540
 65 TTAGCAGTCT TATCTAACTA TGATGCAAT AAAACCGGAC TGAAGGAGCT GCCCATGAGA 600
 AATTTACAGG AAATCTGCA TGGCGCGGTG CGGTTACGCA ACAACCTGCG CCTGTGCAAC 660
 GTGGAGAGCA TCCAGTGGCG GGACATAGTC AGCAGTGACT TTCTCAGCAA CATGTGATG 720
 GACTTCCAGA ACCACTGGG CAGCTGCCAA AAGTGTGATC CAAGCTGTCC CAATGGGAGC 780
 TGCTGGGGTG CAGGAGAGGA GAACTGCCAG AAATGACCA AAATCATCTG TGCCGAGCAG 840
 70 TGCTCGGGCG GCTGCGGTGG CAAGTCCCC AGTGACTGCT GCCACAACCA GTGTGCTGCA 900
 GGCTGCACAG GCCCCCGGGA GAGCGACTGC CTGGTCTGCC GCAATTTCCG AGACGAAGCC 960
 ACGTGCAGG ACACCTGCC CCCACTCATG CTCTACAACC CCACACAGTA CCAGATGGAT 1020
 GTGAACCCCG AGGGCAAAAT CAGCTTTGGT GCCACCTGCG TGAAGAAGTG TCCCCGTAAT 1080
 TATGTGTGA CAGATCACGG CTCGTGCGTC CGAGCCTGTG GGGCCGACAG CTATGAGATG 1140
 75 GAGGAAGAG GCGTCCGCAA GTGTAAAGAG TGGGAAGGGC CTGCGCGCAA AGTGTGTAA 1200
 GGAATAGGTA TTGGTGAAT TAAAGACTCA CTCTCCATAA ATGCTACGAA TATTAACAC 1260
 TTCAAAAACG GCACCTCCAT CAGTGGCGAT CTCACATCC TGCCGCTGCG ATTTAGGGGT 1320
 GACTCCTTCA CACATACTCC TCCTCTGGAT CCACAGGAAC TGGATATTCT GAAAAACGTA 1380
 AAGGAATAT CAGGGTTTTT GCTGATTGAG GCTTGGCCTG AAAACAGGAG GGAACCTCAT 1440
 80 GCCTTTGAGA ACCTAGAAAT CATACGCGGC AGGACCAAGC AACATGGTCA GTTTTCTCTT 1500
 CGAGTGTGTA GCCTGAACAT AACATCCTTG GGATTACGCT CCCTCAAGGA GATAAGTGAT 1560
 GGAGATGTGA TAATTTACAG AACAAAAAT TTGTGCTATG CAAATACAA AAACCTGAAA 1620
 AAACCTTTTG GACCTCCCG TCAGAAAAAC AAAATTATTA GCAACAGAGG TGAACACAG 1680
 TGCAAGGCCA CAGGCCAGGT CTGCCATGCC TTGTGCTCCC CGAGGGGCTG CTGGGGCCCG 1740
 GAGCCACAGG ACTGCGTCTC TTGCGGGAAT GTCAGCGGAG GCAGGGAATG CGTGGACAG 1800

	TGCAAGCTTC	TGGAGGGTGA	GCCAAGGGAG	TTTGTGAGAG	ACTCTGAGTG	CATACAGTGC	1860
	CACCCAGAGT	GCCTGCCTCA	GGCCATGAAC	ATCACCTGCA	CAGGACGGGG	ACCAGACAAC	1920
	TGTATCCAGT	GTGCCCCACTA	CATTGACGGC	CCCCACTGCG	TCAAGACCTG	CCCGGCAGGA	1980
5	GTCAATGGAG	AAAACAAAC	CCTGGTCTGG	AAGTACGCG	ACGCCGGCCA	TGTTGTCCAC	2040
	CTGTGCCATC	CAAACTGCAC	CTACGGATGC	ACTGGGCCAG	GTCTTGAAGG	CTGTCCAAAG	2100
	AATGGGCTTA	AGATCCCGTC	CATCGCCACT	GGGATGGTGG	GGGCCCTCCT	CTTGTGCTGT	2160
	GTGGTGGCCC	TGGGGATCGG	CCTCTTCATG	CGAAGGGGCC	ACATCGTTCG	GAAGCGCACG	2220
	CTGCGGAGGC	TGCTGCAGGA	GAGGGAGCTT	GTGGAGCCTC	TTACACCCAG	TGGAGAAGCT	2280
10	CCCAACCAAG	CTCTCTTGAG	GATCTTGAAG	GAACCTGAAT	TCAAAAAGAT	CAAGATGTCT	2340
	GGCTTCGGTG	CGTTTCGGAC	GGTGTATAAG	GGACTCTGGA	TCCCAGAAAG	TGAGAAAGTT	2400
	AAAATTCGCG	TGCGTATCAA	GGAAATTAAG	GAAGCAACAT	CTCCGAAAGC	CAACAAGGAA	2460
	ATCTCTGATG	AAGCCTAAGT	GATGGCCAGC	GTGGACAACC	CCCACGTGTG	CCGCTGTGCT	2520
	GGCATCTGCC	TCACCTCCAC	CGTGCAACTC	ATCACGCAGC	TCATGCCCTT	CGGCTGCCTC	2580
15	CTGGACTATG	TCCGGGAACA	CAAAGACAAT	ATTGGCTCCG	AGTACCTGCT	CAACTGGTGT	2640
	GTGCAGCAGG	AGATCTCTTC	GAACTACTTG	GAGGACCGTG	GCTTGGTGCA	CCGCGACCTG	2700
	GCAGCCAGGA	ACGTACTGGT	GAAACACCG	CAGCATGTCA	AGATCAGACA	TTTTTGGGCT	2760
	GCCAAACTGC	TGGGTGCGGA	AGAGAAAGAA	TACCATGCAG	AAGGAGGCAA	AGTGCCCTATC	2820
	AAGTGGATGG	CATTGGAATC	AATTTTACAC	AGAATCTATA	CCCACAGAGG	TGATGTCTGG	2880
20	AGCTACGGGG	TGACCGTTTG	GGAGTTGATG	ACCTTTGGAT	CCAAGCCATA	TGACGGGAATC	2940
	CCTGCCAGCG	AGATCTCTTC	CATCCTGGAG	AAAGGAGAAC	GCCCTCCCTCA	GCCACCCATA	3000
	TGTACCATCG	ATGTCTACAT	GATCATGGTC	AAGTGTCTGA	TGATAGACGC	AGATAGTCGC	3060
	CCAAAGTTCC	GTGAGTTGAT	CATCGAATTC	TCCAAATGCG	CCCGAGACCC	CCAGCGCTAC	3120
	CTTGTCTATC	AGGGGATGTA	AAGAATGCAT	TTGCCAAGTC	CTACAGACTC	CAACTTCTAC	3180
25	CGTGCCCTGA	TGGATGAAGA	AGACATGGAC	GACGTGGTGG	ATGCCGACGA	GTACCTCATC	3240
	CCACAGCAGG	GCTTCTTCAG	CAGCCCTCC	ACGTACCGGA	CTCCCTCTCT	GAGCTCTCTG	3300
	AGTGCAACCA	GCAACAAATC	CACCGTGGCT	TGCAATGATA	GAAATGGGCT	GCAAGCTGTG	3360
	CCCATCAAGG	AAGACAGCTT	CTTGCAAGCA	TACAGCTCAG	ACCCACAGCG	CGCCTTGACT	3420
	GAGGACAGCA	TAGACGACAC	CTTCTCCCA	GTGCCTGAAT	ACATAAACCA	GTCCGTTCCC	3480
30	AAAAGGCCCG	CTGGCTCTGT	GCAGAATCCT	GTCTATCACA	ATCAGCCTCT	GAACCCCGCG	3540
	CCACAGCAGG	ACCCACATGA	CCAGGACCCC	CACAGCACTG	CAGTGGGCAA	CCCCGAGTAT	3600
	CTCAACACTG	TCCAGCCCA	CTGTGTCAAC	AGCACATTGG	ACAGCCCTGC	CCACTGGGCC	3660
	CAGAAAGCAA	GCCACAAAT	TAGCCTGGAC	AACCTGACT	ACCAGCAGGA	CTTCTTTCCC	3720
	AAGGAAGCCA	AGCCAAATGG	CATCTTTAAG	GGCTCCACAG	CTGAAAATGC	AGAATACCTA	3780
35	AGGCTGCGCC	CACAAAGCAG	TGAATTTATT	GGAGCATGAC	CACGGAGGAT	AGTATGAGCC	3840
	CTAAAATCC	AGACTCTTTC	GATACCCAGG	ACCAAGCCAC	AGCAGGTCTC	CCATCCCCAAC	3900
	AGCCATGCCC	GCATTAGCTC	TTAGACCCAC	AGACTGGTTT	TGCAACGTTT	ACACCGACTA	3960
	GCCAGGAAGT	ACTTCCACCT	CGGGCACATT	TTGGGAAGTT	GCATTCTTTT	GTCTTCAAA	4020
	TGTGAAGCAT	TTACAGAAAC	GCATCCAGCA	AGAATATTGT	CCCTTTGAGC	AGAAATTTAT	4080
40	CTTTCAAGA	GGTATTTTGG	AAAAAAGTATA	TGTGAGGATT	TTTATTTGAT	TTTATTTGAT	4140
	GGGGATCTTG	GAGTTTTCAT	TGTGCTATAT	TGATTTTAC	TTCAATGGGC	TCTTCAACCA	4200
	AGGAAGAAGC	TTGCTGGTAG	CACCTTGCTAC	CCTGAGTTCA	TCCAGGCCCA	ACTGTGAGCA	4260
	AGGAGACAAA	GCCACAAAGT	TTCCAGAGGA	TGCTTGATTC	CAGTGGTTCT	GCTTCAAGGC	4320
	TTCCATGCA	AAACACTAAA	GATCCCAAGAA	GGCTTTCATG	GCCCCAGCAG	GCCGGATGGG	4380
45	TACTGTATCA	AGTCATGGCA	GGTACAGTAG	GATAAGCCAC	TCTGTCCCTT	CCTGGGCAAA	4440
	GAAGAAACGG	AGGGGATGAA	TTCTTCTTTA	GACTTACTTT	TGTAAAAATG	TCCCCACGGT	4500
	ACTTACTCCC	CATGATGGGA	CCAGTGGTTT	CCAGTCAATG	GCGTTAGACT	GACTTGTGTT	4560
	TCTTCAATTC	CATTGTTTTG	AAACTCAGTA	TGCCGCCCTC	GTCTTGCTGT	CATGAAATCA	4620
	GCAAGAGAGG	ATGACACATC	AAATAATAAC	TCCGATTCCA	GCCCCACATT	GATTCATCAG	4680
50	CATTGGGACC	AATAGCCCCA	AGCTGAGAA	GTGGAATACC	TAAGGATAAC	ACCGCTTTTG	4740
	TTCTCGCAAA	AACGATCTCT	CTAATTTGAG	GCTCAGATGA	AATGCATCAG	GTCTTTTGGG	4800
	GCATAGATCA	GAGACTTACA	AAAATGAAGC	TGCTCTGAAA	TCTCTTTAG	CCATCACCCC	4860
	AACCCGCCCA	AATTAGTTTG	TGTTACTTAT	GGAAGATAGT	TTTCTCTTTT	TACTTCACTT	4920
	CAAAAGCTTT	TACTCAAG	AGTATATGTT	CCCTCCAGGT	CAGCTGCCCC	CAAAACCCCT	4980
55	CCTTACGCTT	TGTCACACAA	AAAGTGTCTC	TGCCCTGAGT	CATCTATTCA	AGCATTTACA	5040
	GCTCTGGCCA	CAACAGGGCA	TTTTACAGGT	GCGAATGACA	GTAGCATTAT	GAGTAGTGTG	5100
	AATTACAGTTA	GTAATATATG	AACTAGGGTT	TGAAATGAT	AATGCTTTCA	CAACATTTTG	5160
	AGATGTGTTT	GAAAGAAAAG	AGTTCCCTCC	TAAAATAATT	TCTCTACAT	TGGGAAGATT	5220
	GAAATTCAG	CTAGTTAGGA	GCCCATTTTT	TCCTAATCTG	TGTGTGCCCT	GTAACCTGAC	5280
60	TGGTTAACAG	CAGTCTTTTG	TAAACAGTGT	TTTAAACTCT	CCTAGTCAAT	ATCCACCCCA	5340
	TCCAATTTAT	CAAGGAAGAA	ATGGTTTCAG	AAATATTTTC	AGCCTACAGT	TATGTTTCA	5400
	CACACACACA	TACAAAATGT	TCCTTTTGCT	TTTAAAGTAA	TTTTTGACTC	CCAGATCAGT	5460
	CAGAGCCCTC	ACAGCATGTT	TAAGAAAGTA	TTTGATTTTT	GTCTCAATGA	AAATAAAACT	5520
	ATATTCATT	CC					
65	Protein sequence 10						
	Gene name: epidermal growth factor receptor (avian erythroblastic leukemia						
	Unigene number: Hs.77432						
	Protein Accession #: NP_005219						
	Signal sequence: 1-27						
70	Pfam domain: Recep_L domain [57-190, 372-492]						
	Transmembrane domains: 646-668						
	1	11	21	31	41	51	
75	MRPSGTAGAA	LLALLAALCP	ASRALEEKV	CQCTSNKLTQ	LGTFFEDHFLS	LQRMFNNECV	60
	VLGNLEITYV	QRNYDLSFLK	TIQEVAGYVL	IALNTVERIP	LENLQIIRGN	MYEENSIALA	120
	VLSNYDANKT	GLKELPMRNL	QEILHGAVRF	SNPALCNVE	SIQWRDIVSS	DFLSNMSMDF	180
	QNHLSGCKQC	DPSCPNSSCW	GAGEENCQKL	TKIIICAQCS	GRCRKSPSD	CCHNQCAAGC	240
	TGPRESDCLV	CRKRFDEATC	KDTCPPPLMLY	NPTTYQMDVN	PEGKYSFGAT	CVKCKPRNYV	300
80	VTDHGSCVRA	CGADSYEMEE	DGVRKCKKCE	GPRKVCNGI	GIGEFKDSLS	INATNIKHFK	360
	NCTISISGLH	ILPVAFRGDS	FHTHPPLDPQ	ELDILKTVKE	ITGFLLIQAW	PENRTDLHAF	420
	ENLEIIRGRT	KQHGQFSLAV	VSLNITSLGL	RSLEKISDGD	VIIISGNKNC	YANTINWKKL	480
	FTSGQKTKI	ISNRGENSKC	ATGQVCHALC	SPEGCWGPEP	RDCVSCRNV	RGRECVDKCK	540
	LLLEGPRFV	ENSECIQCHP	ECLPQAMNIT	CTGRGPDNCI	QCAHYIDGPH	CVKTCAPGVM	600
	GENNTLVWKY	ADAGHVCHLC	HPNCTYGCTG	PGLEGCPING	PKIPSATGTM	VGALLLLLVV	660

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ALGIGLFMR RHIVRKRTLRLQLERELVE PLTPSGEAPN QALLRILKET EFKKIKVLGS 720
GAFGTVYKGL WIPBGEKVKI PVAIKELREA TSPKANKEIL DEAYVMASVD NPHVCRLLGI 780
CLTSTVQLIT QIMPFGLLD YVREHKDNIG SQYLLNWCQ IAKGMNYLED RRLVHRDLAA 840
RNVLVKTPQH VKITDFGLAK LLGAEEKEYH AEGKVPPIKM MALESILHRI YTHQSDVWSY 900
GVTWELMTF GSKPYDGIPI SEISSILEKG ERLPQPPICT IDVYIMMVKC WMIDADSRPK 960
FRELIIEFSK MARDPQRYLV IQGDERMHLP SPTDSNFYRA LMDEEDMDV VDAEYLIPO 1020
QGFFSSPSTS RTPLLSSLSA TSNNSTVACI DRNLQSCPI KEDSFLQRYSDPTGALTED 1080
SIDDITFLVP EYINQSVFKR PAGSVQNPVY HNQPLNPAPS RDPHYQDPHS TAVGNPEYLN 1140
TVQPTCVNST FDSAPHWAQK GSHQISLDNP DYQDFFPKE AKPNGIFKGS TAENAEYLRV 1200
APQSSEFIGA

DNA sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiiofacial syndrome)

Unigene number: Hs.110903

Probeset Accession #: AW245805

Nucleic Acid Accession #: NM_003277

Coding sequence: 121-777

1 11 21 31 41 51
AGGGGACTGG GGCCAAGAGC CGGAGAGCGG GGCSCAAAGS CACCAAGGCC CGCCAGGGC 60
GCCGCGCAGC ACGCCCTTGG GGGTCTGCGG GGCCTTCGGG TGCGGCTCTC GCCTCTAGCC 120
ATGGGGTCCG CAGCGTTGGA GATCCTGGGC CTGGTCTGT GCCTGGTGGG CTGGGGGGGT 180
CTGATCTCGG CGTGGCGGTG GCCCATGTGG CAGGTGACCG CCTTCTCTGA CCACAACATC 240
GTGACGCGCC AGACCACTG GAAGGGCCTG TGGATGTCG CGGTGGTGCA GAGCACGGGG 300
CACATGCAGT GCAAGTGTGA CGACTCGGTG CTGGCTCTGA GCACCGAGGT GCAGGCGGCG 360
CGGGGCTCA CGGTAGAGCG CGTGTGCTG CGGTCTGTG CGCTCTCTGT GACCTTGGCG 420
GGCGGCGAGT GCACCACTG CGTGGGCGCG GCGCGGCGCA AGGCGGCTGT GGCCTCTCAG 480
GGAGGCGTGC TCTACCTGTT TTGCGGGCTG CTGGCGCTCG TGCCACTCTG CTGGTTCGCC 540
AACATTGTCG TCCGCGAGTT TTACGACCCG TCTGTGCGCG TGTGCGAGAA GTACGAGCTG 600
GGCGCAGCGC TGTACATCGG CTGGGCGGCG ACCGCGCTGC TCATGCTAGG CGGCTGCCTC 660
TTGTGCTCGG GCGCCTGGGT CTGACCCGCG CGTCCCGACC TCAGCTTCCC CGTGAAGTAC 720
TCAGCGCGCG GCGGCGGCGC GCGCACCGGC GACTACGACA AGAAGAACTA CGTCTGAGGG 780
CGCTGGGCGC GCGCGGCGCG CTCTGCGCAG CCACGCTGCG GAGGCGTTGG ATAAGCCTGG 840
GGAGCCCCCG ATGAGCCGCG GCTTCCGCGG GGTAGCGCGG CGCGCAGGCT CCGGGAAGG 900
TCGGGCTCTG CGCCCGGAGC CGGCTCTCTG ATCCGCTCCT GCCTGCGCCC GCAGCTGACC 960
TTCTCTCTGC ACTAGCCCGG CCCTGCGCTT AACAGACGGA ATGAAGTTTC CTTTCTCTGT 1020
CGCGGCGCTG TTTCCATAGG CAGAGCGGGT GTCAGACTGA GGATTTCGCT TCCCTCCAA 1080
GACGCTGGGG GTCTTGGCTG CTGCTTACT TCCAGAGGCG TCCTGTCTAG TTCGAGGGGG 1140
CGGATGCAGA GCCCGGGGCG CCCACCGGAA GATGTGTACA GCTGCTCTT ACTCCATCGG 1200
CAGGCGCGAG CCGAGGAGCC AGTGACTTGG CCTGGACCTC CCGGTCTCAC TCCAGCATCT 1260
CCCCAGGCAA GGCTTGTGGG CACCGGAGCT TGAGAGAGGG CGGAGTGGG AAGGCTAAGA 1320
ATCTGCTTAG

Protein sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiiofacial syndrome)

Unigene number: Hs.110903

Protein Accession #: NP_003268

Signal sequence: none found

Pfam domain: PMP22 Claudin [4-181]

Transmembrane domains: 5-27, 74-96, 123-145, 164-186

Cellular Localization: plasma membrane

1 11 21 31 41 51
MGSAALIEIL LVLCVWGWS LILACGLPMW QVTAFLDHNI VTAQTWVGL WMSCVVQSTG 60
HMQCKVYDSV LALSTEVQAA RALTVSAVLL AFVALFVTLA GAQCTTCVAP GPAPARVALT 120
GGVLYLFCGL LALVPLCWFA NIVVREFYDF SVPVSQKYEL GAALYIGWAA TALIMVGGL 180
LCCGAWVCTG RPLDSFPVKY SAPRRPTATG DYDKKNYV

DNA sequence 12

Gene name: vascular endothelial junction-associated molecule

Unigene number: Hs.54650

Probeset Accession #: AA410345

Nucleic Acid Accession #: AF255910

Coding sequence: 241-1137

1 11 21 31 41 51
TTACCATGT GTTGGGCTGC GAGAAGACGA CAGAAGGGGG ACCCGCCTCT TGGCAGCCAG 60
CTGAGAAGGC GCCCGGGGA GGGGAAACT GACATCCCAT CTAGAGCCGT CCTCCTCTT 120
CCTCCCTCC CGACTCTCTG CTCTTTTCCC GCGCCAGAA GTTAAGGGCC CCGGCGCTCC 180
TGCGCTCTCG CGCGCGGAG CCGGACCTC CTCAGAGCAG CCGGCTGCCG CCGCGGGAAG 240
ATGGCGAGGA GAGGCGGCA CCGCTCCTC CTGCTGCTGC TGCGCTACCT GGTGGTGGCC 300
CTGGGCTATC ATAAGGCTA TGGGTTTCT GCGCCAAAG ACCAACAGGT AGTCACAGCA 360
GTAGAGTACC AAGAGGCTAT TTTAGCTGC AAAACCCCA AGAAGACTGT TTCCTCCAGA 420
TTAGAGTGA AAGAACTGGG TCGGAGTGT TCCTTTGTCT ACTATCAACA GACTCTTCAA 480
GGTGATTTA AAAAGCAGC TGAGATGATA GATTTCATA TCGGATCAA AAATGTGACA 540
AGAAGTGATG CGGGGAAATA TCGTTGTGAA GTTAGTGCCC CATCTGAGCA AGGCCAAAC 600
CTGGAAGAGG ATACGCTAC TCTGGAAGTA TTAGTGGCTC CAGCAGTTCC ATCATGTGAA 660
GTACCTCTT CTGCTCTGAG TGGAACTGTG GTAGAGCTAC GATGTCAAGA CAAAGAAGGG 720
AATCCAGCTT CTGAATACAC ATGGTTTAA GATGGCATCC GTTGTCTAGA AAATCCGAGA 780
CTGGCTCCC AAAGCACCAC CAGCTCATAC ACAATGAATA CAAAACTGG AACTCTGCAA 840
TTTAATACTG TTTCCAACT GGCACTGGA GAATATTCCT GTGAAGCCCG CAATCTGTGT 900
GGATATCCGA GGTGTCTCG GAAACGAATG CAAGTAGATG ATCTCAACAT AAGTGGCATC 960
ATAGCAGCG TAGTAGTTGT GGCCTTAGTG ATTTCCGTTT GTGGCCTTGG TGTATGCTAT 1020

5 GCTCAGAGGA AAGGCTACTT TTCAAAGAA ACCTCCTTCC AGAAGAGTAA TTCTTCATCT 1080
 AAAGCCACGA CAATGAGTGA AATGATTTC AAGCACACAA AATCCTTTAT AATTAAAGA 1140
 CTCCACTTTA GAGATACACC AAAGCCACCG TTGTTACACA AGTTATTAAA CTATTATAAA 1200
 ACTCTGCTTT GTCCGACATT TGCAAAGAGG TACACGAGGA AATGGAATTG GTATTTCATT 1260
 TTAATTTTCA TGAATACTAA CTACCTGAA CTTGCTATT TAAAMAATA GTTCTGTCGA 1320
 CACCTAAAAT ATAATCTGCG TTCTGTGTC TGGACTAAGT TAAAGAATT AAAATACTTT 1380
 GTAATGTCAA AAAAAA

Protein sequence 12

Gene name: vascular endothelial junction-associated molecule

Unigene number: Hs.54650

Protein Accession #: AAF81223

Signal sequence: 1-22

Igc2 domain: 41-116, 146-221

Transmembrane domains: 239-261

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 20 MARRSRHRL LLLRLYLVA LGYHKAYGFS APKDQQVVTA VEYQBAIAC KTPKKTVSSR 60
 LEWKKLGRSV SFVYYQQTLL GDFKNRAEMI DFNIRIKNVT RSDAGKYRCE VSAPSEQQQN 120
 LEEDVTTLLEV LVAPAVPSC VPSSALSGTV VELRCQDKEG NPAPEYTWFK DGIRLLENPR 180
 LGSQSTNSSY TMNTKTGTLQ FNTVSKLDTG EYSCEARNVS GYRRCPGKRM QVDDLNLISGI 240
 IAAVVVVALV ISVCGLGVCY AQRKGYFSKE TSFQKSNSSS KATTMSENDF KHTKSFII

DNA sequence 13

Gene name: solute carrier family 11 (proton-coupled divalent metal ion

Unigene number: Hs.182611

Probeset Accession #: D50402

Nucleic Acid Accession #: NM_000578

Coding sequence: 1-1653

1 11 21 31 41 51
 | | | | |
 35 ATGACAGGTG ACAAGGGTCC CCAAAGGCTA AGCGGGTCCA GCTATGGTTC CATCTCCAGC 60
 CCGACACGCC CGACACGCC AGGGCCACAG CAAGCACCTC CCAGAGAGAC CTACCTGAGT 120
 GAGAAGATCC CCATCCCAGA CACAAAACCG GGCACCTTCA GGTCTCGGAA GCTATGGGCC 180
 TTCACGGGGC CTGGCTTCCT CATGAGCAIT GCTTTCCTGG ACCCAGGAAA CATCGAGTCA 240
 GATCTTCAGC TNGNCCNGT GCGGGGATTC AAACCTCTCT GGGTGTCTGT CTGGGCCACC 300
 GTGTTGGGCT TGCTCTGCA CCGACTGGCT GCACGTCTGG GCGTGGTGAC AGGCAAGGAC 360
 TTGGGCGAGG TCTGCCATCT CTACTACCTC AAGGTGCCCC GCACCGTCTC CTGGCTGACC 420
 40 ATCGAGCTAG CCATTGTGGG CTCGACATG CAGGAAGTCA TCGGCACGCG CATTCGATTTC 480
 AATCTGTCTC CAGCTGGAGC AATCCCACTC TGGGGTGGCG TCCTCATCAC CATCGTGGAC 540
 ACCTTCTTCT TCCTCTTCCT CGATAACTAC GGGCTGCGGA AGCTGGGAAGC TTTTITTTGA 600
 CTCCTTATAA CCATTATGCG CTTGACCTTT GGCTATGAGT ATGTGGTGGC GCGTCTTGAG 660
 45 CAGGGAGCGC TTCTTCGGGG CCTGTTCCCTG CCTCGTGGC GGGGTGCGG CCACCCGAG 720
 CTGCTGCGAG CGGTGGGCAT TGTGTGGCGC ATCATCATGC CCCACACAT CTACCTGCAC 780
 TCGGCCCTGG TCAAGTCTCG AGAGATAGAC CGGCCCGGCC GAGTCGACAT CAGAGAAGCC 840
 AACATGTACT TCCTGATTGA GGCCACCATC GCGCTGTCCG TCTCCTTTAT CATCAACCTC 900
 TTTGTATGG CTGCTATTGG GCAGGCTTTC TACCAGAAAA CCAAGCAGGC TCGTTCACAC 960
 50 ATCTGTGCCA ACAGCAGCCT CCACGACTAC GCTAAGATCT TCCCCATGAA CAAGCCACCC 1020
 GTGGCCGTGG ACATTACCA GGGGGCGGTG ATCCTGGGCT GCTGTTCGG CCCCGCGGCC 1080
 CTCTACATCT GGGCCATAGG TCTCCTGGCG GCTGGGCGA GCTCCACCAT GACGGGACCC 1140
 TACGCGGGAC AGTTCGTGAT GGAGGGCTTC CTGAGGCTGC GGTGGTCAAG CTTCCGCGCT 1200
 GTCCCTCTCA CCGCTCTCTG CGCCATCCTG CCCACGCTGC TCGTGGCTGT CTTCCGGGAC 1260
 55 GTGAGGACT TGTCCGGCCT CAATGATCTG CTCAACGTGC TGCAGAGCTC GCTGCTCCCG 1320
 GTTCCGCTGC TGCCCATCTC CACGTTTACC AGCATGCCCA CCTCATGCA GGAGTTTGCC 1380
 AATGGCTGCG TGAACAAGGT CGTCACTCT TCCATCATGG TGCTAGTCTG CACCATCAAC 1440
 CTCTACTTCG TGGTCAGCTA TCTGCCAGC CTGCCCCACC CTGCTACTTT CGGCTTGCA 1500
 GCCTTGCTGG CCGCAGCTA CTTGGGCTC AGCACCTACC TGGTCTGAC CTGTTGCCTT 1560
 60 GCCCAGGAG CCACCTTCTT GGGCCACAGC TCCACCACC ACTTCTGTA TGGGCTCCTT 1620
 GAAGAGGACC ACAAAGGGA GACCTCTGGC TAG

Protein sequence 13

Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1

Unigene number: Hs.182611

Protein Accession #: NP_000569

Signal sequence: none found

Pfam domain: Nramp [78-463]

Transmembrane domains: 58-80, 88-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 70 MTGDKGPQRL SGSSYGSISS PTSPTSPGPQ QAPPRETYLS EKIPIDTPK GTFRLRLKLA 60
 FTGPGFLMSI AFLDPGNIES DLQLGPVAGF KLLVLLWAT VLGLLCQRLA ARLGVVTGKD 120
 75 LGEVCHLYVP KVPRTVLWLT IELAIVGSDM QEVIGTAIAF NLLSAGRIPL WGGVLITIVD 180
 TFFFLFDNY GLRLEAFPG LLITIMALT GYEVVVARPE QGALLRGLFL PSCPGCGHPE 240
 LLQAVGIVGA IIMPHNIYLH SALVKSREID RARRVDIREA NMYFLIEATI ALSVSFIINL 300
 FVMAAFQAF YQKTKQAAF ICANSSSLHDY AKIFPMNAT VAVDIYQGGV ILGCLFGPAA 360
 LYIWAIGLLA AGQSSMTGT YAGQFVMEGF LRLRWSSPAR VLLTRSCAIL PTVLVAVFRD 420
 80 LRDLSGLNDL LNLVQLLLP VAVLPILTFT SMPILMQEFA NGLLNKVVTS SIMVLVCTIN 480
 LYFVSVLPS LPHPAYFGLA ALLAAAYLGL STYLVMTCC LAGATFLAHS SHHFLYGLL 540
 EEDHKGETSG

DNA sequence 14

Gene name: solute carrier family 7 (cationic amino acid transporter, y+

Unigene number: Hs.184601
 Probeset Accession #: AF104032
 Nucleic Acid Accession #: NM_003486
 Coding sequence: 53-1576

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      GCTCGCTGGG CCGCTGCTCC CGGGTGTCCT AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
      TGC GGCCCGG AAGCGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG 120
      GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG 180
10     CGTGACCTCG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
      TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCG GCTCGCGCGG 300
      GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGCGCG CGCTCTGCTA 360
      CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
      CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCCTT 480
15     ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCCG TCTTCCCCAC 540
      CTGCCCGGTG CCGGAGGAGG CAGCCAAAGT CGTGGCCTGC CTGTGCGTGC TGCTGCTCAC 600
      GGCGGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TGGCGCGCG 660
      CAAGCTCCTG GCCCTGGCCC TGATCATCTC GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
      TGTGTCCAAT CTAGATCCCA AGTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780
20     TGTGTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCGT 840
      CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
      CATCGTGACG CTGGTGTAGC TGCTGACCAA CTGGGCTTAC TTCAACCCCG TGTCCACCGA 960
      GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
25     GTCCTGGATC ATCCCGCTCT TCGTGGCGCT GTCTGCTTTT GGCTCCGTCA ATGGGTCCCT 1080
      GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
      CTCATGATC CACCCACAGC TCCTCACCCC CGTCCCGTCC CTCTGTTCAT CGTGTGTGAT 1200
      GACGCTGCTC TACGCTTCTT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
      CAACTGGCTG TCGTGGCCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
30     TGAGCTTGA CCGCCCATCA AGGTGAACCT GGCCTGCCTT GTGTTCTTCA TCCTGGCCTG 1380
      CCTCTTCCTG ATCGCCGTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
      CATCATCTC AGCGGGCTGC CCGTCTACTT CTTCCGGGTC TGGTGGAAAA ACAAGCCCAA 1500
      TGGGCTCTC CAGGGCATCT TCTCCACGAC GTCTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
      CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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35     Protein sequence 14
      Gene name: solute carrier family 7 (cationic amino acid transporter, y+
      Unigene number: Hs.184601
      Protein Accession #: NP_003477
      Pfam domain: aa permeases [46-481]
40     Transmembrane domains: 52-74, 82-104, 120-142, 145-167, 169-191, 200-222, 237-259, 275-297, 323-345, 371-393,
      398-419, 430-452, 455-476
      Cellular Localization: plasma membrane
      1      11      21      31      41      51
      |      |      |      |      |      |
45     MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
      GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
      LEVYGSLEPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLV 180
      LLTAVNCSYV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPK FSPFEGTKLDV 240
50     GNIVLALYSG LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
      STEQMLSEEA VAVDFGNVHL GVMSSWII PVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
      SILSMIHQL LTPVPSLVFT CVMTLIYAFS KDIFSVINFF SFFNWLCLVAL AIIIGMIWLR 420
      RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVKN 480
      KPKWLLQGI STTVLCQKLM QVVPQET

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55     DNA sequence 15
      Gene name: Glutamate receptor subunit
      Unigene number: Hs.249141
      Nucleic Acid Accession #: S40369
      Coding sequence: 1-2943
60     1.      11      21      31      41      51
      |      |      |      |      |      |
      ATGCGGCTG AGCTGCTGCT GCTGCTGATT GTTGCCTTCG CCAGCCCCAG CTGCCAGGTG 60
      CTCTCATCAC TGCGCATGGC TGCAATCCTG GATGATCAGA CAGTGTGTGG CCGCGGTGAG 120
65     CGTCTGGCCT TGCCTTTGGC CCGGGAGCAG ATCAACGGGA TCATCGAGGT CCCAGCCAAG 180
      GCCCGAGTGG AAGTAGACAT CTTTGAAGCT CAGCGGGACA GCCAGTACGA GACCACGGAC 240
      ACCATGTGTC AGATCTTACC CAAAGGGGTT GTGCTGTGCC TTGGGCCCTC CTCTAGCCCA 300
      GCATCTGCCT CCACCGTGAG CCATATCTGT GGAGAGAAGG AGATCCCCCA CATCAAGGTG 360
      GGTCCCGAGG AGACACCCCG CTTTCAGTAC CTTGCTTCG CGTCTGTGAG CCGTATCCCC 420
70     AGTAACGAGG ACGTCAGCTT GCGGTCTCC CGAATCCTCA AGTCCTTCAA CTACCCCTCG 480
      GCCAGCCTCA TCTGCGCCAA GGCTGAGTGC CTGCTGCGAT TGGAGGAACT GGTGCGTGGC 540
      TTCTCATCT CCAAGGAGAC GCTGTCACTG AGGATGTTGG AGCAGACCCG GGACCCCA 600
      CCACTGCTCA AGGAGATCCG TGATGACAAG GTGTCCACCA TCATCATCGA CGCCAAACGCC 660
      TCCATCTCCC ACCTCATCTT CCGTAAGGCC TCGGAACCTG GAATGACCTC AGCGTTTAC 720
75     AAGTACATCC TCACCAACAT GGACTTCCCC ATCCTGCATC TGGACGCTAT TGTGGAGGAC 780
      TCTCCAAACA TCTTGGGCTT CTCCATGTTT AACACGTCCC ACCCTTCTA CCTGAGTTT 840
      GTCCGAGGCC TCAACATGTC CTGAGGGGAG AACTGTGAAG CCAGCACCTA CCTGGGCCCT 900
      GCGCTGTGAG CCGCCCTGAT GTTTGAGGCC GTGCACGTGG TGGTAGCGCG TGTCCGAGAG 960
      CTGAACCGCA GCCAGGAGAT CGGTGTGAAG CCTTGGCCT GTACATCGGC CAACATTG 1020
80     CCCCACGGGA CCAGCCTCAT GAACTACCTG CGCATGGTAG AGTATGATGG GCTGACCGGG 1080
      CGGTCGAGT TCAACAGCAA AGGGCAGAGA ACCAACTACA CCTGCGCAT CTTAGAAAG 1140
      TCCCGGCAGG GCCACCGTGA GATTGGGGTG TGGTACTCTA ACCGCACCTT GGCCATGAAT 1200
      GCCACACCCC TGGACATCAA CTGTGCGCAG ACACCTGGCA ACAAGACCTT GTTGGTCACA 1260
      ACCATCTTGG AGAAACCATTA OGTATGCGC CGGCCCAACT TCCAGGGCTT TCGGGGAAC 1320
      GAACGCTTCG AGGGCTTCTG CTGGGACATG CTGCGGGAGC TGGCCGAGCT GCTGCCGTTT 1380

```

5 CCGTACCGCC TCGGTTGGT GGAGGATGGG CTGTACGGGG CGCCGAGCC CAACGGCTCC 1440
 TGGACGGGCA TGGTTGGCGA GCTCATCAAC CGGAAGGCAG ACCTGGCTGT GGCCGCTTC 1500
 ACCATCACAG CTGAGCGGGA GAAGGTCACT GACTTTTCCA AGCCCTTTAT GACCCCTGGG 1560
 ATCAGCATCC TCTACGAGT GCACATGGCG CGCAAGCCTG GCTACTTCTC CTTCCTGGAC 1620
 CCCTTCTCCC CTGCTGTGTG GCTCTTCATG CTCTTTGCTT ACCTGGCTGT CAGCTGCGTC 1680
 CTGTTTCTGG CTGCCAGGCT GAGCCCTAT GAGTGGTATA ACCACACCC ATGCTTGGCG 1740
 GCACGCCCCC ACATCTGGA GAACCACTAC ACGCTGGGCA ACAGCTGTG GTTCCCGTG 1800
 GGGGGCTTCA TGCAGCAGGG CTGGAGATC ATGCCCGGG CGCTGTCCAC GCGCTGTGTC 1860
 10 AGCGGAGTCT GGTGGGCTT CACCTTGATC ATCATCTCTT CCTACACGGC CAACCTGGCC 1920
 GCCTTCTCTA CCGTGCAGCG CATGGAGGTG CCTGTGGAGT CGGCCGATGA CCTGGCAGAT 1980
 CAGACCAACA TCGAGTATGG CACCATCCAC GCGGCTCCA CCATGACCTT CTTCAGAAAT 2040
 TCACGATACC AAACGTACCA GCGCATGTGG AACTACATGC AGTCGAAGCA GCCCAGCGTG 2100
 TTGCTCAAGA GCACAGAAGA GGGCATGTCC GCGCTCTCA ACTCCCGCTA GCGCTTCTCT 2160
 CTGAGTCCA CCATGAACGA ATACCACCG CGCCTCAACT GCAACCTCAC CCAGATCGGG 2220
 15 GGACTCTCTG ACACCAAGGG CTACGGCATT GGCATGCGGC TGGGCTCCCC GTTCGGGAT 2280
 GAGATCACAC TGGCCATCCT GCAGCTTCAG GAGAACAAAC GGCTGGAGAT CCTGAAGCGC 2340
 AAGTGTGTC AGGGGGGCGG GTGCCCAAG GAGGAGGACC ATCGAGCTAA AGGTTTGGCG 2400
 ATGAGGAACA TTGTTGGCAT TTTTATCGTG CTCTCTGTG GCGCTCATAT TGCTGTCTTC 2460
 20 GTGGCGGTCA TGAATTCTAT ATGGTCCACA CGGAGGTGAG CTGAGTCCGA GGAGGTGTGG 2520
 GTGTGCCAGG AGATGCTGCA GGAGCTGCGC CACGCGGTTT CTTCGCGCAA GACGTGCGGT 2580
 TCCCGCGCGG GCGGAGCGCC GGGCGGCGCG AGCGGGGCGG TGCTGTCACT GCGCGCGGTC 2640
 CGCGAGATGC GCGTCAGCAA CGGCAAGCTC TACTCGGCGG GCGCGGCGCG GATGCGGCG 2700
 AGCGGCGCAG GGGGCGCGCA GCGCTCTCTG GACGACCGCG GCGCGCGCGG CCGAGCGCGA 2760
 25 CCGCGCGCGG CACCCCTCTG CACCCACGTG CCGCTCTGCC AGGAGTGGCG GCGCATCCAG 2820
 GCGCTGCGGG CCTCGGGGGG CCGCGCGGCT CCGCGTGGCC TGGGCGTCCC CGCCGAGGCC 2880
 ACCAGCGCGG CCGCGCGCGG GCGTGGCGCC GCGCGCGCCC GGGAGCTGGC GGAGCACGAG 2940
 TGA

30 **Protein sequence 15**
 Gene name: Glutamate receptor subunit
 Unigene number: Hs.249141
 Protein Accession #: AAB22591
 Signal sequence: 1-27
 Pfam domain: ANF receptor [343-400]; PBPe domain [416-785, 799-838]
 35 Transmembrane domains: 297-319, 544-566, 624-646, 803-825
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
 40 MPAELLLLLL VAFASPSQCV LSSLRMAAIL DDQTVCGRGE RLALALAREQ INGIIEVPAK 60
 ARVEVDIFEL QRDSQYETTD TMCQILPKGV VSVLGPSSSP ASASTVSHIC GEKEIPHIKV 120
 GPEETPRLQY LRFASVSLYP SNEDVSLAVS RILKSPNYPS ASLICKAKAEC LLRLLEELVRG 180
 FLISKETLSV RMLDDSRDPT PLLKEIRDDEK VSTIIIDANA SISHILIRKA SELGMTSAFY 240
 KYLLTTMDFP ILHLDGIVED SSNILGFSMF NTSHPFYPEF VRSLNMSWRE NCEASTYLGP 300
 45 ALSAALMFDA VHVVSVAVRE LNRSGEIGVK PLACTSANIW PHGTSMLNLY RMVEYDGLTG 360
 RVEFNSKQGR TNYTLRILEK SRQGHREIGV WYSNRTLAMN ATTLDINLSQ TLANKTLVVT 420
 TILNPYVMR RPNFQGLSGN ERFEGFCVDM LRELAELLPE PYRLRLVEDG LYGAPEFNGS 480
 WIGMVGELIN RKADLAVAAF TITAEREKVI DPKFPMTLG ISILYRVHMG RKPGYFSPFD 540
 PFSPAVLWFM LLAYLAVSCV LFLAARLSPY EWNYPHPCLR ARPHILENQY TLGNLSLWFPV 600
 50 GGFMMQGSSEI MPRLSTRVCV SGVWNAFTLI IISYNTANLA AFLTVQRMEV PVESADDLAD 660
 QTNIEYGTIH AGSTMTTFQON SRYQTYQRMW NYMQSKQPSV FVKSTEEGIA AVLNSRYAFL 720
 LESTMWEYHR RLWNLTLQIG GLLDTKGYGI GMLPGSPFRD EITLAILQLQ ENNRLEILKR 780
 KHWGGRCPK EBDHRAKGLG MENIGGIFIV LICGLIIAVF VAVMEFIWST RRSASEEVS 840
 VCQEMLEQLR HAVSCRKTSR SRRRRRPGGP SRALLSLRAV REMRLSNGKL YSAGAGGDAG 900
 55 SAHGGPQRLD DDPGPSPGAR PAAPTPCTHV RVCQECRIQ ALRASGAGAP PRGLGVPAEA 960
 TSPPRPRPGP AGPRELAEHE

60 **DNA sequence 16**
 Gene name: adenosine A3 receptor
 Unigene number: Hs.258
 ProbeSet Accession #: NM_000677
 Nucleic Acid Accession #: NM_000677
 Coding sequence: 768-1724
 1 11 21 31 41 51
 65 ATCTTTGCTG CAAAGGCTGG GTATCGGCTG TGCTCAGCAA AGCGTCAACT CGTGCAAGAA 60
 CITAGCAGGA ATAGTTCTGG CTAAGGTTAG GAGGCTGCCA CCAAAGTCTC TTTTGTGTTT 120
 CTCTGCTTCT CCCGTTTGCC TCCTTATCAT GAGATCTTTT TGCTAAGCTG GCAGAAAGAT 180
 TGCAATAGTCA GTGCTTCCAG CTCTGCTCCC ACCTGATCCT GCACTGTCTT CTGGTCCCTG 240
 70 AATGAATGAA CTCTGATACC CAATCTTGTC TCGAGCCTTC TCTATGCCAC TCATGGCTCC 300
 TCTTCTGCTC TTTCATCTTT TTTGCTGAGA GTTCTGAGCT CTGTACTTCC TCTTGGCCCA 360
 TCTCACTTCC TGAACACCC CTGAAGAGGG TTGCTTATCT TGATGGAAC CAAAAGGCCA 420
 AAAAGCTGCA GGCAGAGGCG TTGAGGACAT CTGTTTGGGG AACTAAGAGC AGCAGCACTT 480
 TCAGATTTCG TCCATATAGA GCTGTCTTAC AGCATTCTGG AACTTGGAG ATGTGCGGTG 540
 75 CATAAAGGGG CTGGAAGTGA CCCACCTGTG ATGAGCCCTT TCTAAGGAGA AGGCTTTCCA 600
 AGAGATCACC CCACCAGAAA AGGGTAGGAA TGAGCAAGTT GGGAAATTTA GACTGTCACT 660
 GCACATGGAC CTCTGGGAAG ACGTCTGGCG AGAGCTAGGC CCACTGGCCC TACAGACGGA 720
 TCTTGTCTGC TCACCTGTCC CTGTGGAGGT TCCCTGGGA AGGCAAGATG CCCAACAAACA 780
 GCACTGTCTT GTCAATGGCC AATGTTACCT ACATCACCAT GGAATTTTCT ATTGGACTCT 840
 80 GCGCATGATG GGGCAAGCTG CTGGTCACTT GCGTGGTCAA GCTGAACCCC AGCCTGCAGA 900
 CCACCACCTT CTATTTCAAT GTCTCTCTAG CCCTGGCTGA CATGTCTGTT GGGGTGCTGG 960
 TCATGCTTTT GGCCATTTGT GTCAGCCTGG GCATCACAAT CCCTTCTAC AGCTGCTTTT 1020
 TTATGACTTG CCTACTGCTT ATCTTTACCC ACGCCTCCAT CATGTCTCTG CTGGCCATCG 1080
 CTGTGACCGC ATACTTGCGG GTCAAGCTTA CCGTCAGATA CAAGAGGGTC ACCACTCACA 1140
 GAAGAATATG GCTGGCCTTG GGCCTTTGCT GGCTGGTGTG ATTCTGGTGG GATTGACCC 1200

	CCATGTTTGG	CTGGAACATG	AAACTGACCT	CAGAGTACCA	CAGAAATGTC	ACCTTCCTTT	1260
	CATGCCAATT	TGTTTCCGTC	ATGAGAAATGG	ACTACATGGT	ATACTTCAGC	TTCTCACCT	1320
	GGATTTTCAT	CCCCCTGGTT	GTCATGTGCG	CCATCTATCT	TGACATCTTT	TACATCATTC	1380
5	GGAACAACT	CAGTCTGAAC	TTATCTAACT	CCAAAGAGAC	AGGTGCATTT	TATGGACGGG	1440
	AGTTCAAGAC	GGCTAAGTCC	TGTTTCTGCG	TTCTTTTCTT	GTTTGCTCTG	TCATGGCTGC	1500
	CTTTATCTAT	CATCAACTGC	ATCATCTACT	TAAATGGTGA	GGTACCACAG	CTTGTGCTGT	1560
	ACATGGGCAT	CCTGCTGTCC	CATGCCAACT	CCATGATGAA	CCCTATCGTC	TATGCCTATA	1620
	AAATAAGAA	GTTCAAGGAA	ACCTACCTTT	TGATCCTCAA	AGCCTGTGTG	GTCTGCCATC	1680
10	CCTCTGATTC	TTTGGACACA	AGCATTGAGA	AGAATTCTGA	GTAGTTATCC	ATCAGAGATG	1740
	ACTCTGTCTC	ATTGACCTTC	AGATTCCCCA	TCAACAAACA	CTTGAGGGCC	TGTATGCCTG	1800
	GGCCAAGGGA	TTTTTACATC	CTTGATTACT	TCCACTGAGG	TGGGAGCATC	TCCAGTGCTC	1860
	CCCAATTATA	TCTCCCCAC	TCCACTACTC	TCTTCCTCCA	CTTCATTTT	CCTTGTCTCT	1920
	TTCTCTCTAA	TTCACTGTTT	TGGAGGCGCTG	ACTTGGGGAC	AACGTATTAT	TGATATTATT	1980
	GTCTGTTTTT	CTTCTTCCCA	ATAGAAGAAT	AAGTCATGGA	GCCTGAAGGG	TGCCTAGTTG	2040
15	ACTTGTGAC	AAAAGGCTCT	AGTTGGGCTG	AACATGTGTG	TGGTGGTGAC	TCATTCCAT	2100
	GCCATTGTGG	AATTGAGCAG	AGAACCTGCT	CTCGGAGGAT	GCCTAGAAGA	TGTTGGGAAC	2160
	AGAAGAAATA	AATCTAGATT	AAGGGGACT	TAACTGCTG	AATTCACCTG	TGGATGTTTT	2220
	TGAGTAAATA	AAAGCTAATA	G				
20	Protein sequence 16						
	Gene name: adenosine A3 receptor						
	Unigene number: Hs.258						
	Protein Accession #: NP_000668						
	Signal sequence: none found						
25	Pfam domain: 7tm_1 [29-282]						
	Transmembrane domains: 12-34, 50-72, 86-108, 120-150, 179-201, 229-251						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
30	MPNNSTALS	LVNTYITMEI	FIGLCAIVGN	VLVICVVKLN	PSLQITTFYF	IVSLALADIA	60
	VGVLVMEPLAI	VVSLGITIH	YSLCFMTCLL	LIFTHASIMS	LLAIADVRYL	RVKLTVRYKR	120
	VTHRRILWA	LGLCWLVSFL	VGLTPMFQWN	MKLITSEYHRN	VTFLSCQFVS	VMRMDYMYFP	180
	SFLTWIFPL	VVMCAIYLDI	FYIIRNKLSL	NLSNSKETGA	FYGREFTAK	SLFLVLFLFA	240
	LSWLPLSIIN	CIIFYNGEVP	QLVLYMGILL	SHANSMMMPI	VYAYKIKKFK	ETYLILKAC	300
35	VVCHPSDSL	TSIEKNS					
	DNA sequence 17						
	Gene name: glypican 1						
	Unigene number: Hs.2699						
40	Probeset Accession #: X54232						
	Nucleic Acid Accession #: NM_002081						
	Coding sequence: 222-1898						
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	CGGACCTTG	GCTCTGCCCT	TGCGGGCGCG	GAACCTCGCA	GGACCGCGCC	AGGATCCGAG	180
	AGAGGCGCG	GCGGCGCGCG	GGGGCGCGCG	CGCGCCCGC	CATGGAGCTC	CGGCGCGAG	240
50	GCTGGTGGT	GCTATGTGCG	GCGCGAGCGC	TGGTGGCTG	CGCCGCGCGG	GACCGCGCCA	300
	GCAAGAGCG	GAGCTGCGCG	GAGGTCCGCG	AGATCTACGG	AGCCAAGGCG	TTACGCTCAG	360
	GCGACGTGCC	CCAGGCGGAG	ATCTCGGGTG	AGCACCTGCG	GATCTGTCCC	CAGGGCTACA	420
	CCTGCTGCAC	CAGCGAGATG	GAGGAGAACC	TGGCCAAACG	CAGCCATGCC	GAGCTGGAGA	480
	CGCGCTCGC	GCGACAGCAG	CGCGTCTGCG	AGGCCATGCT	TGCCACCCAG	GTCGCGAGCT	540
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	CGCGCGCTT	CGGAGAGCTG	TACACGCAGA	ACGCGAGGCG	CTTCCGGGAC	GCTGTACTCAG	660
	AGCTGCGCT	GTACTACCGC	GGTGCCAACC	TGCACCTGGA	GGAGACGCTG	CGCGAGTTCT	720
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	ACTACCTGGA	CTGCTTGGCG	AAGCAGGCGG	AGGCGCTGCG	GCCCTTGGGG	GAGGCGCGCA	840
	GAGAGCTGG	CCTGCGGGCG	ACCGGTGCTC	TGCTGGCTGC	TGCTCTCTTT	GTGACGGGCC	900
60	TGGCGTGGC	CAGCGAGCTG	GTCCGGAAG	TGGCTCAGGT	CCCGCTGGCG	CGGAGTGTCT	960
	CGAGAGCTGT	CATGAAGCTG	GTCTACTGTG	CTCACTGCCT	GGGAGTCCCC	GGCGCCAGGC	1020
	CCTGCCCTGA	CTATTGCCGA	AATGTGCTCA	AGGCTGCCT	TGCCAACAG	GCGACCTGG	1080
	ACGCGAGTG	GAGGAACCTC	CTGGACTCCA	TGGTGTCTAT	CACCGACAAG	TTCTGGGGTA	1140
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65	CCCTCCAGGA	CAACAGGAGC	ACGCTCACGG	CCAAGTCTAT	CCAGGCTGCG	GGGAACCCCA	1260
	AGGTCAACCC	CCAGGCGCCT	GGGCTGAGG	AGAAGCGGCG	CGGGGCAAG	CTGGCCCGCG	1320
	GGGAGAGGCC	ACCTTCAGGC	ACGCTGGAGA	AGCTGGTCTC	TGAAGCCAAG	GCCAGCTGCC	1380
	GCGACGTCCA	GGAATCTTGG	ATCAGCCTCC	CAGGGACACT	GTGCACTGAG	AAGATGGCCC	1440
	TGAGCACTGC	CAGTGATGAC	CGCTGCTGGA	ACGGGATGGC	CAGAGGCGCG	TACCTCCCGG	1500
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	CCAAGCCGGA	CATGACCATC	CGGCAGCAGA	TCATGCAGCT	GAAGATCATG	ACCAACCGGC	1620
	TGCGCAGCGC	CTACAACGGC	AACGACGTGG	ACTTCCAGGA	CGCCAGTGAC	GACGCGAGCG	1680
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	GCTCCAGCTC	CGGACGCCCC	TTGACCCATG	CCCTCCAGG	CCTGTACAGG	CAGGAAGGAC	1800
75	AGAAGACCTC	GGCTGCCAGC	TGCCCCAGC	CCCGACCTT	CCTCTGCCCC	CTCTCTCTCT	1860
	TCTCTGCTCC	TACAGTAGCC	AGGCCCGGCT	GGCGTAACT	GCCTCAAGGC	CCGAGGACA	1920
	GAGGCCAAGG	ACTGACTTTG	CCAAAAATAC	AACACAGACG	ATATTTAATT	CACCTCAGCC	1980
	TGGAGGCGCC	TGGGTGGGGA	CAGGGAGGGC	CGCGGCTCT	GAGCAGGGGC	AGGCGCAGAG	2040
	GTCCAGCCCC	CAGGCTGGCG	CTGCTGCTCC	TTTCTGCTCT	TTAATTTTGT	ATGAGTCTCT	2100
80	CAGGTGACGT	GGGAGCCAGT	GTGCCCAAAA	GCCATGTATT	TCAGGGACCT	CAGGGGCACC	2160
	TCCGCTGCTC	TAGCCTCTCC	CCCAGCTCCC	TGCACCGCGC	CAGAAGCAGC	CCTCGAGGCG	2220
	CTACAGAGGA	GGCCTCAAAG	CAACCCGCTG	GAGCCCAACG	CGAGCCTGTG	CCTTCTCTCC	2280
	CGCTCTCTCC	CACTGGGACT	CCCAGCAGAG	CCCACAGGCC	AGCCTGTGCC	CACCCCGGAC	2340
	CCTCCAGAGA	AGCCCGGCAC	GGGCTGCTCG	GGTGTCCGCC	ATCCAGGGTC	TGCAGAGGCC	2400

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 10 CCCCCTACTG CACACGGGAA TGCTTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG 2940
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 15 TCCTGAACCG ACTGACCTGT AGGAGGCCGC TTAGTGTGTC TTTGCTTTTC ATCACGCTCC 3300
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 20 TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
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 TCCTTGTATG AATAAAGGC TGGAAACCTA AA

25 Protein sequence 17
 Gene name: glypican 1
 Unigene number: Hs.2699
 Protein Accession #: NP_002072
 Signal sequence: none found
 Pfam domain: Glypican protein [2-490]
 30 Transmembrane domains: none found
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
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 35 ICPQSYTCCT SEMEENLANR SHAELETALR DSSRLVQAML ATQLRSFDDH FQHLLNDSER 120
 TLQATFPFAG GELYTQNARA FRDLYSELRL YYRGAHLLE ETLAEFWARL LERLKFQLHP 180
 QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFLVAA RSFVQGLGVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGLC ANQADLDAEW RNLLDSMVL 300
 40 TDKFWGTSGV ESVGISVHTW LAEAINALQD NRDTLTAKVI QCGGNPKVNP QGPGPEEKRR 360
 RGLAPRPREP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRWNMGMA 420
 RGRYLPVEMG DGLANQINNP EVEVDITKPD MTIRQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDGSGSGS

45 DNA sequence 18
 Gene name: NY-REN-24 antigen
 Unigene number: Hs.128425
 Nucleic Acid Accession #: AF155102
 Coding sequence: 27-908
 1 11 21 31 41 51
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 AGGTACGGGG AGACGCCAGC GAGAGCGCCG AGGACATCTT CTTCGGCGCG GCCAAGGAGG 240
 55 GCATGGGCCA GGACGAGGCG CAGTTCAGCG TGGAGATGCC ACTCACCGGC AAGGCCTACC 300
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70 Protein sequence 18
 Gene name: NY-REN-24 antigen
 Unigene number: Hs.128425
 Protein Accession #: AAD42868
 Signal sequence: none found
 75 Transmembrane domains: none found
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
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 80 GEGEAVLME EDLIQQLDD YDAGRYSPRL LTAHELPLDA HVLEPDEDLQ RLQLSRQQLQ 60
 TGDASESAE DIFERRAKG MQQDEAQFSV EMPLTKAYL WADKYRPRKP RFFNRVHTGF 120
 WNKYNQTHY DFDNPPPKIV GQYKFNIFYP DLIDKRSTPE YFLEACADNK DFAILRFTRG 180
 LRGHRFQDR QPRVGTILAPP RLPLFVQQRH LPAVLSLQAL PLSAVTALGN GRPGGPRATR 240
 PQPRSEWPS RQACSSASDG NISNRSKTES ASRTPRGPPN LTSHQPQTTH SPSTPRLTW 300

DNA sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A
 Unigene number: Hs.159

Probeset Accession #: BE295782

Nucleic Acid Accession #: NM_001065

Coding sequence: 256-1623

5
 10
 15
 20
 25
 30
 35
 40
 45
 T

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CGGGAAGCCC	CAGCACTGCC	GCTGCCACAC	TGCCCTGAGC	CCAAATGGGG	GAGTGAGAGG	240
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CTCTCCTGCC	AGGAGAAACA	GAACACCGTG	TGCACCTGCC	ATGCAGGTTT	CTTTCTAAGA	780
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CTGGTCATT	TCITTTGGTCT	TTGCTTTTA	TCCCTCCTCT	TCATTGGTTT	AATGTATCGC	960
TACCAACGGT	GGAAGTCCAA	GCTCTACTCC	ATTGTTTGTG	GGAAATCGAC	ACCTGAAAAA	1020
GAGGGGAGAC	TTGAAGGAAC	TACTACTAAG	CCCCCTGGCC	CAAAACCAAG	CTTCAGTCCC	1080
ACTCCAGGCT	TCACCCCCAC	CCTGGGCTTC	AGTCCCGTGC	CCAGTTCAC	CTTCACCTCC	1140
AGCTCCACCT	ATACCCCGGG	TGACTGTCCC	AACCTTGCGG	CTCCCGCAG	AGAGGTGGCA	1200
CCACCCCTATC	AGGGGGCTGA	CCCCATCCTT	GCGACAGCCC	TGCGCTCGA	CCCCATCCCC	1260
AACCCCTTTC	AGAAGTGGGA	GGACAGCGCC	CACAAGCCAC	AGAGCCTAGA	CACTGATGAC	1320
CCGCGACGCG	TGTACGCCCT	GGTGGAGAAC	GTGCCCCCGT	TGCGCTGGAA	GGAATTGCTG	1380
CGGCGCCTAG	GGCTGAGCGA	CCACGAGATC	GATCGGCTGG	AGCTGCAGAA	CGGCGCTGCG	1440
CTGCGCGAGG	CGCAATACAG	CATGCTGGCG	ACCTGGAGGC	GCGCACGCCC	CGGCGCGAG	1500
GCCACGCTGG	AGCTGCTGGG	ACGCGTGCTC	CGCGACATGG	ACCTGCTGGG	CTGCGTGGAG	1560
GACATCGAGG	AGGCGCTTTG	CGGCCCGGCC	GCCCTCCCGC	CGCGGCCAG	TCTTCTCAGA	1620
TGAGGCTGCG	CCCTCGCGGG	CAGCTCTAAG	GACCGTCTGT	CGAGATCGCC	TTCCAAACCC	1680
ACTTTTCTTG	GGAAAGGAGG	GGTCTGCGAG	GGGCAAGCAG	GAGCTAGCAG	CGCGCTACTT	1740
GGTGCTAACC	CCTCGATGTA	CATAGCTTTT	CTCAGCTGCC	TGCGCGCCGC	CGACAGTCAG	1800
CGCTGTGCGC	GCGGAGAGAG	GTGCGCCGTG	GGCTCAAGAG	CCTGAGTGGG	TGGTTTGCGA	1860
GGATGAGGGA	CGCTATGCTC	CATGCCCGTT	TTGGGTGTCC	TCACCAGCAA	GGCTGCTCGG	1920
GGGCGCCCTG	TTGCTCCCTG	AGCCTTTTTC	ACAGTGCATA	AGCAGTTTTT	TTTGTTTTGT	1980
TTTTGTTTTG	TTTTGTTTT	AAATCAATCA	TGTTACACTA	ATAGAAACTT	GGCACTCCTG	2040
TGCCCTCTGC	CTGGACAAGC	ACATAGCAAG	CTGAACCTGC	CTAAGGCAGG	GGCGAGCACG	2100
GAACAATGGG	GCCTTCAGCT	GGAGCTGTGG	ACTTTGTATC	ATACACTAAA	ATTCTGAAGT	2160

Protein sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A
 Unigene number: Hs.159

Protein Accession #: NP_001056

Signal sequence: 1-29

TNFR domain: 44-81, 84-125, 127-166, 168-195

Transmembrane domains: 211-234

Cellular Localization: plasma membrane

50
 55
 60
 65

1	11	21	31	41	51	
MGLSTVPDLL	LPLVLELLV	GIYPSGVIGL	VPHLGDEKR	DSVCPQGYI	HPQNNISICT	60
KCHKGTLYLN	DCPGPGQDID	CRECESGSFT	ASENHLRHCL	SCSKCRKEMG	QVEISSCTVD	120
RDIVCGCRKN	QYRHYNSNL	PQCFNCSLCL	NGTVHLSQCE	KQNTVCTCHA	GFFLRENECV	180
SESNCKKSL	CTRLCLPQIE	NVKGTEDSGT	TVLLPLVIF	GLCLLSLLFI	GLMYRYQRWK	240
SKLYSIVCGK	STPEKEGELE	GTTTKPLAPN	PSPSPPTPGT	PTLGFSPVPS	STFTSSSTYT	300
PGDCPNFAAP	RREVAFFYQG	ADPILATALA	SDPIPPLQK	WEDSAHKPQS	LDTDDPATLY	360
AVVENVPPLR	WKEFVRRLGL	SDHEIDRLLE	QNGRCLREAO	YSMLATWRRR	TPRREATLEL	420
LGRVLRLMDL	LGCLIEDIEA	LOGPAALPPA	PSLLR			

DNA sequence 20

Gene name: prominin (mouse)-like 1

Unigene number: Hs.112360

Probeset Accession #: R40057

Nucleic Acid Accession #: NM_006017

Coding sequence: 38-2635

70
 75
 80

1	11	21	31	41	51	
CCAAGTTCTA	CCTCATGTTT	GGAGGATCTT	GCTAGCTATG	GCCCTCGTAC	TGGGCTCCCT	60
GTTCGTGCTG	GGGCTGTGCG	GGAATCTCTT	TTCAAGGAGG	CAGCCTTCAT	CCACAGATGC	120
TCCTAAGGCT	TGGAATTATG	AATTGCCTGC	AACAATTAT	GAGACCCAG	ACTCCATAA	180
AGCTGGACCC	ATTGGCATTG	TCTTTGAAC	AGTGCAATC	TTTCTCTATG	TGGTACAGCC	240
CGGTGATTTC	CCAGAGATA	CTTTGAGAAA	ATTCTTACAG	AAGGCATATG	AATCCAAAT	300
TGATTATGAC	AAGCCAGAAA	CTGTAATCTT	AGGTCTAAG	ATTGTCTACT	ATGAAGCAGG	360
GATTATTCTA	TGCTGTGTCC	TGGGGCTGCT	GTTTATTATT	CTGATGCCTC	TGGTGGGGTA	420
TTTCTTTTGT	ATGTGTCTGT	GCTGTAAACA	ATGTGGTGGG	GAAATGCACC	AGCGACAGAA	480
GGAAAATGGG	CCCTTCCTGA	GGAAATGCTT	TGCAATCTCC	CTGTTGGTGA	TTGTATATAAT	540
AATAAGCATT	GGCATCTTCT	ATGGTTTGT	GGCAATCAC	CAGGTAAGAA	CCCGGATCAA	600
AAGGAGTCGG	AACTGGCAG	ATAGCAATTT	CAAGGACTTG	CGAACTCTCT	TGAATGAAAC	660

	TCCAGAGCAA	ATCAAAATATA	TATTGGCCCA	GTACAACACT	ACCAAGGACA	AGGCGTTCAC	720
	AGATCTGAAC	AGTATCAATT	CAGTGTAGG	AGGCGGAATT	CTTGACCGAC	TGAGACCCAA	780
	CATCATCCCT	GTCTCTGATG	AGATTAAATG	CATGGCAACA	GCGATCAAGG	AGACCAAGA	840
5	GGCGTGGAG	AACATGAACA	GCACCTTGAA	GAGCTTGCAC	CAACAAAGTA	CACAGCTTAG	900
	CAGCAGTCTG	ACCAGCGTGA	AAACTAGCCT	GCGGTCTATCT	CTCAATGACC	CTCTGTGCTT	960
	GGTGCATCCA	TCAAGTGAAA	CCTGCAACAG	CATCAGATTG	TCTCTAAGCC	AGCTGAATAG	1020
	CAACCCCTGAA	CTGAGGCAGC	TTCCACCCGT	GGATGCAGAA	CTTGACAACG	TTAATAACGT	1080
	TCTTAGGACA	GATTITGGATG	GCCTGGTCCA	ACAGGGCTAT	CAATCCCTTA	ATGATATACC	1140
10	TGACAGAGTA	CAACGCCAAA	CCACGACTGT	CGTAGCAGGT	ATCAAAAGGG	TCTTGAATTC	1200
	CATTGGTTC	GATATCGACA	ATGTAACCTA	GCGTCTTCCT	ATTCAGGATA	TACTCTCAGC	1260
	ATTCTCTGTT	TATGTTAATA	ACACTGAAAG	TTACATCCAC	AGAAATTAC	CTACATTGGA	1320
	AGAGTATGAT	TCATACTGGT	GGCTGGGTGG	CCTGGTCTATC	TGCTCTCTGC	TGACCCCTCAT	1380
	CGTGATTITT	TACTACCTGG	GCTTACTGTG	TGGCGTGTGC	GGCTATGACA	GGCATGCCAC	1440
15	CCCGACCACC	CGAGGCTGTG	TCTCCAACAC	CGAGGGCGTC	TTCTCTATGG	TTGGAGTTGG	1500
	ATTAAGTTTC	CTCTTTTGCT	GGATATTGAT	GATCAITGTG	GTCTTACCT	TGTCTTTTGG	1560
	TGCAAAATGTG	GAAAAACCTGA	TCTGTGAACC	TTACACGAGC	AAGGAATTAT	TCCGGGTTTT	1620
	GGATACACCC	TCTTACTATA	ATGAAGACTG	GGAATACTAT	CTCTCTGGGA	AGCTATTATA	1680
	TAAATCAAAA	ATGAAGCTCA	CTTTGAACA	AGTTTACAGT	GACTGCAAAA	AAAATAGAGG	1740
20	CACTTACGGC	ACTCTTCACC	TGCAGAACAG	CTTCAATATC	AGTGAACATC	TCAACATTAA	1800
	TGAGCATACT	GGAAGCATAA	GCAAGTGAAT	GGAAAGTCTG	AAGGTAAATC	TTAATATCTT	1860
	TCTGTGGGT	GCACGAGGAA	GAAAAAACCT	TACGATTITT	GCTGCTTGTG	GAATAGACAG	1920
	AATGAATTAT	GACAGCTACT	TGGCTCAGAC	TGGTAAATCC	CCCCCAGGAG	TGAATCTTTT	1980
	ATCATTTGCA	TATGATCTAG	AAGCAAAAGC	AAACAGTTTG	CCCCCAGGAA	ATTGAGGAA	2040
25	CTCCCTGAAA	AGAGATGCAC	AAACTATTAA	AACAATTCAC	CAGCAACGAG	TCCTTCCTAT	2100
	AGAACAATCA	CTGAGCAGCT	TATACCAAAG	CGTCAAGATA	CTTCAACGCA	CAGGGAATGG	2160
	ATTGTTGGAG	AGAGTAACCT	GGATTCTAGC	TTCTCTGGAT	TTTGCTCAGA	ACTTCTATCAG	2220
	AAAACAATCT	TCTCTGTGTA	TTATTGAGGA	AACTAAGAAG	TATGGGAGAA	CAATAATAGG	2280
	ATATTTTGAA	CAITATCTGC	AGTGGATCGA	GTTCTCTATC	AGTGAGAAAG	TGGCATCGTG	2340
30	CAAACCTGTG	GCCACCGCTC	TAGATACTGC	TGTTGATGTC	TTTCTGTGTA	GCTACATTAT	2400
	CGAACCCCTG	AATTTGTTTT	GGTTTGGCAT	AGGAAAAGCT	ACTGTATTTT	TACTTCCGGC	2460
	TCTAATTTTT	GGGCTAAAAC	TGGCTAAGTA	CTATCGTCGA	ATGATTCCGG	AGGACGTGTA	2520
	CGATGATGTT	GAAACTATAC	CCATGAAAAA	TATGGAAAAA	GGTAATAATG	GTTATCATAA	2580
	AGATCATGTA	TATGGTATTC	ACAATCCTGT	TATGACAAGC	CCATCACAAAC	ATTGATAGCT	2640
35	GATGTTGAAA	CTGCTTGAGC	ATCAGGATAC	TCAAAGTGGA	AAGGATCACA	GATTTTGTGT	2700
	AGTTTCTGGG	TCTACAAGGA	CTTTCCAAAT	CCAGGAGCAA	CGCCAGTGGC	AACGTAGTGA	2760
	CTCAGGCGGG	CACCAAGGCA	ACGGCACCAT	TGGTCTCTGG	GTAGTGCTTT	AAGAATGAAC	2820
	ACAATCACTG	TCTATCCAT	GGTCCATCAC	TATTCAAGGA	TGACTCCCTC	CCTTCTGTGC	2880
	TATTTTGTGT	TTTTACTTTT	TTACACTGAG	TTTCTATTTA	GACACTACAA	CATATGGGGT	2940
40	GTTTGTTCCT	ATTGGATGCA	TTTCTATCAA	AACTCTATCA	AATGTGATGG	CTAGATTCTA	3000
	ACATATTGCC	ATGTGTGGAG	TGTGCTGAAC	ACACACCAGT	TTACAGSAAA	GATGCATTTT	3060
	GTGTACAGTA	AACGGTGTAT	ATACCTTTTG	TTACCAACAGA	GTTTTTFAAA	CAAAATGAGTA	3120
	TTATAGAGCT	TTCTTCTAAA	TGAGCTAAAT	AAGTCACCAT	TGACTCTCTG	GTGCTGTGTA	3180
	AAATAATCCA	TTTTCTACTA	AAGTGTGTGA	AACCTACAGC	ATATTCTTCA	CGCAGAGATT	3240
45	TTCACTTATT	ATACTTTATC	AAAGATTGGC	CATGTTCCAC	TTGGAAATGG	CATGCAAAAG	3300
	CCATCATAGA	GAAACCTGCG	TAACCTCCATC	TGACAAATTC	AAAAGAGAGA	GAGAGATCTT	3360
	GAGAGAGAAA	TGCTGTTTCT	TCAAAAGTGG	AGTTGTTTTA	ACAGATGCCA	ATTACGGTGT	3420
	ACAGTTTAAC	AGAGTTTCTT	GTTGCATTAG	GATAAACATT	AATTGGAGTG	CAGCTAACAT	3480
	GAGTATCATC	AGACTAGTAT	CAAGTGTCTT	AAAATGAAAT	ATGAGAAGAT	CCTGTACAAA	3540
50	TTCTTAGATC	TGGTGTCCAG	CATGGATGAA	ACCTTTGAGT	TTGGTCCCTA	AATTTGCATG	3600
	AAAGCACACG	GTAATATATC	ATTGCTTCTA	GGAGTTTCAT	GTTGGATCTG	TCATTATCAA	3660
	AAGTGATCAG	CAATGAAGAA	CTGGTCGGAC	AAAATTTAAC	GTTGATGTAA	TGGAATTCCA	3720
	GATGTAGGCA	TTCCCCCCAG	GTCTTTTCAT	GTGCAGATTG	CAGTTCTGAT	TCATTTGAAT	3780
	AAAAAGGAAC	TTGGC					
55	<u>Protein sequence 20</u>						
	Gene name: prominin (mouse)-like 1						
	Unigene number: Hs.112360						
	Protein Accession #: NP_006008						
	Signal sequence: 1-21						
60	Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
65	MALVLGSLLL	LGLCGNSFSFG	GQPSSTDAPK	AWNYELPATN	YETQDSHKAG	PIGILFELVH	60
	IFLVVQPRD	FPEDTLRKFL	QKAYESKIDY	DKPETVILGL	KIVYYEAGII	LCCVLGLLFI	120
	ILMPLVGYYF	CMCRCCNKG	GEMHQKQEN	GPFLRKCFAI	SLLVICIIIS	IGIFYGFVAN	180
	HQVTRIKRS	RKLADSNFKD	LRTLNETPE	QIKYILAQYN	TTKDKAFTDL	NSINSVLGGG	240
	ILDLRLPNII	PVLDEIKSMA	TAIKETKEAL	ENMNSTLKS	HQSTQLSSS	LTSVKTSLS	300
70	SLNDPLCLVH	PSSETCNSIR	LSLSQLNSNP	ELRQLPPVDA	ELDNVNVNLR	TDLDGLVQGG	360
	YQSLNDIPDR	VQRQTITVVA	GIKRVLNSIG	SDIDNVTQRL	PIQDILSAFS	VYVNNTESYI	420
	HRNLPTLEBY	DSYWWLGGVL	ICSLTLIVI	FYYLGLLCGV	CGYDRHATPT	TRGCVSNTGG	480
	VFLMVGVLGS	FLFCWILMII	VVLTFVFGAN	VEKLICEPYT	SKELFRVLD	PYLLNEDWEY	540
	YLSGKLFNKS	KMKLTPEQVY	SDCKKNRGTY	GTLLHQNFSN	ISEHLNINEH	TGSISSELES	600
75	LKVNLIIFLL	GAAGRNLQD	FAACGIDRMN	YDSYLAQTKG	SPAGVNLFS	AYDLEAKANS	660
	LPPGNLRNSL	KRDAQTIKTI	HQQRVLPBIEQ	SLSTLYQSVK	ILQRTGNLL	ERVTRILASL	720
	DFAQNFITNN	TSSVIIIEETK	KYGRITIGYF	EHYLNQIEFS	ISEKVASCKP	VATALDTAVD	780
	VFLCSYIDP	LNLFWFGIGK	ATVFLLPALI	FAVKLAKYYR	RMDSEIDVYD	VETIPMKMNE	840
	NGNNGYHKDH	VYGIHNPVMT	SPSQH				
80	<u>DNA sequence 21</u>						
	Gene name: G protein-coupled receptor 39						
	Unigene number: Hs.85339						
	Nucleic Acid Accession #: NM_001508						
	Coding sequence: 1-1362						

	1	11	21	31	41	51	
	ATGGCTTCAC	CCAGCCTCCC	GGGCGTGC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
	CCCGAGTTTG	AGGTGGCCAC	CTGGATCAA	ATCACCCCTA	TTCTGGTGTA	CCTGATCATC	120
5	TTCTGTGATG	GCCTTCTGGG	GAACAGCGCC	ACCATGCGG	TCACCCAGGT	GCTGCAGAAG	180
	AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
	TTGGTGTTC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTGACC	300
	ACGTCCAGCT	ACACCTGTCT	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
	GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTACCCCC	420
10	TTCAAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTGTCTGCG	480
	GTCACCTCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGTACTGA	GTACCCCTTG	540
	GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCAAGAG	600
	CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
	CAGTCCAGCA	TCTTCGGGCG	CTTCGTGGTC	TACCTCGTGG	TCCTGCTCTC	CGTAGCCCTTC	720
15	ATGTGTCTGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780
	ACGCGGCTCT	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
	ACCATCATCT	TCTCTGAGGT	GATTGTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACAG	900
	ATTCGGAGGA	TCATGGCTGC	GGCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCGG	960
	GCGTACATGA	TCCTCTCTCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
20	CCGCTCCTGT	ACACGGTGTCT	CTCGCAGCAG	TTTCGGCGGG	GGTTCGTGCA	GGTGTCTGTC	1080
	TGCCCGCTGT	CGCTGCAGCA	CGCAACCCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
	ACCAACGATG	CGCCCGCTCT	TGTGCAGCGC	CCGTTGCTCT	TGCGCTCCCG	GCGCCAGTCC	1200
	TCTGCAAGGA	GAAGTGAAGA	GATTTTCTTA	AGCACTTTTC	AGACGAGGTC	CGAGCCCCAG	1260
25	TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1320
	AATTCGTCTG	CAGAGAAATG	TTTTCAGGAG	CATGAAGTTT	GA		

Protein sequence 21

Gene name: G protein-coupled receptor 39

Unigene number: Hs.85339

Protein Accession #: NM_001508, NP_001409

Signal sequence: none found

Pfam domains: 7tm_1 [72-172, 224-344]

Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342

Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MASPSLPQSD	CSQIIDHSV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60
	KGYLQKEVD	HMVSLACSDI	LVFLIGMPME	FYSIIWNPLT	TSSYTLSCKL	HTFLFEACSY	120
40	ATLLHLVLTLS	FERYIAICHP	FRYKAVSGPC	QVKLLIGFVW	VTSALVALPL	LFAMGTETPL	180
	VNVPSSHRLT	CNRSSTRHHE	QPETSNMSIC	TNLSRRWTFV	QSSIFGAFVU	YLVVLLSVAF	240
	MCWNMMQVLM	KSQKSLAGG	TRPPQLRKSE	SEESRTARRQ	TIIFLRLLIVV	TLAVCWMPNQ	300
	IRIRMAAAKP	KHDWTRSYFR	AYMILLPFSE	TFFYLSSVIN	PLLYTVSSQQ	FRRVFVQVLC	360
	CRSLQHANH	EKRLRVHAHS	TTDSARFVQR	PLLEASRRQS	SARRTEKIFL	STFQSEAEPE	420
45	SKSQSLSLSES	LEPNSGAKPA	NSAAENGFBQ	HEV			

TABLE 8A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 8A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of 75th percentile tumor to 85th percentile normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
60	431917	D16181	Hs.2868	peripheral myelin protein 2	75.2
	427343	A1880044	Hs.176977	protein kinase C binding protein 2	74.6
	455601	A1368680	Hs.816	SRY (sex determining region Y)-box 2	74.2
	428321	A1699994	Hs.2868	peripheral myelin protein 2	71.6
	412719	AW016610	Hs.129911	ESTs	70.7
65	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	66.3
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-1	64.3
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	60.1
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	52.3
70	435147	AL133731	Hs.4774	Homo sapiens mRNA: cDNA DKFp761C1712 (f	46.7
	425842	A1587490	Hs.159623	NK-2 (Drosophila) homolog B	40.1
	412733	AA984472	Hs.74554	KIAA0080 protein	39.0
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	38.7
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	37.2
75	423849	AL157425	Hs.133315	Homo sapiens mRNA: cDNA DKFp761J1324 (f	36.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	31.8
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	31.8
	436878	BE465204	Hs.47448	ESTs	31.4
80	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	30.9
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	30.4
	446711	AF169692	Hs.12450	protocadherin 9	30.2
	439415	F05538	Hs.12825	ESTs	28.3
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	26.9

	429466	M85835	Hs.12827	ESTs	25.9
	447004	AW296968	Hs.157539	ESTs	25.3
	424581	M62062	Hs.150917	calenin (cadherin-associated protein), a	24.8
5	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	24.8
	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.3
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	24.3
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	24.2
	450133	AW969769	Hs.105201	ESTs	24.2
10	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	23.3
	448672	AI955511	Hs.225106	ESTs	22.7
	435708	AI362949	Hs.75169	ESTs	22.0
	407034	U84540		gb.Human dystrobrevin isoform DTN-3 (DTN	21.9
	407168	R45175	Hs.117183	ESTs	21.7
15	431019	NM_005249	Hs.2714	forkhead box G1B	21.5
	409049	AI423132	Hs.146343	ESTs	21.4
	433896	AW294729	Hs.274461	ESTs	21.1
	445041	T64183	Hs.282982	solute carrier	21.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	20.4
20	444378	R41339	Hs.12569	ESTs	20.0
	411305	BE241596	Hs.69547	myelin basic protein	19.9
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	19.8
	441016	AW138653	Hs.25845	ESTs	19.6
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	18.5
25	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	18.4
	452461	N78223	Hs.108106	transcription factor	18.1
	409395	U46745	Hs.54435	dystrobrevin, alpha	18.1
	417183	R52089	Hs.172717	ESTs	18.0
	409638	AW450420	Hs.21335	ESTs	18.0
30	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	18.0
	449611	AI970394	Hs.197075	ESTs	17.0
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	16.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9
	444471	AB020684	Hs.11217	KIAA0877 protein	16.8
35	421659	NM_014459	Hs.105511	protocadherin 17	16.7
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	16.6
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
	441440	AI807981	Hs.30495	ESTs	15.7
40	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	15.7
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	15.5
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885	Hs.117183	ESTs	15.1
	424945	AI221919	Hs.173438	hypothetical protein FLJ10582	14.9
45	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	14.9
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
	416857	AA188775	Hs.292453	ESTs	14.7
	419721	NM_001650	Hs.288650	aquaporin 4	14.6
	411078	AI222020	Hs.182364	CocoaCrisp	14.4
50	453924	R49295	Hs.24886	ESTs	14.4
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	14.3
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266	N59006	Hs.26133	ESTs	14.0
55	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	14.0
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	14.0
	439239	AI031540	Hs.235331	ESTs	14.0
	441497	R51064	Hs.23172	ESTs	14.0
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	14.0
60	414245	BE148072	Hs.75850	WAS protein family, member 1	13.7
	429900	AA460421	Hs.30875	ESTs	13.6
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	449605	AW138581	Hs.198416	ESTs	13.6
	452526	W38537	Hs.280740	hypothetical protein MGC3040	13.6
65	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	13.3
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	13.3
	420077	AW512260	Hs.87767	ESTs	13.2
	424120	T80579	Hs.290270	ESTs	13.2
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	13.2
70	423361	AW170055	Hs.47628	ESTs	13.1
	428409	AW117207	Hs.98523	ESTs	12.9
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	12.6
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	12.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
75	436954	AA740151	Hs.130425	ESTs	12.4
	430691	C14187	Hs.103538	ESTs	12.4
	433551	AI985544	Hs.12450	protocadherin 9	12.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	12.2
	427540	R12014	Hs.20976	ESTs	12.1
80	435624	AF218942	Hs.24889	formin 2	12.1
	415849	R20529	Hs.6806	ESTs	12.1
	428845	AL157579	Hs.153610	KIAA0751 gene product	11.9
	442671	AI005668	Hs.134779	EST	11.9
	444396	T65213	Hs.4257	ESTs	11.8

	452752	AW044058	Hs.33578	KIAA0820 protein	11.8
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
5	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
	428976	AL037824	Hs.194695	ras homolog gene family, member I	11.6
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	11.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	11.6
	414214	D49958	Hs.75819	glycoprotein M6A	11.5
10	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
	405238				11.4
	420362	U79734	Hs.97205	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	11.4
15	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
	451952	AL120173	Hs.301663	ESTs	11.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTs	11.3
20	429918	AW873986	Hs.119383	ESTs	11.3
	443912	R37257	Hs.184780	ESTs	11.3
	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092	AAB14043	Hs.88045	ESTs	11.2
	408081	AW451597	Hs.167409	ESTs	11.2
25	411642	NM_014932	Hs.71132	neuroigin 1	10.9
	415170	R44386	Hs.164578	ESTs	10.9
	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fs, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8
30	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	10.7
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	10.7
	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
35	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	10.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3
	440471	AA886146	Hs.307944	ESTs	10.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.1
40	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	10.1
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	10.1
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fs, clone L	9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AI538323	Hs.52620	integrin, beta 8	9.8
45	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
	436511	AA721252	Hs.291502	ESTs	9.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	9.7
	449539	W80363	Hs.58446	ESTs	9.7
	412959	D87458	Hs.75090	KIAA0282 protein	9.6
50	412811	H06382	Hs.21400	ESTs	9.6
	449300	AI656959	Hs.222165	ESTs	9.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
55	451516	AI800515	Hs.12024	ESTs	9.4
	422656	AI870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	9.3
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	9.2
60	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	9.2
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
	424641	AB001106	Hs.151413	glia maturation factor, beta	9.1
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9.1
65	408508	AI806109	Hs.135736	KIAA1580 protein	9.0
	452785	AL359942	Hs.298434	erythroid differentiation and denucleati	9.0
	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	8.9
70	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
	449625	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	8.8
	400292	AA250737	Hs.72472	ESTs	8.7
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	8.7
	420345	AW295230	Hs.25231	ESTs	8.7
75	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	8.7
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	400780				8.6
80	434891	AA814309	Hs.123583	ESTs	8.6
	449277	AA001064	Hs.172976	ESTs	8.6
	415709	AA649850	Hs.278558	ESTs	8.5
	439947	AB006627	Hs.6788	astrotactin	8.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5

	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	8.4
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	8.4
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	8.4
	415796	R87548	Hs.78854	ATPase, Na+/K+ transporting, beta 2 poly	8.3
5	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	8.3
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	8.3
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	8.3
	433447	U29195	Hs.3281	neuronal pentraxin II	8.3
10	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	8.3
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
	414300	AI304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
15	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	8.1
	442710	AI015631	Hs.23210	ESTs	8.1
	425048	H05468	Hs.164502	ESTs	8.1
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	8.0
	445740	T76281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neurofilin	7.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
25	446619	AI076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
	435501	AW051819	Hs.129908	KIAA0591 protein	7.8
	423600	AI633559	Hs.310359	ESTs	7.8
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	7.8
30	415314	N88802	Hs.5422	glycoprotein M6B	7.7
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp5861823 (f	7.7
	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	AI962493	Hs.197647	ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.7
35	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
	439779	NM_003787	Hs.6414	nucleolar protein 4	7.6
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	7.6
	448555	AI536697	Hs.159863	ESTs	7.5
40	439662	H97552	Hs.269060	ESTs	7.5
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	7.5
	410099	AA081630	Hs.169387	KIAA0036 gene product	7.5
	431592	R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
45	405819				7.4
	407886	AW969688	Hs.100826	ESTs	7.4
	437416	AL359605	Hs.283851	Homo sapiens mRNA; cDNA DKFZp547G036 (fr	7.4
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	7.4
	408604	D51408	Hs.21925	ESTs	7.4
50	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
	447499	AW262580	Hs.147674	protocadherin beta 16	7.3
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.2
	410037	AB020725	Hs.58009	KIAA0918 protein	7.2
55	419318	AW969742	Hs.291005	ESTs	7.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.2
	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52620	integrin, beta 8	7.2
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	7.2
60	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	7.2
	407182	AA312551	Hs.230157	ESTs	7.1
	415293	R49462	Hs.106541	ESTs	7.1
	422764	AI767727	Hs.47522	ESTs	7.1
	451592	AI805416	Hs.213897	ESTs	7.1
65	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0
	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
	434149	Z43829	Hs.19574	hypothetical protein MGC5469	7.0
	436726	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypotheti	7.0
	417632	R20855	Hs.5422	glycoprotein M6B	7.0
70	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	6.9
	435267	N23797	Hs.110114	ESTs	6.9
	437117	AL049256	Hs.122593	ESTs	6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
	445745	AB007924	Hs.13245	KIAA0455 gene product	6.9
75	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.9
	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	6.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.7
80	443297	AI049864	Hs.133029	ESTs	6.7
	443992	AW022228	Hs.322922	ESTs	6.7
	453096	AW294631	Hs.11325	ESTs	6.7
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	6.7
	443761	AI525743	Hs.160603	ESTs	6.6

5	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	6.6
	435056	AW023337	Hs.5422	glycoprotein M6B	6.5
	453431	AF094754	Hs.32973	glycine receptor, beta	6.5
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	6.5
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.5
10	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805	L10333	Hs.99947	reticulon 1	6.4
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothe	6.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
	407866	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.3
15	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
	445102	AW204610	Hs.22270	ESTs	6.2
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	6.2
20	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	6.2
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2N6HM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
25	424997	AL138167	Hs.96920	ESTs	6.1
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	6.1
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.1
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
30	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.0
	444170	AW613879	Hs.102408	ESTs	6.0
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	6.0
35	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H05626	Hs.6921	ESTs	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.9
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.9
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
40	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	5.9
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9
	447350	AI375572	Hs.172634	ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9
	447101	N72185	Hs.44189	ESTs	5.9
45	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.9
	438451	AW075485	Hs.286049	phosphoserine aminotransferase	5.9
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	5.8
	437036	AI571514	Hs.133022	ESTs	5.7
50	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	5.7
	445828	F05802	Hs.81907	ESTs	5.7
	447198	D61523	Hs.283435	ESTs	5.7
55	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.9567	butyrobetaine (gamma), 2-oxoglutarate di	5.6
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	5.6
	435718	R06569	Hs.269534	ESTs	5.6
60	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW514021	Hs.245510	ESTs	5.6
	422411	AW749443	Hs.22511	ESTs	5.6
	438328	AI492261	Hs.32450	ESTs	5.6
65	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	5.5
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
	400859				5.5
	413625	AW451103	Hs.71371	ESTs	5.5
70	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	AI879064	Hs.54618	ESTs	5.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	5.5
	430979	AI479755	Hs.129010	ESTs	5.5
75	412709	AL022327	Hs.74518	KIAA0027 protein	5.5
	439920	H05430	Hs.288433	neurotrimin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
	419235	AW470411	Hs.288433	neurotrimin	5.4
80	418030	BE207573	Hs.83321	neuromedin B	5.4
	410330	AW023630	Hs.46786	ESTs	5.4
	410781	AI375672	Hs.165028	ESTs	5.4
	420658	AW965215	Hs.336656	ESTs	5.4
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4
	443740	R56434	Hs.21062	ESTs	5.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	5.4
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	5.4

5	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.4
	424432	AB037821	Hs.146858	protocadherin 10	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
10	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	404584				5.3
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3
	439845	AL355743	Hs.55653	Homo sapiens EST from clone 41214, full	5.3
	424001	W67883	Hs.137476	paternally expressed 10	5.3
15	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitter)	5.3
	426625	T78300	Hs.300642	serologically defined colon cancer antigen	5.3
	428137	AA421792	Hs.170999	ESTs	5.3
	428679	AA431765		gbzw80c03.s1 Soares_testis_NHT Homo sap	5.3
	438176	AW138970	Hs.122113	ESTs	5.3
20	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.3
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340	N31772	Hs.79226	fasciculation and elongation protein zeta	5.3
	435244	N77221	Hs.187824	ESTs	5.3
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
25	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secretion	5.3
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillator	5.3
	430437	A1768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.3
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian)	5.2
	453941	U39817	Hs.36820	Bloom syndrome	5.2
30	424998	U58515	Hs.154138	chitinase 3-like 2	5.2
	423419	R55336	Hs.23539	ESTs	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	5.2
	409206	AF041853	Hs.43670	kinesin family member 3A	5.2
35	421013	M62397	Hs.1345	mutated in colorectal cancers	5.2
	429443	AB028967	Hs.202687	potassium voltage-gated channel, Shal-re	5.2
	434367	AB020700	Hs.3830	KIAA0893 protein	5.2
	444861	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	5.2
	446142	A1754693	Hs.145968	ESTs	5.2
40	448816	AB033052	Hs.22151	KIAA1226 protein	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related	5.2
	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
	416737	AF154335	Hs.79691	LIM domain protein	5.2
45	424800	AL035588	Hs.153203	MyoD family inhibitor	5.2
	443695	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	5.2
	415257	F03016	Hs.27513	ESTs	5.2
	433929	A1375499	Hs.27379	ESTs	5.1
	415651	A1207162	Hs.3815	stathmin-like-protein RB3	5.1
50	451027	AW519204	Hs.40808	ESTs	5.1
	409172	Z99399	Hs.118145	ESTs	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	429172	AA447417	Hs.285491	ESTs	5.1
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	5.1
55	451270	AW341392	Hs.235795	ESTs	5.1
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (f	5.1
	420560	AW207748	Hs.59115	ESTs	5.1
	418097	R45137	Hs.21868	ESTs	5.1
	442910	A1365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.1
60	434849	AW292765	Hs.8053	ESTs	5.1
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.1
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	5.0
	413627	BE182082	Hs.246973	ESTs	5.0
65	418661	NM_001949	Hs.1189	E2F transcription factor 3	5.0
	422438	AA445925	Hs.270896	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
	435087	AW975241	Hs.23567	ESTs	5.0
70	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (5.0
	410434	AF051152	Hs.63568	toll-like receptor 2	4.9
	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	4.9
	407808	AA663559	Hs.279789	histone deacetylase 3	4.9
	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	4.9
75	425977	R15138	Hs.165570	Homo sapiens clone Z5052 mRNA sequence	4.9
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
	447112	H17800	Hs.7154	ESTs	4.9
	449574	F05048	Hs.175373	ESTs	4.9
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	4.9
80	423869	BE409301	Hs.134012	C1q-related factor	4.9
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.9
	449176	A1633545	Hs.198072	ESTs	4.9
	448451	AW015994		gb:UL-H-B10p-abh-g-09-0-UI.s1 NCI_CGAP_S	4.8
	402604				4.8
	436039	AW023323	Hs.121070	ESTs	4.8
	448769	N66037	Hs.38173	ESTs	4.8
	423578	AW963357	Hs.7847	ESTs	4.8

	439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.8
	425870	R13406	Hs.56782	ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
5	413409	AI638418	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.8
	413623	AA825721	Hs.246973	ESTs	4.8
	417246	AI760098	Hs.21411	ESTs	4.8
	420900	AL045633	Hs.44269	ESTs	4.8
	424153	AA451737	Hs.141496	MAGE-like 2	4.8
10	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
	454030	AW021429	Hs.231980	ESTs	4.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.8
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	4.8
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
	431103	M57359	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956	AI374651	Hs.22542	ESTs	4.7
	435060	AI422719	Hs.233349	ESTs, Weakly similar to fork head like p	4.7
20	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7
	449353	AA001220	Hs.271369	ESTs	4.7
25	452022	AW072330	Hs.293875	ESTs	4.7
	454269	AI951060	Hs.129908	KIAA0591 protein	4.7
	404541				4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125	R17268	Hs.259873	axonal transport of synaptic vesicles	4.7
30	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.6
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.6
	413492	D87470	Hs.75400	KIAA0280 protein	4.6
	419629	AB020695	Hs.91662	KIAA0888 protein	4.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.6
35	436140	W87355	Hs.269587	ESTs	4.6
	439169	AI912122	Hs.41095	ESTs	4.6
	443150	AI034467	Hs.34650	ESTs	4.6
	451073	AI758905	Hs.208063	ESTs	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
40	452106	AI141031	Hs.21342	ESTs	4.6
	451407	AA131376	Hs.326401	fibroblast growth factor 12B	4.6
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	4.6
	437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	4.6
45	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.5
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5
	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	4.5
	419343	AA456245	Hs.85603	down-regulated by Ctnnb1, a	4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
50	429399	AA452244	Hs.16727	ESTs	4.5
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
	453118	AW195849	Hs.252757	ESTs	4.5
	443455	AB001025	Hs.9349	ryanodine receptor 3	4.4
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	4.4
55	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.4
	435202	AI971313	Hs.170204	KIAA0551 protein	4.4
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4
60	451254	AI571016	Hs.172967	ESTs	4.4
	439039	AI656707	Hs.48713	ESTs	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	AI742434	Hs.169911	ESTs	4.4
65	410611	AW954134	Hs.20924	KIAA1628 protein	4.4
	402605				4.4
	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222	AI061301	Hs.164773	ESTs	4.4
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.4
70	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	4.4
	442832	AW206560	Hs.253569	ESTs	4.4
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279	AW959861	Hs.290943	ESTs	4.3
	427194	AA399018	Hs.250835	ESTs	4.3
75	419723	AL120193	Hs.92614	longevity assurance (LAG1, S. cerevisiae	4.3
	445810	AW265700	Hs.155660	ESTs	4.3
	409734	BE161664	Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	4.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.3
80	433024	AA573847	Hs.26549	KIAA1708 protein	4.3
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	4.3
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.3
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3

	444600	R41398	Hs.6996	ESTs	4.3
	454042	H22570	Hs.172572	hypothetical protein FLJ20093	4.3
	441899	AJ372588	Hs.8022	TU3A protein	4.3
5	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
	430291	AV660345	Hs.238126	CGI-49 protein	4.2
	433597	AA708205	Hs.100343	ESTs	4.2
	444127	N63620	Hs.13281	ESTs	4.2
10	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	4.2
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	4.2
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.2
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	4.2
	428536	AI143139	Hs.2288	visinin-like 1	4.2
15	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	4.2
	447138	AJ439112	Hs.93828	ESTs, Weakly similar to Z109260A B cell	4.2
	450648	AI703366	Hs.26766	ESTs	4.2
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2
20	421686	AB011156	Hs.106794	KIAA0584 protein	4.2
	452776	AA194540	Hs.13522	ESTs, Weakly similar to I38022 hypotheti	4.2
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	4.2
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibitor	4.2
25	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.2
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
	439607	BE540565	Hs.159460	ESTs	4.1
	424028	AF055084	Hs.153592	Homo sapiens cDNA FLJ14354 fis, clone Y7	4.1
	446936	H10207	Hs.47314	ESTs	4.1
30	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.1
	412445	AI768015	Hs.92127	ESTs	4.1
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.1
	419683	AA248897	Hs.48784	ESTs	4.1
	426071	AW138057	Hs.163835	ESTs	4.1
35	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.1
	432809	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	4.1
	452039	AI922988	Hs.172510	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.1
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433932	AW954599	Hs.169330	neuronal protein	4.1
	436637	AI783629	Hs.26766	ESTs	4.1
45	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.1
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	4.1
	410486	AW235094	Hs.69233	zinc finger protein	4.0
50	413916	N49813	Hs.75615	apolipoprotein C-II	4.0
	438703	AI803373	Hs.31599	ESTs	4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	405771				4.0
	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	4.0
55	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.0
	424176	AL137273	Hs.142307	hypothetical protein	4.0
	425773	N21279	Hs.237749	ESTs	4.0
	427304	AA761526	Hs.163853	ESTs	4.0
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	4.0
60	452834	AI538627	Hs.105685	KIAA1688 protein	4.0
	453745	AA952989	Hs.63908	hypothetical protein MGC14726	4.0
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0
65	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
	439199	R40373	Hs.26299	ESTs	4.0
	439450	R51613	Hs.125304	ESTs	4.0
	446782	AI653048	Hs.144006	ESTs	4.0
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9
70	402408				3.9
	453362	H14988	Hs.107375	ESTs	3.9
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	3.9
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	3.9
	425010	T16837	Hs.4241	ESTs	3.9
75	444230	H95537	Hs.146067	ESTs	3.9
	441736	AW292779	Hs.169799	ESTs	3.9
	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.9
	406311				3.9
	408460	AA054726	Hs.285574	ESTs	3.9
80	410658	AW105231	Hs.192035	ESTs	3.9
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.9
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.9
	429477	AI275514	Hs.6658	ESTs	3.9
	433766	AA609234	Hs.112669	ESTs	3.9

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	3.9
	447891	R41754	Hs.6496	ESTs	3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9
	404283				3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.9
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.9
	445314	AI689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.9
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9
10	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.9
	438054	AA776526	Hs.62183	ESTs	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157646	Hs.153506	ESTs	3.9
	432590	AI609273	Hs.110783	ESTs	3.9
15	453331	AI240665	Hs.8895	ESTs	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.8
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.8
20	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	3.8
	417355	D13168	Hs.82002	endothelin receptor type B	3.8
	446727	AB011095	Hs.16032	KIAA0523 protein	3.8
	424340	AA339036	Hs.7033	ESTs	3.8
25	423346	AI267677	Hs.127416	synaptotagmin 1	3.8
	412788	AA120960	Hs.198416	ESTs	3.8
	404593				3.8
	416856	N27833	Hs.269028	ESTs, Weakly similar to I38022 hypotheti	3.8
30	429896	AA460367	Hs.224223	ESTs, Moderately similar to I38022 hypot	3.8
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	3.8
	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
	440322	AA879430		gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	447761	AF061573	Hs.19492	protocadherin 8	3.8
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	3.8
35	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.8
	447028	AI973128	Hs.167257	brain link protein-1	3.8
40	449458	AI805078	Hs.208261	ESTs	3.8
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.8
	428841	AI418430	Hs.104935	ESTs	3.8
	430643	AW970065	Hs.287425	MEGF10 protein	3.8
45	422263	AA307639	Hs.129908	KIAA0591 protein	3.8
	451625	RS6793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.8
	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	3.8
	441928	AI370188	Hs.211454	ESTs	3.8
	441797	AI369333	Hs.214635	ESTs	3.7
50	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.7
	425588	F07396	Hs.46751	ESTs	3.7
	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
55	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	3.7
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.7
	440080	AW051597	Hs.143707	ESTs	3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.7
60	409234	AI879419	Hs.27206	ESTs	3.7
	420489	AA815089	Hs.193513	ESTs	3.7
	426890	AA393167	Hs.41294	ESTs	3.7
	438849	W28948	Hs.10762	ESTs	3.7
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.7
65	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.7
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.7
	459518	AI937419	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	3.7
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL135740	Hs.102447	TSC-22-like	3.7
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.7
70	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.7
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.7
	420807	AA280627	Hs.57846	ESTs	3.7
	449961	AW265634	Hs.133100	ESTs	3.7
75	422634	NM_016010	Hs.118821	CGI-62 protein	3.7
	421030	AW161357	Hs.101174	microtubule-associated protein tau	3.7
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	3.7
	440483	AI200836	Hs.150386	ESTs	3.7
80	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.7
	423756	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	3.6
	425187	AW014486	Hs.22509	ESTs	3.6
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	3.6
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.6

	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.6
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5H85	3.6
	429239	AA448419	Hs.45209	ESTs	3.6
5	419086	NM_000216	Hs.89591	Kalman syndrome 1 sequence	3.6
	446659	AJ335361	Hs.226376	ESTs	3.6
	426757	AW205640	Hs.158206	ESTs	3.6
	418819	AA228776	Hs.191721	ESTs	3.6
	458332	AI000341	Hs.220491	ESTs	3.6
10	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.6
	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	3.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.6
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	3.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.6
15	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	3.6
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	3.6
	430530	AA480870	Hs.47660	ESTs	3.6
	436425	AJ913146	Hs.318725	CGI-72 protein	3.6
	438078	AJ016377	Hs.131693	ESTs	3.6
20	442927	AJ024347	Hs.131519	ESTs	3.6
	446242	N66336	Hs.7360	ESTs	3.6
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.6
	450474	AW872844	Hs.201919	ESTs	3.6
	452198	AJ097560	Hs.61210	ESTs, Weakly similar to I38022 hypothesi	3.6
25	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
	436443	AW138211	Hs.128746	ESTs	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.6
	456038	AA203285	Hs.294141	ESTs, Weakly similar to alternatively sp	3.6
	408902	AW014869	Hs.5510	ESTs	3.6
30	442950	AI500417	Hs.46764	ESTs	3.6
	442905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.6
	425478	AB007953	Hs.268840	ESTs	3.6
	453884	AA355925	Hs.36232	KIAA0186 gene product	3.6
	404721				3.6
35	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	440553	AA889416	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.5
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	3.5
	413999	N46124	Hs.34460	ESTs	3.5
40	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.5
	425017	AL119305	Hs.288405	ESTs	3.5
	435958	H98180	Hs.117975	ESTs	3.5
	415101	R45531	Hs.144534	ESTs	3.5
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.5
45	430290	AJ734110	Hs.136355	ESTs	3.5
	416836	D54745	Hs.80247	cholecystokinin	3.5
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.5
	419412	AW161058	Hs.90297	synuclein, beta	3.5
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.5
	452689	F33868	Hs.284176	transferrin	3.5
50	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	3.5
	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypothesi	3.5
	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.5
	444584	AI168422		gb:rok30e11.x1 Soares_NSF_FB_9W_OT_PA_P_S	3.5
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.5
55	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.5
	412659	AW753865	Hs.74376	olactomedin related ER localized protei	3.5
	429077	AB028983	Hs.2352	adenylate cyclase 2 (brain)	3.5
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	3.5
	450784	AW246803	Hs.47289	ESTs	3.5
60	446827	AW451243	Hs.157069	ESTs	3.5
	436434	N50465	Hs.92927	putative 47 kDa protein	3.5
	412777	AJ335773	Hs.270123	ESTs	3.5
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.5
	408601	U47928	Hs.86122	protein A	3.4
65	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	3.4
	448425	AI500359	Hs.233401	ESTs	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	451729	AW160725	Hs.312469	ESTs	3.4
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.4
70	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.4
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.4
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.4
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	3.4
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (f	3.4
75	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.4
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.4
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.4
	435061	AI651474	Hs.163944	ESTs	3.4
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.4
80	449714	AB033015	Hs.23941	KIAA1189 protein	3.4
	443392	AI055821	Hs.293420	ESTs	3.4
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.4
	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.4
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.4

5	432731	R31178	Hs.287820	fibronectin 1	3.4
	448758	AB018311	Hs.21917	KIAA0768 protein	3.4
	432613	AW081698	Hs.80712	KIAA0202 protein	3.4
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
10	410108	AA081659	Hs.318775	OSBP-related protein 6	3.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	3.4
	402855				3.3
	422170	AI791949	Hs.112432	anti-Müllerian hormone	3.3
	445034	AW293376	Hs.143659	ESTs	3.3
15	424378	W28020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	3.3
	404819				3.3
	436607	AW661783	Hs.211061	ESTs	3.3
20	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.3
	452693	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW850180		gb:IL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	3.3
25	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.3
	421192	AA833718	Hs.204529	KIAA1806 protein	3.3
	426695	AW118191	Hs.112729	ESTs	3.3
	438885	AI886558	Hs.184987	ESTs	3.3
30	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypotheti	3.3
	453590	AF150278	Hs.33578	KIAA0820 protein	3.3
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.3
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.3
35	436045	AB037723	Hs.5028	DKFZP564O0423 protein	3.3
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.3
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.3
	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3
40	443898	AW804296	Hs.9950	Sec61 gamma	3.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3
	445953	AI612775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.3
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
	436556	AI364997	Hs.7572	ESTs	3.2
50	424369	R87622	Hs.26714	KIAA1831 protein	3.2
	457065	AI476318	Hs.192480	ESTs	3.2
	440210	AW674562	Hs.125296	ESTs	3.2
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	3.2
55	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
	439924	AI985897	Hs.125293	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	3.2
	415115	AA214228	Hs.127751	hypothetical protein	3.2
60	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437762	T78028	Hs.154679	synaptotagmin I	3.2
	438944	AA302517	Hs.92732	KIAA1444 protein	3.2
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
65	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2
	410953	AW811766	Hs.334858	hypothetical protein MGC12250	3.2
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin tyrosine ligase-like 1	3.2
	429496	AA453800	Hs.192793	ESTs	3.2
70	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
	439274	AF086092	Hs.48372	ESTs	3.2
75	440847	AA907511	Hs.130178	ESTs	3.2
	447750	AI422234	Hs.143434	contactin 1	3.2
	455350	AW901809		gb:QVO-NN1020-170400-195-h02 NN1020 Homo	3.2
	430890	X54232	Hs.2699	glypican 1	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
80	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450	AB014526	Hs.178121	KIAA0626 gene product	3.2
	430456	AA314998	Hs.241503	hypothetical protein	3.2
	430181	AF065314	Hs.234785	cyclic nucleotide gated channel alpha 3	3.2
	418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.2
	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (3.2
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.2
	424899	AL119387	Hs.119062	ESTs	3.2

	436277	R88520	Hs.120917	ESTs	3.2
	451455	AJ937227	Hs.8821	hepcidin antimicrobial peptide	3.2
	445078	AI869975	Hs.4775	junctophilin 3	3.2
5	447746	AW015920	Hs.161359	ESTs	3.2
	435458	F11872	Hs.4892	Homo sapiens clone 24841 mRNA sequence	3.2
	427729	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	3.2
	417417	F05745	Hs.89512	ATPase, Ca ⁺⁺ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
10	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	432527	AW975028	Hs.102754	ESTs	3.1
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	3.1
	421988	AW450481	Hs.161333	ESTs	3.1
	426509	M31165	Hs.2050	pentactin-related gene, rapidly induced b	3.1
15	408786	AA773187	Hs.294027	ESTs	3.1
	433494	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	3.1
	412723	AA648459	Hs.335951	hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439456	AI752409	Hs.109314	hypothetical protein FLJ20980	3.1
20	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
	452780	BE171598	Hs.13522	ESTs, Weakly similar to I38022 hypothe	3.1
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1
	424939	AK000059	Hs.153881	Homo sapiens NY-REN-82 antigen mRNA, par	3.1
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	3.1
25	404299				3.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.1
30	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	3.1
	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	414705	AW340125	Hs.76989	KIAA0097 gene product	3.1
35	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1
	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.1
	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	3.1
	410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.1
40	425491	AA883316	Hs.255221	ESTs	3.1
	456273	AF154846	Hs.1148	zinc finger protein	3.1
	412140	AA219691	Hs.73625	RAB6 interacting, kinasin-like (rabkines	3.1
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.1
	432154	AI701523	Hs.112577	ESTs	3.1
45	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.1
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.1
	448616	AF035621	Hs.21611	kinesin family member 3C	3.0
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	3.0
	443906	AA348031	Hs.7913	ESTs	3.0
50	417318	AW953937	Hs.12891	ESTs	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.0
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44888	Homo sapiens clone TCCTA00151 mRNA sequ	3.0
55	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	422758	AF152329	Hs.284180	protocadherin gamma subfamily C, 3	3.0
	421633	AF121860	Hs.106260	sorting nexin 10	3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.0
60	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.0
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.0
	422709	AA315331	Hs.153485	ESTs	3.0
	423135	N67655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	3.0
65	426617	W58006	Hs.266258	endonuclease G-like 1	3.0
	427386	AW836261	Hs.337717	ESTs	3.0
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	3.0
	435071	D60883	Hs.35495	ESTs	3.0
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.0
70	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.0
	436936	AL134451	Hs.197478	ESTs	3.0
	445855	BE247129	Hs.145569	ESTs	3.0
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
75	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypothe	3.0
	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	3.0
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.0
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.0
80	416586	D44643	Hs.14144	secreted modular calcium-binding protein	3.0
	416874	H98752	Hs.42568	ESTs	3.0
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypothe	3.0

	404048				3.0
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	454117	BE410100	Hs.40358	adaptor-related protein complex 1, sigma	3.0
	418196	A1745649	Hs.26549	KIAA1708 protein	3.0
5	434131	A1858275	Hs.143659	ESTs	3.0
	441255	R06350	Hs.171635	ESTs	2.9
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.9
	453905	NM_002314	Hs.36566	LIM domain kinase 1	2.9
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	2.9
10	431173	AW971198	Hs.294068	ESTs	2.9
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	436401	A1087958	Hs.29088	ESTs	2.9
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.9
15	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	2.9
	433149	BE257672	Hs.42949	hypothetical protein HES6	2.9
	434811	AW971205	Hs.114280	ESTs	2.9
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
20	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.9
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!	2.9
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	2.9
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	2.9
25	435741	A1240668	Hs.113099	ESTs	2.9
	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypothe	2.9
	422939	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothe	2.9
	439376	AA883521	Hs.222064	ESTs	2.9
	439935	S75105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
30	437267	AW511443	Hs.258110	ESTs	2.9
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 fami	2.9
	400250				2.9
	400992				2.9
35	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	2.9
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.9
40	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	2.9
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.9
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9
	428500	A1815395	Hs.184641	fatty acid desaturase 2	2.9
	421641	A1638184	Hs.106334	Homo sapiens clone 23836 mRNA sequence	2.9
	421141	AW117261	Hs.125914	ESTs	2.9
45	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	2.9
	436456	AW292577	Hs.248122	G protein-coupled receptor 24	2.9
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9
	412190	R16180	Hs.274461	ESTs	2.9
50	446131	NM_000929	Hs.290	phospholipase A2, group V	2.9
	441668	A1611973	Hs.127525	ESTs	2.9
	437387	A1198874	Hs.28847	AD026 protein	2.9
	423420	A1571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp7611224 (f	2.9
55	427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	2.9
	447067	R42098	Hs.21964	ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
	424126	AA335635	Hs.96917	ESTs	2.9
60	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	2.9
	447422	BE618703	Hs.98258	orthopedia (Drosophila) homolog	2.9
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-tik	2.9
	446997	AA383439	Hs.16758	Spir-1 protein	2.9
65	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	2.9
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.9
	419586	A1088485	Hs.144759	ESTs, Weakly similar to I38022 hypothe	2.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	2.8
	408432	AW195262		gb:xm67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.8
70	420320	AB002361	Hs.96633	KIAA0363 protein	2.8
	425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	2.8
	428670	AA431682	Hs.134832	ESTs	2.8
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.8
	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	2.8
	411555	AF113537	Hs.70669	HMP19 protein	2.8
75	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	2.8
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	2.8
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.8
	424572	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.8
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.8
80	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	2.8
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.8
	440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	2.8
	408554	AAB36381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8

	403056	R58624	Hs.2186	eukaryotic translation elongation factor	2.8
	423449	AI497900	Hs.33067	ESTs	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.8
5	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.8
	434981	AW182577	Hs.293077	ESTs	2.8
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	2.8
	442748	AI016713	Hs.135787	ESTs	2.8
	443312	N52025	Hs.46616	ESTs	2.8
10	450940	AI744943	Hs.143209	ESTs, Weakly similar to I38022 hypotheti	2.8
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.8
	409182	AA064970	Hs.118145	ESTs	2.8
	439793	AA018825	Hs.7934	Kruppel-like factor 4 (gulf)	2.8
	432683	AW995441	Hs.10475	ESTs	2.8
15	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	2.8
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin)	2.8
	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	2.8
	434276	AF123659	Hs.33605	leucine zipper, putative tumor suppresso	2.8
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8
20	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.8
	425168	R96366		gb:Yq37d04.s1 Soares fetal liver spleen	2.8
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.8
	409348	AI401535	Hs.146090	ESTs	2.8
	409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8
25	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.8
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	2.8
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	2.8
	434008	AA740878	Hs.112982	ESTs	2.8
30	446776	AW293417	Hs.156455	ESTs	2.8
	408838	AI669535	Hs.40369	ESTs	2.8
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	2.8
	447397	BE247676	Hs.18442	E-1 enzyme	2.8
	412530	AA766268	Hs.265273	hypothetical protein FLJ13346	2.8
35	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fts, clone PL	2.8
	446377	AW014022	Hs.170953	ESTs	2.8
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	2.8
	447710	AI420523	Hs.328241	ESTs	2.8
	404049				2.8
40	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8
	426400	M78361	Hs.169743	Homo sapiens clone 25121 neuronal olfact	2.8
	413264	W26456	Hs.134757	hypothetical protein FLJ20033	2.8
	458997	AW937420	Hs.69662	ESTs	2.7
	422864	AA318323		gb:EST20390 Retina II Homo sapiens cDNA	2.7
45	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
	452023	AB032999	Hs.27566	KIAA1173 protein	2.7
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
	452438	BE514230	Hs.29595	JM4 protein	2.7
	435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypotheti	2.7
50	418791	AA935633	Hs.194628	ESTs	2.7
	438821	AA826425	Hs.291829	ESTs	2.7
	423464	NM_016240	Hs.128656	CSR1 protein	2.7
	442091	AW770493	Hs.182874	guanine nucleotide binding protein (G pr	2.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fts, clone H	2.7
55	412436	AA665089		gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens	2.7
	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	2.7
	416404	AA180138	Hs.107924	ESTs	2.7
	441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	2.7
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	2.7
60	426304	AA374532	Hs.124673	Homo sapiens cDNA FLJ11477 fts, clone HE	2.7
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	2.7
	449701	AW952323	Hs.129908	KIAA0591 protein	2.7
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.7
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	2.7
65	414603	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
	416096	H18577	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.7
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fts, clone H	2.7
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.7
	436304	AA339622	Hs.108887	ESTs	2.7
70	441027	AI911412	Hs.126444	ESTs	2.7
	452545	N31940	Hs.14434	ESTs, Weakly similar to I38022 hypotheti	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	448560	BE613183	Hs.23213	ESTs	2.7
	426807	AA385315	Hs.156682	ESTs	2.7
75	425825	AI929508	Hs.159590	lymphocyte antigen 6 complex, locus H	2.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.7
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.7
	427624	AA406245	Hs.24895	ESTs	2.7
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.7
80	422491	AA338548	Hs.117546	neuronatin	2.7
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	2.7
	415827	H17462	Hs.23079	ESTs	2.7

	445568	H00918	Hs.268744	KIAA1796 protein	2.7
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	2.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
5	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	2.7
	426420	BE383808	Hs.322430	NDRG family, member 4	2.7
	436899	AA764852	Hs.291567	ESTs	2.7
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.7
	426501	AW043782	Hs.293616	ESTs	2.7
10	449092	U91641	Hs.22985	alpha2,8-sialyltransferase	2.7
	427311	AB020672	Hs.175411	KIAA0865 protein	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	404029				2.7
	416289	W26333	Hs.337438	ESTs	2.7
15	439108	AW163034	Hs.6467	synaplogyrin 3	2.6
	418746	AI955289	Hs.300759	ribosomal protein L36	2.6
	412046	Y07847	Hs.73088	RAS-related on chromosome 22	2.6
	435040	AI932350	Hs.152825	ESTs	2.6
	453083	U87223	Hs.31622	contactin associated protein 1	2.6
20	428167	AA770021	Hs.16332	ESTs	2.6
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.6
	443715	AI583187	Hs.9700	cydin E1	2.6
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
25	415056	AB004662	Hs.77867	adenosine A1 receptor	2.6
	451697	AW449774	Hs.295380	POM (POM121 rat homolog) and ZP3 fusion	2.6
	433701	AW445023	Hs.15155	ESTs	2.6
	457358	AI479755	Hs.129010	ESTs	2.6
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.6
30	418027	AB037807	Hs.83293	hypothetical protein	2.6
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16365	ESTs	2.6
	459335	AW298545	Hs.250726	EST	2.6
	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	2.6
35	453169	AB037815	Hs.32156	KIAA1394 protein	2.6
	433647	AA603367	Hs.222294	ESTs	2.6
	450414	AI907735	Hs.21446	KIAA1716 protein	2.6
	446233	AI282028	Hs.25205	ESTs	2.6
	415446	F08898	Hs.66075	ESTs	2.6
40	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.6
	413012	D83777	Hs.75137	KIAA0193 gene product	2.6
	428671	BE297851	Hs.189482	zinc finger protein 179	2.6
	427158	AA935603	Hs.166231	ESTs	2.6
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.6
45	459516	AI049662	Hs.246858	EST	2.6
	402693				2.6
	408039	AA131424	Hs.50340	ESTs	2.6
	422896	AW961489	Hs.154116	ESTs	2.6
	423130	AW897586	Hs.21213	ESTs	2.6
50	438796	W67821	Hs.109590	genethonin 1	2.6
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.6
	440192	AA872282	Hs.190596	ESTs	2.6
	419708	AK000753	Hs.92374	hypothetical protein	2.6
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	2.6
55	436870	AW204219	Hs.155560	calnexin	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	401324				2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	2.6
60	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.6
	429139	F09092	Hs.66087	ESTs	2.6
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.6
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.6
65	412049	N53437	Hs.18268	adenylate kinase 5	2.6
	441783	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence	2.6
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.6
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.6
70	453478	AF083898	Hs.33021	neuro-oncological ventral antigen 2	2.6
	418962	AA714835	Hs.271863	ESTs	2.6
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.6
	443257	AI334040	Hs.11614	HSPC065 protein	2.6
	428748	AW593206	Hs.98785	Ksp37 protein	2.6
75	444984	H15474	Hs.132898	fatty acid desaturase 1	2.6
	433404	T32982	Hs.102720	ESTs	2.6
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	2.6
80	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	2.6
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	2.6
	433216	AF217412	Hs.47320	neuroigin 3	2.6
	435380	AA679001	Hs.192221	ESTs	2.6
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.6

	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.6
	419304	AI271326	Hs.146101	ESTs, Weakly similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.6
5	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	2.6
	435370	AI964074	Hs.225838	ESTs	2.6
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.5
	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	2.5
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	2.5
10	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.5
	427951	AI826125	Hs.43546	ESTs	2.5
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.5
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451422	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-i	2.5
15	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.5
	428826	AL048842	Hs.194019	atractin	2.5
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	2.5
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.5
	429550	AW293055	Hs.119357	ESTs	2.5
20	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.5
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.5
	427513	AI476318	Hs.192480	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2.5
25	417123	BE326521	Hs.159450	ESTs	2.5
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	412980	AI815750	Hs.20977	hypothetical protein MGC3129 similar to	2.5
	427209	H06509	Hs.92423	KIAA1566 protein	2.5
	424327	AA431707	Hs.31209	ESTs	2.5
30	436340	R42246	Hs.21605	ESTs	2.5
	450650	T65617	Hs.101257	hypothetical protein MGC3295	2.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothei	2.5
	400777				2.5
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.5
35	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.5
	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	2.5
	432558	R97268	Hs.177269	ESTs	2.5
	400860				2.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.5
40	416063	BE047699	Hs.93454	ESTs	2.5
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.5
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.5
	417791	AW965339	Hs.111471	ESTs	2.5
	418079	R40058	Hs.6911	ESTs	2.5
45	408495	W68796	Hs.237731	ESTs	2.5
	442104	L20871	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.5
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.5
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
50	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.5
	408955	BE315170	Hs.8087	NAG-5 protein	2.5
	415261	T40928	Hs.8346	ESTs	2.5
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.5
55	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.5
	421002	AF116030	Hs.100932	transcription factor 17	2.5
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.5
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLL_HUMAN CYTOP	2.5
	427961	AW293165	Hs.143134	ESTs	2.5
60	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothei	2.5
	428508	BE252383	Hs.184668	SBB131 protein	2.5
	428858	AA436760		gbzv67d11.r1 Soares_total_fetus_Nb2HF8_	2.5
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	2.5
	432427	AL037630	Hs.6638	Homo sapiens cDNA FLJ11602 fis, clone HE	2.5
65	435347	AW014873	Hs.116963	ESTs	2.5
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.5
	438208	AL041224	Hs.65379	ESTs	2.5
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	2.5
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	2.5
70	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	442337	AI371029	Hs.129257	ESTs, Weakly similar to TC17_HUMAN TRANS	2.5
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.5
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.5
	449086	AI628357	Hs.208037	ESTs	2.5
75	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5

TABLE 8B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession
408432 1058667_1 AW195262 R27868 AW811262
412225 1284108_1 AW902042 N77591

412436	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
416120	1571266_1	H46739 H51513 H19779
416871	1626761_1	H98716 N90792 N24283
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
422864	222336_1	AA318323 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821
422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
422977	223410_1	AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642
		AW853758 H56414
423756	231725_1	AA828125 AA834883 AA330555
425168	247552_1	R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194
425517	252729_1	AF121179 BE162735 AA358827
426413	266650_1	AA377823 AW954494 AI022688
428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
428679	294049_1	AA431765 AA432015
428858	296453_1	AA436760 AW237453 BE327496 N47347 N56967
429007	298301_1	D80642 AA443145 AL119015 AW904500
429163	300543_1	AA884766 AW974271 AA592975 AA447312
433532	368950_1	AW975367 AA598607 AA742735
436190	41555_1	AK001059 AA633055
437034	431713_1	AA742643 AA808575 AW976568
438458	457837_1	AW975186 AA807807 D29548
438993	467651_1	AA828955 AA834879 AI926361
439566	47387_1	AF086387 W77884 W72711
440322	491965_1	AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400
444584	611496_1	AI168422 D80113 T59074
447197	711623_1	R36075 AI365546 R36167
448451	764066_1	AW015994 R39898 AW000978 AI598202 AI521706
450625	84032_1	AW970107 AA513951 AA010406
452453	918300_1	AI902519 AI902518 AI902516
454996	1248640_1	AW850180 AW850326
455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798

TABLE 8C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

400777	8131663	Plus	70745-71121
400780	8131663	Minus	118372-118619
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400860	9757499	Minus	151830-152104,152649-152744
400992	8098828	Plus	140390-140822
401324	9863791	Plus	234057-234174
402408	9796239	Minus	110326-110491
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973
402693	8569863	Minus	82366-82515
402855	9662953	Minus	59763-59909
404029	7671252	Plus	108716-111112
404048	3688074	Minus	54421-56808
404049	3688074	Minus	75765-78155
404283	2276311	Minus	99460-99564
404299	5738652	Minus	3826-4025
404541	8318559	Plus	103456-103664
404584	9857511	Plus	138651-139153
404593	9944086	Minus	74922-75788
404721	9856648	Minus	173763-174294
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
405238	7249119	Minus	51728-51836
405771	7018349	Plus	91191-91254,91510-91589
405819	4007557	Plus	2830-2967
406311	9211559	Minus	137114-139033

TABLE 9A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 9A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue

452461	N78223	Hs.108106	transcription factor	20.1
435895	AF037335	Hs.5338	carbonic anhydrase XII	15.2
453941	U39817	Hs.36820	Bloom syndrome	14.2

	443247	BE614387	Hs.333893	c-Myc target JPO1	12.4
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.0
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	11.7
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	11.4
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	11.2
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.2
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (10.0
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	9.9
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.9
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	9.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	9.4
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	8.9
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	8.9
15	455516	BE172704	Hs.222746	KIAA1610 protein	8.2
	420092	AA814043	Hs.88045	ESTs	7.9
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	7.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.9
20	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.8
	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8
	440584	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	7.8
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	7.7
	409638	AW450420	Hs.21335	ESTs	7.5
25	444665	BE613126	Hs.47783	B aggressive lymphoma gene	7.5
	456759	BE259150	Hs.127792	della (Drosophila)-like 3	7.5
	412777	AI355773	Hs.270123	ESTs	7.4
	436607	AW661783	Hs.211061	ESTs	7.3
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.3
30	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	7.3
	428976	AL037824	Hs.194695	ras homolog gene family, member 1	7.2
	433244	AB040943	Hs.271285	KIAA1510 protein	7.1
	436726	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypothei	7.1
35	408432	AW195262	Hs.148135	gb:xb67b05.x1 NCL_CGAP_CML1 Homo sapiens	7.1
	434164	AW207019	Hs.251946	serine/threonine kinase 33	7.0
	445873	AA250970	Hs.293707	poly(A)-binding protein, cytoplasmic 1-I	7.0
	439726	AW449893	Hs.3076	ESTs, Weakly similar to I38598 zinc fing	7.0
	432656	NM_000246	Hs.250500	MHC class II transactivator	6.8
	431117	AF003522	Hs.252809	delta (Drosophila)-like 1	6.8
40	453387	AI990741	Hs.183161	ESTs	6.6
	418821	AA436002	Hs.69328	gb:ny91c01.s1 NCL_CGAP_GCB1 Homo sapiens	6.6
	437034	AA742643	Hs.151738	MD-2 protein	6.5
	411252	AB018549	Hs.271741	matrix metalloproteinase 9 (gelatinase B	6.4
45	424687	J05070	Hs.271741	ESTs, Weakly similar to A46010 X-linked	6.3
	452953	AI932884	Hs.38207	gb:EST387475 MAGE resequences, MAGN Homo	6.3
	433532	AW975367	Hs.21668	Human DNA sequence from clone RP4-53015	6.2
	420311	AW445044	Hs.13872	ESTs	6.2
	418097	R45137	Hs.57471	gb:bj32b03.s1 NCL_CGAP_AA1 Homo sapiens	6.1
50	407304	AA565832	Hs.57471	cytokine-like protein C17	6.1
	435256	AF193766		ESTs	6.0
	449448	D60730			6.0
	403790				6.0
	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
55	420674	NM_000055	Hs.1327	butyrylcholinesterase	5.9
	435542	AA687376	Hs.269533	ESTs	5.9
	418216	AA662240	Hs.283099	AF15q14 protein	5.8
	439086	AF085947		gb:Homo sapiens full length insert cDNA	5.8
	408037	AW271720	Hs.42233	hypothetical protein FLJ10300	5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
60	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	5.7
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypothei	5.7
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.6
	405558				5.6
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.5
	420560	AW207748	Hs.59115	ESTs	5.5
	408096	BE250162	Hs.83765	dihydrofolate reductase	5.5
70	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	5.4
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.4
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	5.3
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.3
	444168	AW379879		gb:RC1-HT0256-081199-011-f01 HT0256 Homo	5.3
	432789	D26361	Hs.3104	KIAA0042 gene product	5.3
75	437036	AI571514	Hs.133022	ESTs	5.2
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	5.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	5.2
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	5.1
80	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
	454157	AW162906	Hs.312481	ESTs, Weakly similar to S66668 hydrogen	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.1
	406679	AA070786		gb:zm66b07.r1 Stratagene neuroepithelium	5.1

	442671	AI005668	Hs.134779	EST	5.1
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	5.0
	418819	AA228776	Hs.191721	ESTs	5.0
5	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	4.9
	420730	NM_002691	Hs.99890	polymerase (DNA directed), delta 1, cata	4.9
	441217	AI922183	Hs.213246	ESTs	4.9
	453385	AW296101	Hs.252806	ESTs	4.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.7
10	450813	AI739625	Hs.203376	ESTs	4.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.7
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	4.7
	405771				4.6
15	457065	AI476318	Hs.192480	ESTs	4.6
	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	400859				4.6
	435267	N23797	Hs.110114	ESTs	4.6
20	443454	AI057494	Hs.133421	ESTs	4.5
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5
	437267	AW511443	Hs.258110	ESTs	4.5
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.5
	454269	AI961060	Hs.129908	KIAA0591 protein	4.5
25	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.5
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	4.5
	417308	H60720	Hs.81892	KIAA0101 gene product	4.5
30	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.4
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	4.4
	406568	AF088886	Hs.11590	cathepsin F	4.4
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chloro	4.4
	402516				4.4
35	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	4.4
	413625	AW451103	Hs.71371	ESTs	4.4
	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
40	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	4.3
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3
	444386	BE065183		gb:RC1-BT0314-Q20200-012-c04 BT0314 Homo	4.3
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
45	441020	W79283	Hs.35962	ESTs	4.3
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	405701				4.3
50	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2
	433323	AA805132	Hs.30701	ESTs	4.2
	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.1
55	441269	AW015206	Hs.178784	ESTs	4.1
	418727	AA227609	Hs.94834	ESTs	4.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	4.1
	430786	AA486144	Hs.31293	ESTs	4.1
60	445372	N36417	Hs.144928	ESTs	4.1
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.0
	457465	AW301344	Hs.122908	DNA replication factor	4.0
	422094	AF129535	Hs.272027	F-box only protein 5	4.0
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
65	459321	AW044477	Hs.299538	ESTs	4.0
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.0
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	4.0
	447004	AW296968	Hs.157539	ESTs	4.0
	448295	AI381911	Hs.334859	KIAA1814 protein	3.9
70	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	440704	M69241	Hs.162	insulin-like growth factor binding prote	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
	457026	AA397620	Hs.48692	ESTs	3.9
	404642				3.9
75	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	3.9
	437718	AI927288	Hs.196779	ESTs	3.9
	438490	AW593272	Hs.301299	ESTs	3.9
	429919	AA460692	Hs.278945	hypothetical protein FLJ23024	3.9
80	413604	R51767		gb:y973g11.r1 Soares infant brain 1N1B H	3.9
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.9
	449300	AI656959	Hs.222165	ESTs	3.8
	452203	X57522	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8

	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.8
	404295				3.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.8
5	428728	NM_016625	Hs.191381	hypothetical protein	3.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.8
	430172	AA468591	Hs.161889	ESTs	3.8
	447499	AW262580	Hs.147674	protocadherin beta 16	3.8
	405884				3.8
10	437236	AW137817	Hs.244353	ESTs	3.7
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.7
	425529	NM_014656	Hs.158282	KIAA0040 gene product	3.7
	425502	R98895	Hs.125823	ESTs	3.7
15	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
	402424				3.7
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.7
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.7
	414872	U82010	Hs.77513	COX10 (yeast) homolog, cytochrome c oxid	3.7
20	426071	AW138057	Hs.163835	ESTs	3.7
	419078	M93119	Hs.89584	insulinoma-associated 1	3.7
	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.7
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	3.7
	436899	AA764852	Hs.291567	ESTs	3.6
25	436722	AW975977		gb:EST388086 MAGE resequences, MAGN Homo	3.6
	440552	A1216751	Hs.143977	ESTs	3.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypotheti	3.6
	409048	H59990	Hs.37699	ESTs	3.6
30	439546	AF088056		gb:Homo sapiens full length insert cDNA	3.6
	443544	A1076315	Hs.16359	ESTs	3.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
	435889	A1249107	Hs.269901	ESTs	3.6
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.6
35	438078	A1016377	Hs.131693	ESTs	3.6
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	3.5
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.5
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.5
40	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.5
	436123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5
	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo	3.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	3.5
	435065	BE064391		gb:RC4-BT0310-110300-015-b08 BT0310 Homo	3.5
45	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.5
	447101	N72185	Hs.44189	ESTs	3.5
	410530	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	3.5
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.5
50	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.5
	439743	AL389956	Hs.283858	Homo sapiens mRNA full length insert cDN	3.5
	453884	AA355925	Hs.36232	KIAA0186 gene product	3.5
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.5
	420721	AA927802	Hs.159471	ZAP3 protein	3.5
	426764	AA732524	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!	3.4
55	420649	A1866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.4
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.4
	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604				3.4
	442407	AW469584	Hs.32353	mitogen-activated protein kinase kinase	3.4
60	414300	A1304870	Hs.188680	ESTs	3.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	3.4
	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4
	452211	A1985513	Hs.233420	ESTs	3.4
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.4
65	449961	AW265634	Hs.133100	ESTs	3.4
	413257	BE075035		gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.4
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.4
70	446189	H85224	Hs.214013	ESTs	3.4
	437385	AA757055	Hs.164060	ESTs	3.4
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	3.4
	408298	A1745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.4
	455778	BE088746		gb:CM2-BT0893-210300-123-d09 BT0693 Homo	3.3
75	417546	H65569	Hs.18845	ESTs	3.3
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	3.3
	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	3.3
	454294	AB000734	Hs.50640	JAK binding protein	3.3
	457131	AC002310	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	3.3
80	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
	449676	AW380579	Hs.209657	ESTs	3.3
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.3
	453746	AL120611		gb:DKFZp761H119_r1 761 (synonym: harry2)	3.3
	452799	A1948829	Hs.213786	ESTs	3.3

	435380	AA679001	Hs.192221	ESTs	3.3
	426746	J03626	Hs.2057	uridine monophosphate synthetase (crotal	3.3
	453362	H14988	Hs.107375	ESTs	3.3
5	456473	AI202788	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	3.3
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.3
	445777	AI580371	Hs.145384	ESTs	3.3
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.3
10	404299				3.3
	404108				3.3
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1N1B H	3.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.3
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	3.2
15	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.2
	418958	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	3.2
	449248	M33782	Hs.23391	Homo sapiens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2
20	401596	AA172106	Hs.110950	Rag C protein	3.2
	408380	AF123050	Hs.44532	diubiquitin	3.2
	450325	AI935962	Hs.26289	ESTs	3.2
	428730	AA625947	Hs.25750	ESTs	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
25	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2
	442710	AI015631	Hs.23210	ESTs	3.2
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.2
	430970	AI018210	Hs.144083	ESTs	3.2
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	3.2
30	446676	H09380	Hs.300965	ESTs	3.2
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
	413840	AI301558	Hs.146381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	3.2
35	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.2
	458786	AI457098	Hs.280848	ESTs	3.2
	455909	BE156417	Hs.278798	ESTs	3.2
	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	439710	AF086543		gb:Homo sapiens full length insert cDNA	3.2
40	434559	AF147315		gb:Homo sapiens full length insert cDNA	3.1
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.1
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
45	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.1
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.1
50	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	3.1
	404589				3.1
	421764	AI681535	Hs.148135	serine/threonine kinase 33	3.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.1
	416941	BE000150	Hs.48778	ribon protein	3.1
55	414761	AI077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	449611	AI970394	Hs.197075	ESTs	3.1
	434746	AA648368	Hs.295358	ESTs	3.1
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum amyloid A1	3.1
60	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.1
	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	440052	AI633744	Hs.195648	ESTs, Weakly similar to 138022 hypothe	3.1
	426531	AA381071		gb:EST94100 Activated T-cells XII Homo s	3.1
65	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
	406267				3.1
	447039	AV661798	Hs.282915	ESTs	3.1
	404802				3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
70	419314	AW971924	Hs.87280	ESTs	3.0
	435894	AI076667	Hs.188011	ESTs	3.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.0
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.0
	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypothe	3.0
75	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0
	418241	M26682	Hs.1149	LIM domain only 1 (rhombotin 1)	3.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse	3.0
	412950	BE018581	Hs.245342	hypothetical protein FLJ14642	3.0
	428670	AA431682	Hs.134832	ESTs	3.0
80	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0
	437756	AA767537	Hs.197096	ESTs	3.0
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.0
	402374	AL135225	Hs.301865	dopachrome tautomerase (dopachrome della	3.0
	443885	H91806	Hs.15284	ESTs	3.0

5	434008	AA740878	Hs.112982	ESTs	3.0
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	3.0
	414239	AI288330	Hs.182330	ESTs	3.0
	421013	MG2397	Hs.1345	mutated in colorectal cancers	3.0
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.0
10	410276	AI554545	Hs.68301	ESTs	3.0
	433865	N29862	Hs.44104	ESTs	3.0
	406028				3.0
	401626				3.0
	415949	H10562	Hs.21691	ESTs	3.0
15	418583	AA604379	Hs.86211	hypothetical protein	3.0
	417933	X02308	Hs.82962	thymidylate synthetase	3.0
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.0
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.0
	427940	AA417812	Hs.38775	ESTs	2.9
20	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	2.9
	421988	AW450481	Hs.161333	ESTs	2.9
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	2.9
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.9
25	451189	AA016019	Hs.40905	ESTs	2.9
	401558				2.9
	426207	BE390657	Hs.30026	HSPC182 protein	2.9
	404721				2.9
	401384				2.9
30	417288	AI984792	Hs.108812	hypothetical protein FLJ22004	2.9
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.9
	435928	H64345	Hs.183961	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	2.9
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.9
35	439972	AI348100	Hs.124662	ESTs	2.9
	433112	AA973801	Hs.144553	ESTs, Weakly similar to unnamed protein	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	406748	AW339106	Hs.217493	annexin A2	2.9
	422154	T79045	Hs.126927	ESTs	2.9
40	405588				2.9
	440911	AA909536	Hs.143562	ESTs	2.9
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066	ESTs	2.9
	410114	AW590540	Hs.271280	ESTs	2.9
45	419217	AA504571		gb:aa60e12.r1 NCL_CGAP_GCB1 Homo sapiens	2.9
	415849	R20529	Hs.6806	ESTs	2.9
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.9
	453331	AI240665	Hs.8895	ESTs	2.9
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.9
50	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	2.9
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTs	2.9
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.8
	415446	F08898	Hs.66075	ESTs	2.8
55	439518	W76326		gb:z60d04.r1 Soares_fetal_heart_Nb1H19W	2.8
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.8
	419451	AI907117	Hs.90535	synlexin binding protein 2	2.8
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.8
60	424126	AA335635	Hs.96917	ESTs	2.8
	458895	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypothe	2.8
	418973	AA233056	Hs.191518	ESTs	2.8
	440471	AA886146	Hs.307944	ESTs	2.8
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
65	433647	AA603367	Hs.222294	ESTs	2.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	2.8
	434964	AI638850	Hs.130746	ESTs	2.8
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
70	400517	AF242388	Hs.149585	lengsin	2.8
	433023	AW864793	Hs.87409	thrombospondin 1	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	406736	AI254733	Hs.182426	ribosomal protein S2	2.8
	409207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	2.8
75	440196	N72847	Hs.125221	ESTs	2.8
	403961				2.8
	425193	AW965689	Hs.22509	ESTs	2.8
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20553 fis, clone KA	2.8
	440483	AI200836	Hs.150386	ESTs	2.8
80	412391	AW947710		gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
	448769	N66037	Hs.38173	ESTs	2.8
	411632	AW854829		gb:QV2-CT0261-201099-011-R1 CT0261 Homo	2.8
	438221	AI798853	Hs.122224	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.8
	457578	AA578027		gb:nl20h01.s1 NCL_CGAP_HSC1 Homo sapiens	2.8
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	2.8
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.8
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.8

5	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.8
	439662	H97552	Hs.269060	ESTs	2.8
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.8
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	2.8
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.8
10	447752	M73700	Hs.105938	lactotransferrin	2.8
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	2.8
	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	2.7
	456629	AW891965	Hs.279789	histone deacetylase 3	2.7
	439538	AA837323	Hs.164047	ESTs	2.7
15	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	2.7
	456029	BE255990	Hs.218329	hypothetical protein	2.7
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	2.7
	456412	AW749617	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	2.7
	453536	AA137000	Hs.62578	ESTs	2.7
20	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.7
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
	446322	N23033	Hs.155814	ESTs	2.7
	451592	AI805416	Hs.213897	ESTs	2.7
	429466	M85835	Hs.12827	ESTs	2.7
25	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.7
	455514	AW983871		gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.7
	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.7
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	2.7
30	449655	AI021987	Hs.59970	ESTs	2.7
	422648	D86983	Hs.118893	Melanoma associated gene	2.7
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	2.7
	406895	X60648	Hs.172550	polypyrimidine tract binding protein (he	2.7
	453255	AA278167	Hs.19215	Homo sapiens, clone IMAGE:3605822, mRNA	2.7
35	427348	NM_014137	Hs.177258	PRO0650 protein	2.7
	435370	AI964074	Hs.225838	ESTs	2.7
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV	2.7
	411874	AA096106	Hs.20403	ESTs	2.7
	421192	AA833718	Hs.204529	KIAA1806 protein	2.7
40	435899	W89093	Hs.189914	ESTs	2.7
	414603	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
	453462	AL037291	Hs.236605	ESTs, Moderately similar to ALU4_HUMAN A	2.7
	436554	AI985810	Hs.301173	ESTs	2.7
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7
45	403881				2.7
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.7
	404984				2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.7
50	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.7
	404756				2.7
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.7
	422176	H80977		gb:yu89a11.s1 Soares fetal liver spleen	2.7
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.7
55	436532	AA721522		gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	2.7
	412833	AW960547	Hs.298262	ribosomal protein S19	2.7
	457245	AI745498	Hs.204579	ESTs	2.7
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
	453263	R91778	Hs.99369	ESTs	2.7
60	459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo sapiens c	2.7
	438764	AA824524	Hs.336452	ESTs	2.7
	429285	AI971081	Hs.20432	ESTs, Weakly similar to I38022 hypotheti	2.7
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	2.7
	430037	BE409649	Hs.227789	mitogen-activated protein kinase-activat	2.7
65	449892	N73608	Hs.50309	ESTs	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.7
	427954	J03060	Hs.247551	melaxin 1	2.7
	400371	U80740			2.7
70	452449	AW068658	Hs.20943	ESTs	2.7
	431114	AA492400	Hs.291015	ESTs	2.7
	417088	M54915	Hs.81170	pim-1 oncogene	2.7
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.7
	403680				2.7
75	454679	AW813110		gb:CM4-ST0189-051099-021-R05 ST0189 Homo	2.7
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	2.6
	422240	R60594	Hs.29002	KIAA1706 protein	2.6
	424368	AB037766	Hs.146085	KIAA1345 protein	2.6
	405808				2.6
80	419700	AF084935	Hs.92357	galactokinase 1	2.6
	435972	W95088	Hs.114198	ESTs	2.6
	433568	S70782	Hs.557	adrenergic, alpha-1D-, receptor	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	444156	AW500059	Hs.86437	ESTs, Highly similar to AF219140 1 gastr	2.6
	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin	2.6
	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypotheti	2.6
	453948	AI970797	Hs.64859	ESTs	2.6

	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	2.6
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.6
	418228	AA962181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
5	401324				2.6
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothei	2.6
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.6
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I38022 hypothei	2.6
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	2.6
10	433933	AI754389	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequ	2.6
	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S89890 mitogen i	2.6
	400992				2.6
	455530	AW984744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	2.6
15	436139	AA765786	Hs.120936	ESTs	2.6
	448330	AL036449	Hs.207163	ESTs	2.6
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, completa cds	2.6
	433430	AI863735	Hs.186755	ESTs	2.6
20	436693	AW973223	Hs.303197	B-cell CLL/lymphoma 7C	2.6
	429482	AF076974	Hs.203952	transformation/transcription domain-asso	2.6
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	2.6
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.6
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	2.6
25	414835	AA156720	Hs.185342	ESTs	2.6
	424489	T48851	Hs.149250	D-siglec precursor,	2.6
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797				2.6
	434573	AW372340	Hs.159717	ESTs	2.6
30	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
	415785	R82419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6
	450608	AA010365	Hs.193229	ESTs	2.6
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.6
	432268	BE311856	Hs.274230	3'-phosphoadenosine 5'-phosphosulfate sy	2.6
35	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	2.6
	420917	AW135716	Hs.117330	ESTs	2.6
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	2.6
	446089	AI860021	Hs.270651	ESTs, Moderately similar to A47582 B-cel	2.6
40	440829	AF136407	Hs.7446	chromosome 6 open reading frame 5	2.6
	408475	AA315514	Hs.47986	hypothetical protein MGC10940	2.6
	450946	AA374569	Hs.127698	ESTs, Moderately similar to Z109260A B c	2.6
	421462	AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	2.6
45	422887	AI751848	Hs.49215	ESTs	2.6
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	2.5
	408981	AW500797	Hs.49427	Gem-interacting protein	2.5
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.5
50	418079	R40058	Hs.6911	ESTs	2.5
	437820	AA769062	Hs.323836	ESTs, Weakly similar to alternatively sp	2.5
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	2.5
	425681	AB018297	Hs.159183	KIAA0754 protein	2.5
	435177	AI018174	Hs.42936	ESTs	2.5
55	437323	AA371145	Hs.226627	leptin receptor	2.5
	422114	AW194851	Hs.111801	arsenate resistance protein ARS2	2.5
	448478	AI523218	Hs.203456	ESTs	2.5
	426623	AA382826	Hs.132793	ESTs	2.5
	448764	AI568607	Hs.182112	ESTs	2.5
60	458385	AI051489	Hs.246214	ESTs	2.5
	403726	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
	444888	AI651039	Hs.148559	ESTs	2.5
	456179	H75490	Hs.271930	ESTs	2.5
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.5
65	406273	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	2.5
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	2.5
	454967	AW848276		gb:LL3-CT0214-150200-074-E06 CT0214 Homo	2.5
	442303	AA989289	Hs.129169	ESTs	2.5
70	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	2.5
	434263	N34895	Hs.44648	ESTs	2.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	2.5
	406038	Y14443	Hs.88219	zinc finger protein 200	2.5
75	413495	Y12395	Hs.315177	interferon-related developmental regulat	2.5
	423098	AA321980	Hs.204682	ESTs	2.5
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	2.5
	439841	AF038961	Hs.6710	mannose-P-dolichol utilization defect 1	2.5
	453828	AW970960	Hs.293821	ESTs	2.5
80	445034	AW293376	Hs.143659	ESTs	2.5
	449620	BE407797	Hs.23794	checkpoint with forkhead and ring finger	2.5
	406876	AI382286	Hs.180842	ribosomal protein L13	2.5
	412370	AW946614		gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.5

	430357	AW976789	Hs.165607	ESTs	2.5
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.5
	416097	BE387371	Hs.118964	hypothetical protein FLJ120085	2.5
5	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	2.5
	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.5
	445223	AW291553	Hs.254983	ESTs	2.5
	423926	X03833	Hs.1722	interleukin 1, alpha	2.5
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	2.5
	406474				2.5
10	433908	AW298141	Hs.157975	ESTs	2.5
	439755	AW748482	Hs.77873	B7 homolog 3	2.5
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	ESTs	2.5
	415346	Z43108		gb:HSC13E071 normalized infant brain cDN	2.5
15	419337	AW291112	Hs.209978	ESTs	2.5
	444606	R09478	Hs.18041	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
	411965	BE467339	Hs.280115	ESTs	2.5
20	409278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5
	403142				2.5
	401714				2.5
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.5
25	416505	H66470	Hs.16004	ESTs	2.5
	431518	AA743462	Hs.165337	ESTs	2.5
	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	2.5
	404366				2.5
30	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HE	2.5
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
	402856	AW939659		gb:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	2.4
	436805	AA731533	Hs.270751	ESTs	2.4
35	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
	453496	AA442103	Hs.330084	solute carrier family 2 (facilitated glu	2.4
	453853	AL040600	Hs.188083	ESTs	2.4
	407909	AW103986		gb:xd63e06.x1 NCL_CGAP_Ov23 Homo sapiens	2.4
	454630	BE142075		gb:CM3-HT0137-170999-012-02 HT0137 Homo	2.4
40	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	2.4
	420779	L12398	Hs.99922	dopamine receptor D4	2.4
	438322	AA804170	Hs.221349	ESTs	2.4
	455808	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	2.4
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4
45	440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	2.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.4
	451802	AI817711	Hs.209374	ESTs	2.4
50	419417	R92491	Hs.39429	ESTs	2.4
	407094	AF000574	Hs.22405	leukocyte immunoglobulin-like receptor,	2.4
	423567	BE252949	Hs.69331	hypothetical protein FLJ13633	2.4
	427501	AI369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2.4
55	436845	AA732297	Hs.113928	ESTs	2.4
	431584	AW296121	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	2.4
	440614	AA781530	Hs.127236	hypothetical protein FLJ12879	2.4
	423721	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotrophi	2.4
	452125	BE312642	Hs.28077	GDP-mannose pyrophosphorylase B	2.4
60	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.4
	453446	BE299996		gb:600944574F1 NIH_MGC_17 Homo sapiens c	2.4
	419792	AA250890	Hs.190037	ESTs	2.4
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.4
	410447	AW816134		gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
65	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.4
	402408				2.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.4
	414625	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403048				2.4
70	432088	AA525454		gb:ni85c09.s1 NCL_CGAP_Pr20 Homo sapiens	2.4
	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	2.4
	455023	AW850907		gb:IL3-CT0220-310100-065-H11 CT0220 Homo	2.4
	426249	F05422	Hs.168352	nucleoporin-like protein 1	2.4
	446795	AI797713	Hs.156471	ESTs	2.4
75	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
	414252	AA346483	Hs.126191	ESTs	2.4
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.4
	427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DE	2.4
	404020				2.4
80	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.4
	417222	AI525424	Hs.42053	hypothetical protein MGC2383	2.4
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.4
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	401676				2.4

	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	436277	R88520	Hs.120917	ESTs	2.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
5	405353				2.4
	409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithelium	2.4
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	453335	AW857376	Hs.169238	fucosyltransferase 3 (galactoside 3(4)-L	2.4
10	450621	AW297288	Hs.55918	hypothetical protein FLJ11354	2.4
	419652	AL157485	Hs.91973	hypothetical protein	2.4
	421151	BE174431	Hs.63386	ESTs	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
15	405288				2.4
	453527	R49570	Hs.180236	ESTs	2.4
	429875	AI091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	2.4
	436360	AI962796	Hs.136754	ESTs	2.4
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.4
20	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.4
	449539	W80363	Hs.58446	ESTs	2.4
	419870	AW403911	Hs.265175	phosphoprotein associated with GEMs	2.4
	404584				2.4
	454276	AW294996	Hs.255374	ESTs	2.4
25	423746	AW361817	Hs.132370	NADPH oxidase 1	2.4
	415558	AA885143	Hs.125719	ESTs	2.4
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
	406953	L36847		gb:Human (clone p17/90) rearranged iduro	2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4
30	451031	AI360187	Hs.4254	ESTs	2.4
	455302	AW97641		gb:RC6-BN0052-170200-011-D06 BN0052 Homo	2.4
	449063	AI627352	Hs.236547	Homo sapiens, clone IMAGE:2905978, mRNA,	2.4
	401048				2.4
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
35	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.4
	449086	AI628357	Hs.208037	ESTs	2.4
	415238	R37780	Hs.21422	ESTs	2.4
	448337	AW206453	Hs.3782	ESTs	2.4
	416991	N35389	Hs.141296	KIAA0226 gene product	2.3
40	412600	L28824	Hs.74101	spleen tyrosine kinase	2.3
	418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
	440769	BE561793	Hs.21446	KIAA1716 protein	2.3
	450437	X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3
45	406739	AI566709	Hs.182426	ribosomal protein S2	2.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.3
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	ESTs	2.3
	405605				2.3
50	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	2.3
	445828	F05802	Hs.81907	ESTs	2.3
	457195	AB011099	Hs.195647	KIAA0527 protein	2.3
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.3
55	423198	M81933	Hs.1634	cell division cycle 25A	2.3
	457730	AW753613		gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	2.3
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.3
	446288	AW189209	Hs.149708	ESTs	2.3
60	436954	AA740151	Hs.130425	ESTs	2.3
	411658	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
	404240				2.3
	456094	H95091		gb:yw57a09.r1 Soares_placenta_8to9weeks_	2.3
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.3
65	406737	AI356586		gb:qy15h09.x1 NCL_CGAP_Bm23 Homo sapien	2.3
	458453	AI097452	Hs.135095	ESTs	2.3
	452330	AI879127	Hs.191979	KIAA1733 protein	2.3
	408523	AW833259	Hs.314287	ESTs	2.3
	455470	AW947992		gb:PMO-MT0011-240300-001-c09 MT0011 Homo	2.3
70	436323	R17697	Hs.140963	ESTs, Weakly similar to I38022 hypotheti	2.3
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	2.3
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.3
	419134	T89863	Hs.221771	ESTs	2.3
	445933	AV655733	Hs.293860	spinster-like protein	2.3
75	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.3
	449911	AI262106	Hs.12653	ESTs	2.3
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.3
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.3
80	423491	AA191765	Hs.129673	eukaryotic translation initiation factor	2.3
	407182	AA312551	Hs.230157	ESTs	2.3
	411448	AA178955	Hs.271439	ESTs, Weakly similar to I38022 hypotheti	2.3
	438644	AI126162	Hs.129037	ESTs	2.3
	432691	U29725	Hs.3080	mitogen-activated protein kinase 7	2.3

	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	2.3
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3
	404054				2.3
5	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	2.3
	440210	AW674562	Hs.125296	ESTs	2.3
	446727	AB011095	Hs.16032	KIAA0523 protein	2.3
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.3
10	449919	AI674685	Hs.200141	ESTs	2.3
	415293	R49462	Hs.106541	ESTs	2.3
	441126	NM_000429	Hs.323715	methionine adenosyltransferase I, alpha	2.3
	408203	AA053137	Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
15	450748	AI733093	Hs.130016	ESTs	2.3
	404185				2.3
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
	451370	AI791929	Hs.300782	ESTs	2.3
	400034				2.3
20	407723	AW071161	Hs.252873	ESTs	2.3
	431320	AW959474	Hs.183070	ESTs	2.3
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.3
	419225	U70073		gb:HSU70073 Human Homo sapiens cDNA clon	2.3
25	444656	AI277924	Hs.145199	ESTs	2.3
	405741				2.3
	400917				2.3
	432567	AA736777	Hs.293770	ESTs	2.3
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.3
30	450514	AC005785	Hs.25069	A kinase (PRKA) anchor protein 8	2.3
	418400	BE243026	Hs.301989	KIAA0246 protein	2.3
	444019	BE173977	Hs.10098	putative nucleolar RNA helicase	2.3
	406326				2.3
	412077	N51107	Hs.47199	ESTs, Weakly similar to FLJ00004 protein	2.3
35	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fs, clone KA	2.3
	414528	AA148950	Hs.188836	ESTs	2.3
	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.3
	439467	AW292275	Hs.158355	ESTs	2.3
40	402627				2.3
	451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	2.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.3
	423869	BE409301	Hs.134012	C1q-related factor	2.3
	405915				2.3
45	431503	NM_012129	Hs.258576	claudin 12	2.3
	423306	W88562	Hs.108198	ESTs	2.3
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	2.3
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	2.3
	434437	AI912566	Hs.187813	ESTs	2.3
50	436191	BE407866	Hs.170253	hypothetical protein FLJ23282	2.3
	420006	H14429	Hs.94300	serologically defined colon cancer anti	2.3
	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3
	403166				2.3
	422119	AI277829	Hs.111862	KIAA0590 gene product	2.3
	403751				2.3
55	426451	AI908165	Hs.169946	GATA-binding protein 3	2.3
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.3
	409091	AW970386	Hs.269423	ESTs	2.3
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.3
60	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.3
	405747				2.3
	438210	AA780519	Hs.311601	EST	2.3
	404652				2.3
65	423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.2
	444424	AI654684	Hs.196377	ESTs	2.2
	434031	BE384165	Hs.23723	pseudouridylyl synthase 1	2.2
	427650	AW501245	Hs.252259	ribosomal protein S3	2.2
	435220	D50030	Hs.104	HGF activator	2.2
70	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	2.2
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
	429961	BE246829	Hs.226770	DKFZP566C0424 protein	2.2
	442065	AI831229	Hs.128417	hypothetical protein FLJ14009	2.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.2
75	420536	AL117455	Hs.275438	histone deacetylase 7A	2.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
	443753	AW367578	Hs.134749	ESTs	2.2
	423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	2.2
	446572	AV659151	Hs.282961	ESTs	2.2
80	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.2
	421040	AA715026	Hs.135280	ESTs	2.2
	426212	S71824	Hs.167988	neural cell adhesion molecule 1	2.2
	455584	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	406851	AA609784	Hs.180255	major histocompatibility complex, class	2.2

	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.2
	419575	U43431	Hs.91175	topoisomerase (DNA) III alpha	2.2
	418672	L44284	Hs.159743	ESTs	2.2
5	456261	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0694 protein	2.2
	415737	AA167626	Hs.118743	ESTs	2.2
	447554	AI391598	Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	405159				2.2
	442177	AW661820	Hs.211413	ESTs	2.2
10	446139	H77395	Hs.39749	ESTs	2.2
	458339	AW976853	Hs.172843	ESTs	2.2
	401876				2.2
	439566	AF086387		gb:Homo sapiens full length insert cDNA	2.2
	425079	H09963	Hs.2257	vitronectin (serum spreading factor, som	2.2
15	441837	AA361743	Hs.179881	core-binding factor, beta subunit	2.2
	430644	AB015419	Hs.247710	preprolactin-releasing peptide	2.2
	431474	AL133990	Hs.190642	ESTs	2.2
	407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2.2
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	2.2
20	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORN1	2.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.2
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2.2
	404170				2.2
	406902	M32074		gb:Human retinoic acid receptor gamma 2	2.2
25	437902	AA770599	Hs.144055	ESTs	2.2
	401012				2.2
	446502	AI302654	Hs.208024	ESTs	2.2
	442554	AW467376	Hs.129640	ESTs	2.2
	443021	AA368546	Hs.8904	Ig superfamily protein	2.2
30	421141	AW117261	Hs.125914	ESTs	2.2
	443070	BE388662	Hs.8984	Homo sapiens chromosome 14 BAC 98L12	2.2
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.172662	ESTs	2.2
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	2.2
35	431468	AW248431	Hs.256526	nuclear prelamin A recognition factor	2.2
	416185	AW975861	Hs.47367	KIAA1785 protein	2.2
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	2.2
	402054				2.2
	413335	AI613318	Hs.48442	ESTs	2.2
40	408212	AA297567	Hs.43728	hypothetical protein	2.2
	406169				2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.2
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fis, clone NT	2.2
	409715	W42591	Hs.23892	ESTs	2.2
45	431921	N46466	Hs.58879	ESTs	2.2
	443823	BE089782	Hs.9877	hypothetical protein	2.2
	432458	AI968598	Hs.78768	malignant cell expression-enhanced gene/	2.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	2.2
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (tr	2.2
50	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	2.2
	415216	AI825905	Hs.193211	Homo sapiens cDNA FLJ11421 fis, clone HE	2.2
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.2
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2.2
	406660	X65371	Hs.172550	polypyrimidine tract binding protein (he	2.2
55	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2.2
	432558	R97268	Hs.177269	ESTs	2.2
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.2
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.2
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothi	2.2
60	438407	AI457122	Hs.129673	eukaryotic translation initiation factor	2.2
	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447394, mRNA,	2.2
	409130	BE076601	Hs.75658	phosphorylase, glycogen; brain	2.2
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.2
	429489	AF008203	Hs.204039	aristae-like homeobox 3	2.2
65	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	2.2
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.2
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	2.2
	427498	NM_003926	Hs.178728	methyl-CpG binding domain protein 3	2.2
	408006	H57654	Hs.303345	ESTs, Weakly similar to I38022 hypothi	2.2
70	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	2.2
	431446	AW294929	Hs.255369	Homo sapiens cDNA FLJ10265 fis, clone HE	2.2
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	2.2
	433099	NM_002504	Hs.3187	nuclear transcription factor, X-box bind	2.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.2
75	415245	N59650	Hs.27252	ESTs	2.2
	443657	R14973		gb:y42f10.s1 Soares fetal liver spleen	2.2
	402521	AW501216	Hs.108945	KIAA0515 protein	2.2
	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	2.2
	446530	AV658909	Hs.282642	ESTs	2.2
80	415797	AI291896	Hs.72800	ESTs	2.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.2
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.2

	437033	AW248364	Hs.5409	RNA polymerase I subunit	2.2
	422732	AA577455	Hs.24937	transformer-2 alpha (htra-2 alpha)	2.2
	416388	AI417358	Hs.73677	ESTs	2.2
5	452849	AF044924	Hs.30792	hook2 protein	2.2
	446615	BE513202	Hs.15589	PPAR binding protein	2.2
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.2
	446279	AA490770	Hs.182382	ESTs	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.2
	403969				2.2
10	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	2.2
	447091	AW089648	Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.2
15	438726	AB033103	Hs.6385	KIAA1277 protein	2.2
	453315	BE544203	Hs.24831	ESTs	2.2
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.2
	433610	AA806822	Hs.112547	ESTs	2.2
20	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.2
	417980	R32235		gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
	406347				2.2
	414406	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	2.2
	401827				2.2
25	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr	2.2
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.2
	404084				2.2
	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI632091	Hs.116877	ESTs	2.2
30	442609	AL020996	Hs.8518	selenoprotein N	2.1
	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	2.1
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.1
	439253	AF086064	Hs.332252	ESTs	2.1
	409669	AW177551	Hs.220255	hypothetical protein MGC13098	2.1
	429574	BE268321	Hs.208912	hypothetical protein MGC861	2.1
35	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.1
	408945	AW015089	Hs.4964	DKFZP586J1624 protein	2.1
	447687	AI627947	Hs.150186	hypothetical protein DKFZp566K1946	2.1
	459584	AI910884	Hs.207898	ESTs	2.1
	439130	AA306090	Hs.124707	ESTs	2.1
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.1
	442028	AI239437	Hs.48945	ESTs	2.1
	430958	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	2.1
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	2.1
	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.1
45	444534	AW271626	Hs.42294	ESTs	2.1
	438391	AI262248	Hs.25027	ESTs	2.1
	442003	AW297497	Hs.201891	ESTs	2.1
	456278	BE300369	Hs.289038	hypothetical protein MGC4126	2.1
50	416976	BE243985	Hs.80680	major vault protein	2.1
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	2.1
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452712	AW838616		gb:RCS-LT0054-140200-013-D01 LT0054 Homo	2.1
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	2.1
55	421564	AB007864	Hs.105850	KIAA0404 protein	2.1
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1
	432742	AA564453	Hs.162339	ESTs	2.1
	435958	H98180	Hs.117975	ESTs	2.1
	421531	AA713505	Hs.291769	ESTs	2.1
60	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.1
	420503	AI570943	Hs.337546	ESTs	2.1
	448127	AI478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452897	BE066058	Hs.269233	ESTs, Moderately similar to I78885 serin	2.1
	447112	H17800	Hs.7154	ESTs	2.1
65	406577				2.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
	451460	AI797550	Hs.209652	ESTs	2.1
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	2.1
	435828	AA700705	Hs.13852	ESTs	2.1
70	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.1
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.1
	452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN	2.1
	415586	Z45481		gb:HSC2QE041 normalized infant brain cDN	2.1
	452620	AA436504	Hs.119286	ESTs	2.1
75	457066	BE244613	Hs.158272	ESTs, Weakly similar to CA13 MOUSE COLLA	2.1
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.1
	431741	AA514783	Hs.191701	ESTs	2.1
	446840	AW294828	Hs.209203	ESTs	2.1
	440818	AI147060	Hs.146726	ESTs	2.1
80	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.1
	400822				2.1
	412760	AW379030	Hs.41324	ESTs	2.1
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein binding pr	2.1
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fs, clone H	2.1

	424242	AA337476	Hs.293984	hypothetical protein MGC13102	2.1
	452560	BE077084	Hs.336432	ESTs	2.1
	456437	AJ924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.1
5	458922	BE501831	Hs.282053	ESTs	2.1
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.1
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.1
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	2.1
	457192	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.1
10	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	2.1
	452571	W31518	Hs.34665	ESTs	2.1
	423699	H41850	Hs.131846	PCAF associated factor 65 alpha	2.1
	406610				2.1
	453638	AW814996		gb:MR1-ST0206-170400-024-h09 ST0206 Homo	2.1
15	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	2.1
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.1
	410908	AA121686	Hs.10592	ESTs	2.1
	420221	N25991	Hs.43725	ESTs	2.1
	424739	AA346108	Hs.221610	ESTs	2.1
20	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.1
	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	418181	U37012	Hs.83727	cleavage and polyadenylation specific fa	2.1
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.1
	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1
	400021				2.1
	439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	2.1
30	456505	AA504595	Hs.111418	ESTs	2.1
	405258				2.1
	444645	AI184564	Hs.101654	ESTs	2.1
	430246	AI269069	Hs.109268	hypothetical protein FLJ12552	2.1
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	2.1
	403857				2.1
35	400258				2.1
	422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.1
	441054	AA913591	Hs.126480	ESTs	2.1
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.1
40	454606	AW809752		gb:MR4-ST0124-181299-020-b06 ST0124 Homo	2.1
	448954	AB014564	Hs.22616	KIAA0664 protein	2.1
	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.1
	453486	AL039201	Hs.173554	ubiquinol-cytochrome c reductase core pr	2.1
	437695	AA769202	Hs.192142	ESTs	2.1
	425449	X52056	Hs.157441	spleen focus forming virus (SFFV) provir	2.1
45	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	2.1
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	2.1
	436382	AW977063	Hs.250181	ESTs	2.1
	435837	AI689210	Hs.187276	Homo sapiens cDNA FLJ11431 fis, clone HE	2.1
	458287	AA987556	Hs.12867	ESTs	2.1
50	423794	BE551781	Hs.231895	ESTs	2.1
	408049	AW076098	Hs.74316	desmoplakin (DPI, DPII)	2.1
	402721				2.1
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.1
55	417541	AI992191	Hs.180040	hypothetical protein FLJ22439	2.1
	414857	AW402389	Hs.920	modulator recognition factor I	2.1
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.1
	428086	AL110193	Hs.224137	hypothetical protein	2.1
	447853	AI434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.1
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.1
60	431019	NM_005249	Hs.2714	forkhead box G1B	2.1
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.1
	416435	AI431301	Hs.179703	KIAA0129 gene product	2.1
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	2.1
	459369	T83080		gb:yd40e03.r1 Soares fetal liver spleen	2.1
65	402239				2.1
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	2.1
	426012	AA367507	Hs.75874	pregnancy-associated plasma protein A	2.1
	438885	AI886558	Hs.184987	ESTs	2.1
	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	2.1
70	404561				2.1
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.1
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	2.1
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.1
	458604	W37944	Hs.4007	Sarcolemmal-associated protein	2.1
75	409650	T08490	Hs.288969	HSCARG protein	2.1
	401729				2.1
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.1
	456741	W37608	Hs.184492	ESTs	2.1
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibod	2.1
80	415079	R43179	Hs.22895	hypothetical protein FLJ23548	2.1
	439262	AA832333	Hs.333045	ESTs	2.1
	403108				2.1
	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	2.1
	440696	AI762757	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1

	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	2.1
	453485	BE620712	Hs.33026	hypothetical protein PP2447	2.1
	418177	N44967	Hs.5663	ESTs	2.1
5	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.1
	454434	AA083558	Hs.261286	ESTs	2.1
	406085				2.1
	424441	X14850	Hs.147097	H2A histone family, member X	2.1
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott) sy	2.1
10	424576	BE154142	Hs.96833	ESTs	2.1
	423660	AL045228	Hs.130831	Homo sapiens mRNA; cDNA DKFZp434L137 (fr	2.1
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.1
	441940	AW298115	Hs.128152	ESTs	2.1
	439190	AW978693	Hs.293811	ESTs	2.1
15	417791	AW965339	Hs.111471	ESTs	2.1
	423701	AA329856	Hs.143022	ESTs	2.1
	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.1
	459642	BE243103		gb:TCAAP2E0949 Pediatric acute myelogeno	2.1
	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	2.1
20	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.1
	425591	AW294734	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	2.1
	412811	H06382	Hs.21400	ESTs	2.1
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	2.1
25	435924	AW029203	Hs.191952	ESTs	2.1
	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.1
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	2.1
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	2.1
	450704	H85157	Hs.40696	ESTs	2.1
30	427539	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box	2.1
	402028				2.1
	405362				2.1
	414718	H95348	Hs.107987	ESTs	2.1
	433424	R68252	Hs.163566	ESTs	2.1
35	444875	AI200759	Hs.44737	ESTs	2.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.0
	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen	2.0
	436331	AI239495	Hs.120189	ESTs	2.0
	448418	Z43704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
40	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
	448192	R43915	Hs.4958	ESTs	2.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.0
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.0
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	2.0
45	436872	X15624		gb:Human H1 RNA	2.0
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	2.0
	446307	T50083	Hs.9094	ESTs	2.0
	436588	AA759233	Hs.126506	ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	2.0
50	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.0
	432036	AF224266	Hs.272373	interleukin 20	2.0
	414460	L00727	Hs.898	dystrophin myotonic-protein kinase	2.0
	433507	AI817336	Hs.191791	ESTs	2.0
	427964	AA418082	Hs.98286	ESTs, Weakly similar to T20655 hypotheti	2.0
55	443108	W86975	Hs.203707	ESTs	2.0
	434504	AI887341	Hs.121590	hypothetical protein FLJ12827	2.0
	454310	AW818390	Hs.175613	homolog of Xenopus Caspin	2.0
	443566	AI290284	Hs.159872	ESTs	2.0
	449722	BE280074	Hs.23960	cyclin B1	2.0
60	452682	AA456193	Hs.9071	progesterone membrane binding protein	2.0
	412362	AW945484	Hs.184252	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.0
	435863	AF255346	Hs.62919	Jun dimerization protein p21SNFT	2.0
	400774	R58624	Hs.2186	eukaryotic translation elongation factor	2.0
65	453944	AW975369	Hs.292570	Homo sapiens, clone IMAGE:3502107, mRNA,	2.0
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.0
	448529	T26460	Hs.22550	ESTs	2.0
	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	2.0
	439360	AA448488	Hs.336629	ribosomal protein L44	2.0
70	436660	AI658870	Hs.184513	ESTs	2.0
	449030	AI365582	Hs.57100	Homo sapiens mRNA for FLJ00016 protein,	2.0
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	2.0
	406624	AF052762		gb:Homo sapiens clone csneg8-1 immunoglo	2.0
	450666	T99968	Hs.18799	ESTs, Weakly similar to I38022 hypotheti	2.0
75	446143	BE245342	Hs.306079	sec61 homolog	2.0
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	2.0
	426607	AA382330	Hs.124223	ESTs	2.0
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	2.0
	422564	AI148006	Hs.222120	ESTs	2.0
80	432682	AI376400	Hs.159588	ESTs	2.0
	422140	BE295918	Hs.112193	mutS (E. coli) homolog 5	2.0
	408215	BE614290	Hs.43812	syntaxin 10	2.0
	417129	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	2.0
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.0

5	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	2.0
	411380	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	2.0
	430603	AA148164	Hs.247280	HBV associated factor	2.0
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	2.0
	401125				2.0
10	412939	AW411491	Hs.2186	eukaryotic translation elongation factor	2.0
	448740	BE250632	Hs.8026	sestrin 2	2.0
	454390	AB020713	Hs.56966	KIAA0906 protein	2.0
	415012	NM_004383	Hs.77793	c-src tyrosine kinase	2.0
	410407	X66839	Hs.63287	carbonic anhydrase IX	2.0
15	403478				2.0
	456485	AI393037	Hs.97871	Homo sapiens, clone IMAGE:3845253, mRNA,	2.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.0
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	2.0
	451944	AW445218	Hs.210876	ESTs	2.0
20	436395	AJ227900		gb:Homo sapiens partial mRNA; ID EE2-16B	2.0
	456457	AA252905	Hs.194477	E3 ubiquitin ligase SMURF2	2.0
	449123	D50920	Hs.23106	KIAA0130 gene product	2.0
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957135, mRNA,	2.0
	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	2.0
25	453348	BE272318	Hs.8595	hypothetical protein FLJ12438	2.0
	424382	AA351898	Hs.23539	ESTs	2.0
	447079	AA280057	Hs.105260	ESTs, Weakly similar to dJ963K23.2 [Hsa	2.0
	449501	AI652924	Hs.231942	ESTs	2.0
	422893	X98411	Hs.121555	myosin IF	2.0
30	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	2.0
	434845	BE267057	Hs.325321	hypothetical protein R32184_1	2.0
	410422	AL042014	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	2.0
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.0
	451656	BE327088	Hs.212752	ESTs	2.0
35	442068	BE312873	Hs.314932	ESTs	2.0
	446846	AW197626	Hs.271901	ESTs, Moderately similar to S08686 finger	2.0
	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.0
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.0
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.0
40	402798				2.0
	404554				2.0
	TABLE 9B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
45	Pkey	CAT Number	Accession		
	407909	1025254_1	AW103986 BE156395 BE156391 BE156190 BE156184 BE156388 BE156394		
	408432	1058667_1	AW195262 R27868 AW811262		
	409193	110747_1	AA131483 AA065156 AA076448		
	409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450		
50	410447	1203929_1	AW816134 BE063456 AW748795 BE150839		
	410790	1221131_1	AW803357 AW803423 AW812233 R06814		
	411256	1236790_1	AW834039 AW834040 AW834047 AW845410 BE003128 AW852479		
	411380	1242343_1	AW841619 AW851958 AW851851 AW851985		
	411632	1252361_1	AW854829 AW854805 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826		
55	411658	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605		
	411829	1260309_1	AW865749 BE179419 BE179492		
	412225	1284108_1	AW902042 N77591		
	412370	1291952_1	AW946614 AW946622 AW946663 AW946667 AW946615 AW946619		
	412391	1292625_1	AW947710 AW947698 AW947697 AW947713		
60	413257	1355963_1	BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037		
	413604	1379715_1	RS1767 BE152515 Z44834 H23397		
	414406	1443333_1	BE297904 BE294312		
	414550	1460990_1	BE379808		
	415346	1534581_1	Z43108 F06295 R13085		
65	415406	1536026_1	T26510 F07926 R53367		
	415586	1540116_1	Z45481 F12393 T74437		
	415635	1540853_1	F13168 R21289 T77628		
	416871	1626761_1	H98716 N90792 N24283		
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499		
70	417980	1712954_1	R32235 R32247 R32219		
	418333	173_2	W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353 AW088477		
			AI887846 AW502624 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 AI124782 AA889402		
			AA765804 AA765530 AA055698 AA594019 AI267368 AA456946 R93354 AF264624 AW668618 AA601493		
			AA362858 AW863761 AA229428		
75	418856	179649_1	AA504571 AA235243 AA411737 AW969068 AA406543		
	419217	182954_1	U70073		
	419225	1830274_1	AA689591 AW974261 AA236240 AI077451 AA631399 AW974262		
	419311	183793_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280		
	420352	192979_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991		
80	422128	211994_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512		
	422155	212379_1	AI334966 W32951 H62656 H53902 R88904 AW835732		
			H80977 BE147695 AA305496 AW962366 AA436754		
			AA828125 AA834883 AA330555		
			AA331886 AW962659 AW962655 T89841		
80	422176	212714_1			
	423756	231725_1			
	423867	232732_1			

5	425189	247825_1	H16622 R17322 AA351959
	425517	252729_1	AF121179 BE162736 AA358827
	426076	260504_1	AW962714 AA369277 AA369278
	426413	266650_1	AA377823 AW954494 A1022688
	426503	268283_1	AA380153 AA380233 AW963529
	426531	268760_1	AA381071 AA381084 AA380852
	429875	310034_1	A1091815 AA460162 AA460761
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
10	432088	341195_1	AA525454 H74039 R89502 T77379
	433532	368950_1	AW975367 AA598607 AA742735
	434559	38889_1	AF147315 AW173079 T53029
	435065	399329_1	BE064391 BE064395 AA663613 N99644
	436190	41555_1	AK001059 AA633055
	436395	41905_1	AJ227900 A1094933 AW051119 F00947
15	436532	421802_1	AA721522 AW975443 T93070
	436722	425758_1	AW975977 AA729469 AA747132
	436872	42851_1	X15624
	437034	431713_1	AA742643 AA808575 AW976668
20	439086	46852_1	AF085947 H70981 H78989
	439228	47001_1	N51700 AF086051 N51792
	439518	47334_1	W76326 AF086341 W72300
	439546	47360_1	AF088056 W76297 W72448
	439566	47387_1	AF086387 W77884 W72711
25	439710	47550_1	AF086543 W96291 W96225
	443657	576685_1	R14973 R14967 A1081006
	444168	593829_1	AW379879 A1126285 H12014
	444386	604004_1	BE065183 A1144398 BE065367
	451129	859870_1	BE072881 BE072946 A1762181
30	452712	928309_1	AW838616 AW838660 BE144343 A1914520 AW888910 BE184854 BE184784
	453446	967533_1	BE299996 BE297115 BE270415 BE295214 BE296526
	453638	975649_1	AW814996 AL047199 AW850979
	453746	979731_1	AL120611 BE006190 BE006189
	454377	114761_1	AA076811 AW814764
35	454389	115682_1	AW752571 AW847602 AA077979
	454606	1226149_2	AW809752 AW810271 AW809944 AW810319 AW810215 AW810368 AW810167
	454630	1227352_1	BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142020 BE142074 BE142347 BE142000 BE142375
			AW811189 BE142133
	454631	1227443_1	AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335
40	454679	1228929_1	AW813110 AW813113
	454967	1247021_1	AW848276 AW848416 AW847945 AW847947 AW848063 AW848113
	455023	1249188_1	AW850907 AW850901 AW850877
	455302	1276542_1	AW997641 AW891777
	455470	1292849_1	AW947992 AW947967 AW947950 AW947957 AW947953 AW947973 AW947966 AW947971 AW947947 AW947970 AW947995 AW947979 AW947952
45	455514	1321649_1	AW947956
	455530	1322298_1	AW983871 BE090302 AW983867 AW983845 AW983860 AW983853 AW983852
	455584	1334741_1	AW984744 AW984759
	455778	1364506_1	BE007420 BE007419 BE007421 BE007422
	455908	1382301_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
50	456072	1470256_1	BE156306 BE156188 BE156298 BE156377 BE156374
	456094	1504780_1	H54381 H54463 BE393262
	457374	328758_1	H95091 C01228
	457578	359618_1	AA493662 AW897396 BE154814
55	457730	393905_1	AA578027
			AW753613 AW753857 BE150374 BE150693 BE150394 AA808851 AA650159 AA654653 BE150419

TABLE 9C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400822	7465000	Plus	186223-186402,186878-187275
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400917	7283186	Minus	173258-173631
400992	8096828	Plus	140390-140822
401012	7230838	Minus	736-1137
401048	7232177	Plus	132430-132761
401125	8570296	Minus	126863-126984
401324	9863791	Plus	234057-234174
401384	6850939	Minus	58360-58545
401558	7139678	Plus	103510-104090
401626	8575943	Minus	238100-238432
401676	9965536	Plus	3891-4691
401714	6715702	Plus	96484-96681
401729	8134856	Minus	90651-90878
401827	2262095	Plus	94725-94860,98452-98660
401875	8099107	Plus	95913-96641
402028	7139781	Plus	88749-89237
402064	8117294	Plus	100159-100350,100445-100912
402239	7690131	Plus	38175-38304,42133-42266
402408	9796239	Minus	110326-110491

5	402424	9796344	Minus	64925-65073
	402516	9798099	Minus	195342-195511
	402604	9909420	Plus	20393-20767
	402627	9931216	Plus	12136-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-
10	402721	8969253	Minus	26895,29279-29469
	402798	3355547	Plus	144428-144715
	402856	9801288	Minus	23596-23867
	403048	4210991	Plus	90119-90411
15	403108	8980955	Plus	44275-44592,49656-49955
	403142	9444521	Plus	93253-93667
	403166	9838127	Minus	89286-90131
	403478	9958258	Plus	67762-67940,68695-68856,70394-70507
20	403680	7331517	Minus	116458-116564
	403751	7229815	Minus	157184-157415
	403790	8084957	Minus	158794-160929
	403797	8099896	Minus	87826-87947,89835-90002
25	403857	7708910	Minus	123065-125008
	403881	7710245	Minus	2524-3408
	403961	7596976	Minus	107250-107685,108924-109213
	403969	8569909	Plus	110393-110603
30	404020	8655966	Minus	31237-31375,32405-32506
	404054	3548785	Plus	174449-174663
	404084	9944055	Plus	66713-69175
	404108	8247074	Minus	2795-2969
35	404170	9930793	Plus	63603-64942
	404185	4572584	Minus	168836-169248
	404240	5002624	Minus	129171-129327
	404295	9856663	Minus	116132-116407,116653-116922
40	404299	5738652	Minus	75747-75947
	404366	9964977	Plus	3826-4025
	404554	7243881	Plus	96589-96801
	404561	9795980	Minus	42637-42839
45	404584	9857511	Plus	69039-70100
	404589	9931665	Minus	138651-139153
	404642	9796810	Plus	32824-32985
	404652	9796969	Minus	102999-103145
50	404721	9856648	Minus	108172-108296
	404756	7706327	Plus	173763-174294
	404802	4581357	Minus	82849-83627
	404984	6939882	Plus	30093-30600
55	405159	9966252	Plus	87221-87505
	405258	7329310	Plus	79659-79804
	405288	6139075	Minus	129930-130076
	405353	2811095	Plus	126268-126436
60	405362	2337862	Minus	118525-118892
	405558	1621110	Plus	105008-105142,105980-106091,140445-140556,142519-142641
	405588	5002511	Plus	4502-4644,5983-6083
	405605	5836195	Minus	46180-46366
65	405701	4263751	Plus	117070-117270
	405741	9966947	Minus	93243-93364
	405747	8469069	Minus	156747-156875,156936-157208
	405771	7018349	Plus	153933-154060
70	405808	9929207	Plus	91191-91254,91510-91589
	405884	6758747	Plus	109758-111166
	405915	7712162	Minus	62383-62583
	406028	8312303	Minus	43717-43859
75	406085	9123888	Plus	177469-177829
	406169	6684220	Minus	18665-18843
	406267	7528342	Minus	12620-14251
	406326	9212385	Plus	2570-2731
80	406347	9255981	Plus	84508-84655
	406474	9795567	Plus	90900-91091
	406577	7711730	Plus	52758-53211
	406610	8312226	Plus	11377-11509
				13096-13334

TABLE 10A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 10A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuD3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

Key	ExAccn	UnigenelD	Unigene Title	R1
453655	AW960427	Hs.79059	transforming growth factor, beta recepto	136.7
417275	X63578	Hs.295449	parvalbumin	29.0
430829	AW451999	Hs.194024	ESTs	25.7

	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	18.5
5	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	15.2
	417167	AW206437	Hs.4290	ESTs	14.8
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
10	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6
	408068	AW148652	Hs.167398	ESTs	12.6
	412636	NM_004415	Hs.74316	desmoptakin (DPI, DPII)	12.5
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2
	412638	AA910199	Hs.203838	ESTs	12.2
15	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	12.1
	456844	AL264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	11.9
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39804	Hs.31961	ESTs	10.8
	446353	AI290919	Hs.153661	ESTs	10.4
20	420290	AW977318	Hs.194480	ESTs	10.3
	414220	BE298094		gb:601118Z31F1 NIH_MGC_17 Homo sapiens c	10.3
	414290	AI568801	Hs.71721	ESTs	10.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0
	414937	R38698	Hs.12382	ESTs	10.0
25	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5
	407173	T64349		gb:yc10d08.s1 Stralagene lung (937210) H	9.5
	412454	R55745	Hs.167330	ESTs	9.5
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4
	415315	F12240	Hs.250655	prothymosin, alpha (gene sequence 28)	9.3
30	441790	AW294909	Hs.132208	ESTs	9.2
	448117	H49129	Hs.172982	ESTs	9.1
	400661				9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
35	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
	409031	AA376836	Hs.76728	ESTs	8.7
	428106	BE620016	Hs.182470	PTD010 protein	8.3
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2
40	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.2
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	8.0
	456490	UB3171	Hs.97203	small inducible cytokine subfamily A (Cy	8.0
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	8.0
45	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	7.9
	437073	AI885608	Hs.94122	ESTs	7.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
50	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	7.8
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	7.8
	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	405800				7.7
55	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	7.7
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	7.7
	423440	R25234	Hs.143434	contactin 1	7.7
	445148	AI214510	Hs.146304	ESTs	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
60	424087	N69333	Hs.143434	contactin 1	7.6
	437479	R61866	Hs.101277	ESTs	7.5
	405071				7.5
	421224	AW402154	Hs.125812	ESTs	7.4
	442025	AW887434	Hs.11810	CDA11 protein	7.4
65	459476	BE185844		gb:IL5-HT0731:110500-087-c08 HT0731 Homo	7.2
	430573	AA744550	Hs.136345	ESTs	7.1
	401836				7.1
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152	AB001325	Hs.234642	aquaporin 3	7.1
70	419474	AW968619	Hs.155849	ESTs	7.1
	401780				7.1
	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens c	7.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0
	433098	AW190593	Hs.151143	ESTs	7.0
75	445511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	6.9
	451285	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-	6.8
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.8
	419273	BE271180	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	6.8
	443155	R54485	Hs.23772	ESTs	6.8
80	450561	R49674	Hs.25909	ESTs	6.8
	433068	NM_006456	Hs.288215	sialyltransferase	6.8
	440729	AA904739	Hs.128204	ESTs	6.8
	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	6.7
	423589	AA328082	Hs.209569	ESTs	6.6

	415681	AI379882	Hs.72630	ESTs	
	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.5
	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4
5	453344	BE349075	Hs.44571	ESTs	6.4
	450642	R39773	Hs.7130	copine IV	6.4
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
10	447482	AB033059	Hs.18705	KIAA1233 protein	6.4
	400332	S66407	Hs.248032	FLT4	6.4
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3
	446129	AW244073	Hs.145946	ESTs	6.3
	454076	AW204712	Hs.61957	ESTs	6.3
15	425526	AA359933		gb:EST69040 Fetal lung II Homo sapiens c	6.3
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
	434273	AA913143	Hs.26303	ESTs	6.3
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	AI769514	Hs.209890	EST	6.2
20	430754	AW862610	Hs.157068	ESTs	6.2
	438356	AA805530	Hs.48527	ESTs	6.2
	422743	BE304678	Hs.119598	ribosomal protein L3	6.2
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	426388	AW081394	Hs.97103	ESTs	6.2
25	452502	AI904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1
	402546			ESTs	6.1
	457534	AI761307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958			Homo sapiens mRNA for KIAA1863 protein,	6.1
30	432501	BE546532	Hs.25682	ESTs	6.1
	442979	AW440782	Hs.174743	ESTs	6.1
	422262	AL022315	Hs.113987	lectin, galactoside-binding, soluble, 2	6.0
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sapiens c	6.0
35	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9
	401521			ESTs	5.9
	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	R13727	Hs.21435	ESTs	5.9
40	424806	AA382523	Hs.105689	MSTP031 protein	5.9
	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9
	457483	AB034694	Hs.272558	endomucin-1	5.9
	417175	R44558	Hs.94002	ESTs	5.9
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
45	436427	AI344378	Hs.143399	ESTs	5.8
	411939	AI365585	Hs.146246	ESTs	5.8
	459053	AI807052	Hs.210361	ESTs	5.8
	411052	AW814950		gb:MR1-ST0205-130400-023-d06 ST0206 Homo	5.7
	431063	Z98949	Hs.326843	hypothetical protein bk125H2.1	5.7
50	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7
	442676	AI733585	Hs.130897	ESTs	5.7
	446443	AV659082	Hs.134228	ESTs	5.7
	400865			ESTs	5.7
55	459080	AW192083	Hs.290855	ESTs	5.7
	407952	AI215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256022	5.6
	425705	AF007833	Hs.159265	kruppel-related zinc finger protein hckr	5.6
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	5.6
60	422994	AW891802	Hs.296276	ESTs	5.6
	457148	AF091035	Hs.184627	KIAA0118 protein	5.6
	428356	AL046991	Hs.10338	ESTs	5.6
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	5.5
	402092			ESTs	5.5
65	440526	AI832243	Hs.211471	ESTs	5.5
	444409	AI792140	Hs.49265	ESTs	5.5
	417877	AI025829	Hs.86320	ESTs	5.5
	458238	AW071521	Hs.333541	beta-amyloid binding protein precursor	5.4
	430702	U56979	Hs.250651	H factor 1 (complement)	5.4
70	456189	H91010	Hs.44940	ESTs	5.4
	427424	AA402453	Hs.113011	ESTs	5.4
	437354	AA749215	Hs.291886	ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-f02 BT0614 Homo	5.4
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3
75	427861	AA813185	Hs.98183	ESTs	5.3
	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3
	444209	AI753134	Hs.146494	ESTs	5.3
	422831	R02504	Hs.332943	ESTs	5.3
	403180			ESTs	5.3
80	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	5.3
	430339	W26608	Hs.239625	integral membrane protein 2B	5.2
	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.2
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.2
	437403	AI208149	Hs.121196	ESTs	5.2

	438285	AA782845	Hs.22790	ESTs	5.2
	439901	N73885	Hs.124169	ESTs	5.2
	438507	AA809052	Hs.211275	ESTs	5.2
	449222	AW293984	Hs.197621	ESTs	5.2
5	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	5.2
	419042	T81429	Hs.221055	ESTs	5.2
	436777	AA731199	Hs.293130	ESTs	5.2
	445071	AI280246	Hs.149504	ESTs	5.1
10	408016	AW136827	Hs.256096	ESTs	5.1
	412047	AA934589	Hs.49696	ESTs	5.1
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
15	453830	AA534296	Hs.20953	ESTs	5.1
	459580	AA022888	Hs.176055	ESTs	5.1
	417616	R07728	Hs.268658	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate carrier-6	5.1
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
20	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
	447135	T58148		gb:yb98g06.s1 Stratagene lung (937210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0
	442240	AI791883	Hs.292719	ESTs	4.9
25	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
	427972	AA864870	Hs.181304	putative gene product	4.9
	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093		gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	AI097452	Hs.135095	ESTs	4.9
30	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
	436670	AI690021	Hs.201536	ESTs	4.8
	448072	AI459306	Hs.24908	ESTs	4.8
	408936	AL138043	Hs.293549	ESTs	4.8
35	412622	AW664708	Hs.171959	ESTs	4.8
	414943	D80647	Hs.124193	ESTs	4.8
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
	453567	AI742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8
40	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
	405130				4.7
	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	4.7
	446218	AV657159		gb:AV657159 GLC Homo sapiens cDNA clone	4.7
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.7
45	402176				4.7
	416577	BE063207	Hs.79381	grancalcin	4.7
	436221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fis, clone OV	4.7
	420480	AL137361	Hs.98173	hypothetical protein	4.7
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	4.6
50	435161	AF124150	Hs.272091	ESTs	4.6
	404793				4.6
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6
	438571	AW020775	Hs.56022	ESTs	4.6
	445924	AI264671	Hs.164166	ESTs	4.6
55	444585	AW170015	Hs.6594	ESTs	4.6
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
	418274	AI458587	Hs.128677	Human DNA sequence from clone RP1-500Z4	4.6
	425475	W56339	Hs.107057	ESTs	4.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	4.5
60	414272	AI651603	Hs.46988	ESTs	4.5
	445235	AI564022	Hs.138207	ESTs	4.5
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Homo sapiens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	4.5
65	401024				4.5
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5
	423449	AI497900	Hs.33067	ESTs	4.5
	405138				4.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo	4.5
70	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	4.5
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4
	441184	AA922009	Hs.150269	ESTs	4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4
	445481	AW661846	Hs.148836	ESTs	4.4
75	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	4.4
	404769				4.4
	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW628326	Hs.27151	ESTs	4.4
	449093	AB035356	Hs.22998	neurexin 1	4.4
80	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4
	417888	R23053		gb:yh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4

	435078	AW518888	Hs.40937	ESTs	4.4
	413493	BE144444		gb:MR0-HT0168-141199-002-f09 HT0168 Homo	4.3
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3
5	459650	R25754	Hs.301185	ESTs	4.3
	404828				4.3
	423782	AA72209	Hs.323117	ESTs	4.3
	426867	AA460967	Hs.22668	ESTs	4.3
	426802	AA385182	Hs.46699	ESTs	4.3
10	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	4.3
	412112	BE180342		gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3
	401522	N47812	Hs.306198	CGI-35 protein	4.3
	419055	AI365384	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
	410171	H07892	Hs.12431	ESTs	4.3
15	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	4.3
	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	4.3
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	4.3
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	4.3
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
20	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2
	433389	AF038171		gb:Homo sapiens clone 23671 mRNA sequenc	4.2
	454356	AW390363	Hs.11522	hypothetical protein from Xq28	4.2
	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5'3'	4.2
25	443998	AI620661	Hs.296276	ESTs	4.2
	452197	AW023595	Hs.232048	ESTs	4.2
	451117	AA015752	Hs.205173	ESTs	4.2
	404501	AW247252	Hs.75514	nucleoside phosphorylase	4.2
30	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2
	440323	AA970614	Hs.127992	ESTs	4.2
	425767	AF054176	Hs.159483	chromosome 1 open reading frame 7	4.1
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin 1	4.1
35	413121	T96090	Hs.142678	ESTs	4.1
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	4.1
	450235	AA007512	Hs.17538	ESTs	4.1
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypothe	4.1
40	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	4.1
	408496	AI683802	Hs.136182	ESTs	4.1
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
	434101	AA625205	Hs.259599	KIAA1622 protein	4.1
	451837	T92157	Hs.16970	ESTs	4.1
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1
45	437630	AI252782	Hs.153026	SWAP-70 protein	4.1
	430212	AA469153		gb:nc67f04.s1 NCL_CGAP_Pr1 Homo sapiens	4.0
	400216				4.0
	429830	AI537278	Hs.225841	DKFZP434D193 protein	4.0
50	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0
	405354				4.0
	427931	AW206512	Hs.186996	ESTs	4.0
	428775	AA434579	Hs.143691	ESTs	4.0
	449422	AA001373	Hs.59821	ESTs	4.0
55	453864	AW021407	Hs.21058	hypothetical protein	4.0
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0
	420784	T65158	Hs.102399	ESTs, Moderately similar to S65657 alpha	4.0
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	4.0
60	429628	H09604	Hs.13268	ESTs	4.0
	410087	F12079	Hs.332579	ESTs	4.0
	409840	AW502122		gb:UL-HF-BR0p-ajr-c-08-0-ULr1 NIH_MGC_5	4.0
	452854	AA437061	Hs.14060	prokineticin 1 precursor	4.0
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.0
65	427443	AA402713	Hs.97872	ESTs	4.0
	414990	C17758	Hs.221652	Homo sapiens cDNA FLJ14323 fis, clone PL	3.9
	412678	AA115575	Hs.114914	ESTs	3.9
	405629				3.9
	420299	AI056871	Hs.15276	ESTs	3.9
70	453098	Z25935	Hs.86379	ESTs	3.9
	435752	AF230801		gb:Homo sapiens growth hormone receptor	3.9
	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypothe	3.9
	442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	3.9
75	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.9
	406697	M21388	Hs.123017	Human unproductively rearranged Ig mu-ch	3.9
	443850	AW014723	Hs.334612	ESTs	3.9
	412677	AW029608	Hs.17384	ESTs	3.9
	422788	AL117352	Hs.120828	Human DNA sequence from clone RPS-876B10	3.9
	405377				3.9
80	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [3.9
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9
	431960	AW241821	Hs.301927	c6.1A	3.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9

	427264	AA400117	Hs.125747	ESTs	3.9
	422746	NM_004484	Hs.119651	glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acut	3.9
5	414666	NM_004466	Hs.76828	glypican 5	3.8
	418217	AI910647	Hs.13442	ESTs	3.8
	419118	AA234223	Hs.139204	ESTs	3.8
	445017	AI205493	Hs.176860	ESTs	3.8
	405867				3.8
10	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
	453863	X02544	Hs.572	orosomucoid 1	3.8
	457821	H47166	Hs.124322	ESTs, Weakly similar to A47582 B-cell gr	3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
15	456083	U46922	Hs.77252	fragile histidine triad gene	3.8
	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypothei	3.8
	449057	AB037784	Hs.22941	KIAA1363 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
	414764	AW013887	Hs.72047	ESTs	3.8
	404391				3.7
20	433629	R13140	Hs.13359	ESTs	3.7
	424738	AI963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7
25	440530	AA888646	Hs.174187	ESTs	3.7
	433930	AA620338	Hs.273781	ESTs	3.7
	409662	AW452320	Hs.279726	ESTs	3.7
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	AI248205	Hs.153244	ESTs	3.7
30	408593	R19566	Hs.197617	ESTs	3.7
	417091	AA193283	Hs.291990	ESTs	3.7
	448556	AW885606	Hs.5064	ESTs	3.7
	423135	N67655	Hs.26411	ESTs	3.7
	400135				3.7
35	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	3.7
	457221	AW383197	Hs.218260	ESTs	3.7
	451660	AI807927	Hs.249601	ESTs	3.7
	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.7
	446818	AI342668	Hs.279765	ESTs	3.7
40	447795	AW295151	Hs.163612	ESTs	3.7
	427562	R56424	Hs.26534	ESTs	3.6
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.6
	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	439274	AF086092	Hs.48372	ESTs	3.6
45	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	422897	AA679784	Hs.4290	ESTs	3.6
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6
	421908	AW935200	Hs.285814	sprouty (Drosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
50	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	3.6
	400685				3.6
	417154	AI674701	Hs.21388	ESTs	3.6
	447176	Z42549	Hs.160893	ESTs	3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
55	449231	BE410360	Hs.298573	KIAA1720 protein	3.6
	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
	405977				3.6
	441470	BE503874	Hs.301986	ESTs	3.6
60	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6
	450236	AW162998	Hs.24684	KIAA1376 protein	3.6
	425364	AF052150	Hs.155959	Homo sapiens clone 24533 mRNA sequence	3.6
	426775	AA384564	Hs.108829	ESTs	3.6
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6
65	416876	AW501916	Hs.117897	ESTs	3.6
	400878				3.6
	425153	AW023193	Hs.27046	ESTs	3.6
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	3.5
	415047	F13142		gb:HSC3JD031 normalized infant brain cDN	3.5
70	401532				3.5
	446495	D60923	Hs.153460	ESTs	3.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901	BE155527		gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5
75	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5
	455697	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	3.5
	405678				3.5
	418207	C14685	Hs.34772	ESTs	3.5
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5
80	417027	AA192306	Hs.23926	triadin	3.5
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
	417702	R09935	Hs.191146	ESTs	3.5
	445687	WB0382	Hs.149297	ESTs	3.5
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothei	3.5

	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5
	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo sapiens c	3.5
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5
5	415621	AJ648602	Hs.55468	ESTs	3.5
	454437	AJ248173	Hs.191460	hypothetical protein MGC12936	3.5
	446066	AJ343931	Hs.149383	ESTs	3.5
	423374	AB037770	Hs.127656	KIAA1349 protein	3.5
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5
10	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	3.5
	451776	W45679	Hs.169854	hypothetical protein SP192	3.5
	432305	M62402	Hs.274313	insulin-like growth factor binding prote	3.5
	456995	T89832	Hs.170278	ESTs	3.5
	403323				3.5
15	425022	M95724	Hs.154207	centromere protein C 1	3.5
	439394	AA149250	Hs.56105	ESTs	3.5
	433803	AI823593	Hs.27688	ESTs	3.4
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4
	411474	AW848427		gb:IL3-CT0214-150200-075-H10 CT0214 Homo	3.4
20	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	3.4
	427173	BE255017	Hs.97540	ESTs	3.4
	408112	AW451982	Hs.248613	ESTs	3.4
25	446092	N33522	Hs.145894	ESTs	3.4
	416868	AI656856	Hs.292597	ESTs	3.4
	458234	BE551408	Hs.127196	ESTs	3.4
	419555	AA244416		gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	414314	BE312991		gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
30	400425	AY004252	Hs.287385	PR domain containing 12	3.4
	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	3.4
	434053	AW445136	Hs.134946	ESTs	3.4
	449997	AI683052	Hs.201577	KIAA1829 protein	3.4
	433461	AI636047	Hs.197623	ESTs	3.4
35	428006	AA418743	Hs.98306	KIAA1862 protein	3.4
	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-asso	3.4
	443294	AI733625	Hs.133053	ESTs	3.4
	428212	AW444451	Hs.134812	ESTs	3.4
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	3.4
40	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.4
	428536	AI143139	Hs.2288	visinin-like 1	3.3
	426597	AA382250	Hs.145601	ESTs	3.3
	410366	AI267589	Hs.302689	hypothetical protein	3.3
	458258	AW406546	Hs.127971	ESTs	3.3
45	401738				3.3
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.3
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.3
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3
50	434998	AW975157	Hs.26037	ESTs	3.3
	456359	AI967991	Hs.93574	homeo box D3	3.3
	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type I, b	3.3
	454267	AA437199	Hs.656	cell division cycle 25C	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
55	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	3.3
	436602	AI793222	Hs.166817	ESTs	3.3
	449204	AB000099	Hs.23251	Down syndrome critical region gene 4	3.3
	417935	R53697	Hs.170044	ESTs	3.3
	423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	3.3
60	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	3.3
	453406	AI192987	Hs.61784	hypothetical protein FLJ14451	3.3
	420164	AW339037	Hs.24908	ESTs	3.3
	447826	AW779317	Hs.258556	ESTs	3.3
	419875	AA853410	Hs.93557	proenkephalin	3.3
65	444612	AW138111	Hs.22902	ESTs	3.3
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (I	3.2
	415242	R45986	Hs.295014	ESTs	3.2
	418188	AW139413	Hs.151880	ESTs	3.2
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	3.2
70	421640	AW966652		gb:EST378726 MAGE resequences, MAGI Homo	3.2
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.2
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	3.2
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2
75	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2
	403092				3.2
	452971	AI873878	Hs.91789	ESTs	3.2
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
	401485				3.2
80	401949				3.2
	457452	AW972675		gb:EST384766 MAGE resequences, MAGL Homo	3.2
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2
	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2
	421200	AA284811	Hs.264433	ESTs	3.2

	430142	NM_000437	Hs.234392	platelet-activating factor acetylhydrolase	3.2
	433197	AB040889	Hs.281022	KIAA1456 protein	3.2
	443509	AV645470		gb:AV645470 GLC Homo sapiens cDNA clone	3.2
5	440827	AI733110	Hs.128128	ESTs	3.2
	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferase	3.2
	409257	AW370362		gb:RC1-BT0255-181099-012-d07 BT0255 Homo	3.2
	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLJ00038 protein,	3.2
	416789	AA223439	Hs.79933	cyclin I	3.2
10	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2
	420156	AW449258	Hs.6187	ESTs	3.2
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
	400617	AF151064	Hs.36069	hypothetical protein	3.2
	437129	AL049327	Hs.302057	Homo sapiens mRNA; cDNA DKFZp564E016 (fr	3.2
15	451820	AW058357	Hs.337353	ESTs	3.2
	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2
	419956	AL137939	Hs.40096	ESTs	3.1
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
20	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
	445886	AI793176	Hs.145596	ESTs	3.1
	414401	AI760159	Hs.124833	ESTs	3.1
	441573	BE563966	Hs.6529	ESTs, Weakly similar to I78885 serine/th	3.1
25	450725	R71389	Hs.175951	ESTs	3.1
	458805	AI282933	Hs.23294	hypothetical protein FLJ14393	3.1
	417868	AI078534	Hs.122592	ESTs	3.1
	458391	AI792628	Hs.133273	ESTs	3.1
	423346	AI267677	Hs.127416	synaptotagmin 1	3.1
30	454486	AW857077		gb:RC1-CT0302-140300-016-f04 CT0302 Homo	3.1
	408341	AW182952	Hs.249957	ESTs	3.1
	410669	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	3.1
	404907				3.1
	434910	AI333863	Hs.215474	ESTs, Moderately similar to alternative1	3.1
35	436990	AI149729	Hs.120557	ESTs	3.1
	441921	AI733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	454673	AW812807		gb:RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1
40	404345	AA730407	Hs.159156	protocadherin 11	3.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlled	3.1
	417313	AA195602		gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi	3.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	3.1
	425339	AA936330	Hs.198113	ESTs	3.1
45	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.1
	449078	AK001256	Hs.22975	KIAA1576 protein	3.1
	429608	U49250	Hs.210862	T-box, brain, 1	3.1
	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1
50	428465	AW970976	Hs.293653	ESTs	3.1
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1
	447965	AW292577	Hs.94445	ESTs	3.1
	413918	AW015898	Hs.71245	ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.1
	425810	AI923627	Hs.31903	ESTs	3.1
55	427865	AA416931	Hs.126065	ESTs	3.1
	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	3.1
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
60	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.0
	422963	M79141	Hs.13234	ESTs	3.0
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.0
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	3.0
	414686	BE409757	Hs.23189	ESTs, Moderately similar to TBB2_HUMAN T	3.0
65	458360	AI027207	Hs.132253	ESTs	3.0
	451829	AW964081	Hs.247377	ESTs	3.0
	445179	AI949743	Hs.224768	ESTs	3.0
	433090	AI720050	Hs.145362	immortalization-upregulated protein	3.0
	432018	AA524447	Hs.152377	ESTs	3.0
70	407988	N47760	Hs.285107	hypothetical protein FLJ13397	3.0
	405911				3.0
	418808	AI821836	Hs.10359	ESTs	3.0
	431900	AW972048	Hs.192534	ESTs	3.0
	452893	HI8017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
75	423952	AW877787	Hs.136102	KIAA0853 protein	3.0
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	405793				3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3.0
80	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	427071	AA397958	Hs.192719	ESTs	3.0
	434961	AW974956		gb:EST387061 MAGE resequences, MAGN Homo	3.0

TABLE 108:

		Pkey:	Unique Eos probeset identifier number
		CAT number:	Gene cluster number
		Accession:	Genbank accession numbers
5		Pkey	Accession
		409257	1112994_1 AW370362 AW809101
		409840	1156071_1 AW502122 AW502125 AW501663 AW501720
		411052	1230374_1 AW814950 R98513 H69459 BE176242 H54583
10		411279	1237516_1 AW884776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258
		411474	1247047_2 AW848427 AW848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162
		411607	1251251_1 AW853498 AW853442 AW853590 AW853433 AW853592
		411772	1257386_1 BE170301 AW861539 AW904851 BE154336 BE154090 BE154275
		412112	1277883_1 BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898
15			BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345
	413164	1351422_1	AW893614 AW893615 H85799 H83501 BE180220
			BE068494 BE068414 BE068332 BE068347 BE068706 BE068623 BE068450 BE068480 BE068350 BE068295 BE068498 BE068765 BE068328
			BE068778 BE068671 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068580 BE068445 BE068567 BE068521 BE068549
			BE068392 BE068307 BE068692 BE068473 BE068754 BE068476 BE068685 BE068626 BE068591 BE068745 BE068434 BE068759 BE068628
20			BE068723 BE068529 BE068689 BE068383 BE068422 BE068470 BE068522 BE068618 BE068354 BE068748 BE068683 BE068303 BE068602
			BE068739 BE068374 BE068302 BE068625 BE068596 BE068663 BE068429 BE068605 BE068693 BE068672 BE068401 BE068579 BE068329
			BE068390 BE068419 BE068393 BE068447 BE068675 BE068311 BE068540 BE068301 BE068543 BE068719 BE068369 BE068324 BE068588
			BE068568 BE068317 BE068384 BE068547 BE068674 BE068436 BE068321 BE068361 BE068676 BE068499 BE068299 BE068352 BE068410
			BE068293 BE068418 BE068552 BE068598 BE068327 BE068550 BE068712 BE068661 BE068733 BE068525 BE068752 BE068357 BE068330
25			BE068565 BE068538 BE068340 BE068537 BE068761 BE068632 BE068758
	413493	1373555_1	BE144444 BE144430
	413510	1374377_1	F13044 T77009 BE145525 BE145493
	413544	1375671_1	BE147225 BE147205 BE147234
	414220	1426940_1	BE298094 BE267860
30			BE312991 BE272945
	414314	1435028_1	BE549143 BE390613 BE277344
	414366	1438636_1	H74314 BE299593
	414456	1447655_1	BE386764 BE387560
	414593	1464909_1	BE410857 BE390605
	414630	1468083_1	F13142 Z42926 F06135 F06147 H08517 D51360 T75341
35			AA195602 W01148 N40632
	415047	1517450_1	R23053 R79884 R76271
	417313	166644_1	AA244416 AA244401
	417888	1706092_1	AA285362 AW752386 AW847156 AA285373 AW879575 AW879558
	419555	185884_1	AW966652 AW966653 AA294989 AA385977
40			BE048255 AA313083 AA298419
	421249	200649_1	BE409561 BE162756 AW732798
	421640	204833_1	AA359933 AA358889 AW955306 AW962995 AW837746 AW837755 AW837697
	421813	207654_1	AA469153 A1718503 AA469225
	422760	221034_1	A1204995 AW827539 AW969908 AW440776 AA528756
	425526	252776_1	AF038171 Z43209 F07347
	430212	314437_1	AW974956 AW781075 AA654944
45			AF230801 AF230800 AA401795 AA398260
	432222	343347_1	AL390174 AW898817
	433389	36497_1	BE560093
	434961	396357_1	AV645470 T84636 T82805
	435752	41050_1	AA358760 AA158850 AW062737 AW062738 AV656291
	437483	43756_1	AV657159 BE145509 BE145512 BE145505 BE145507
50			T58148 AW516579 AW059603
	440198	48824_2	BE243534 BE243752 A1880228 L44326
	443509	57199_1	A1904296 BE007223 R30687
	446052	65988_1	BE394588 AW024754 BE183166 BE183167
	446218	66686_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW07582 AW177581
	447135	70963_1	BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
55			BE141749 AW177598
	452346	912206_1	AW381980 BE152244 BE152235 BE152238 BE152232
	452502	919733_1	AW857077 AW861268 AW847383 AW795787
	454065	998401_1	AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801767
	454186	1049791_1	AW812807 AW812815 AW812802
60			AW852286 AW851934 AW852096 AW852274
	454339	1122972_1	AW996689 AW996380 AW996453 BE085650 AW868687 BE085595
	454486	1215703_1	BE006341 BE006307 BE006311
	454506	1219857_1	BE078070 BE061030 BE077927
	454673	1228668_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067953 BE067956 BE067946
65			BE155527 BE155503 BE155188 BE155126
	455040	1250028_1	AA203637 AA832266 H67452
	455225	1262318_1	AW968614 AA243209 AA281411
	455577	1333898_1	AW972675 AA541366 AA523039
	455617	1346117_1	BE155356 BE153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 A1903640 BE155492
	455697	1351148_1	
70			
	455901	1381569_1	
	456235	168686_1	
	456407	184986_1	
	457452	339381_1	
	459150	919196_1	
75		TABLE 10C:	
		Pkey:	Unique number corresponding to an Eos probeset
		Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
80		Strand:	Indicates DNA strand from which exons were predicted.
		Nt_position:	Indicates nucleotide positions of predicted exons.
		Pkey	Ref
		400661	8118474
			Strand
			Plus
			Nt_position
			84912-85187

5	400685	8118768	Minus	72969-73050,73713-73800
	400865	1945037	Minus	44482-45526
	400878	9864757	Plus	31493-32842
	401024	8117489	Plus	60551-60802
	401315	9212516	Minus	198960-199619
	401485	7341723	Plus	68009-68209,68841-69077
	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
10	401738	2982169	Minus	41547-41757
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
15	402176	7543687	Minus	10-750
	402546	7637348	Plus	24673-25170
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
20	403796	8099896	Minus	75073-77664
	404391	3135305	Minus	26030-26173,27852-27997
	404769	8099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
25	404907	7331453	Minus	102880-103828
	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
30	405354	2642452	Plus	52213-53089
	405377	5649375	Plus	216656-216848
	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
35	405800	2791346	Plus	19271-19813
	405867	6758731	Minus	74553-75173
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

40	TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES				
	Table 11A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.				
45	Pkey: Unique Eos probeset identifier number				
	ExAccn: Exemplar Accession number, Genbank accession number				
50	UnigeneID: Unigene number				
	Unigene Title: Unigene gene title				
	R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor				
	R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue				

55	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6	25.8
60	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
65	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6	16.5
	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
70	442593	R39804	Hs.31961	ESTs	10.8	15.0
	446353	AI290919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
75	412454	R55745	Hs.167330	ESTs	9.5	14.1
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0	14.7
80	412453	R20205	Hs.167330	ESTs	9.0	13.7
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
	409031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.2	8.3

	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)		
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	8.0	8.9
	437073	AJ885608	Hs.94122	ESTs	7.9	9.6
5	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9	11.3
	440209	H05049	Hs.22269	neurexin 3	7.9	16.4
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	7.8	34.3
	429611	AJ889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.8	9.0
	423440	R25234	Hs.143434	contactin 1	7.7	5.0
10	445148	AI214510	Hs.145304	ESTs	7.7	9.9
	416294	D86980	Hs.79170	KIAA0227 protein	7.6	9.1
	424087	N69333	Hs.143434	contactin 1	7.6	7.6
	437479	R61866	Hs.101277	ESTs	7.6	10.3
	430573	AA744550	Hs.136345	ESTs	7.5	9.3
15	448958	AB020651	Hs.22653	KIAA0844 protein	7.1	2.8
	419474	AW968619	Hs.155849	ESTs	7.1	10.4
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.1	3.0
	433098	AW190593	Hs.151143	ESTs	7.0	6.9
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	7.0	9.2
20	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.9	3.1
	443155	R54485	Hs.23772	ESTs	6.8	5.0
	450561	R49674	Hs.25909	ESTs	6.8	3.5
	433068	NM_006456	Hs.288215	sialyltransferase	6.8	8.1
	423589	AA328082	Hs.209569	ESTs	6.8	2.0
25	415681	AI379882	Hs.72630	ESTs	6.6	10.5
	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.5	9.0
	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	7.1
	450642	R39773	Hs.7130	copine IV	6.4	9.5
	429322	D86984	Hs.199243	KIAA0231 protein	6.4	5.7
30	447482	AB033059	Hs.18705	KIAA1233 protein	6.4	8.2
	446129	AW244073	Hs.145946	ESTs	6.4	2.3
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3	8.3
	434273	AA913143	Hs.26303	ESTs	6.3	2.1
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2	10.3
35	451301	AI769514	Hs.209890	EST	6.2	3.5
	438356	AA805530	Hs.48527	ESTs	6.2	12.4
	426388	AW081394	Hs.97103	ESTs	6.2	8.1
	452502	AI904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.2	8.6
40	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (I	6.1	2.8
	442979	AW440782	Hs.174743	ESTs	6.1	6.3
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.1	6.3
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	6.0	3.8
	425087	R62424	Hs.126059	ESTs	5.9	21.4
	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9	8.1
45	417175	R44558	Hs.94002	ESTs	5.9	3.1
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8	12.5
	436427	AI344378	Hs.143399	ESTs	5.8	2.2
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.8	13.8
50	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7	4.4
	442676	AI733585	Hs.130897	ESTs	5.7	12.5
	446443	AV659082	Hs.134228	ESTs	5.7	6.8
	459080	AW192083	Hs.290855	ESTs	5.7	6.4
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	5.6	15.6
55	428356	AL046991	Hs.10338	ESTs	5.6	8.2
	417877	AI025829	Hs.86320	ESTs	5.6	6.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.4	4.9
	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3	13.1
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.3	6.6
60	438285	AA782845	Hs.22790	ESTs	5.2	6.0
	439901	N73885	Hs.124169	ESTs	5.2	7.3
	449222	AW293984	Hs.197621	ESTs	5.2	2.7
	408016	AW136827	Hs.256096	ESTs	5.2	8.1
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1	2.5
65	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1	3.0
	409263	AA069573	Hs.50319	ESTs	5.1	7.3
	453830	AA534296	Hs.20953	ESTs	5.1	12.9
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.1	3.4
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0	4.8
70	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0	20.1
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0	3.9
	442240	AI791883	Hs.292719	ESTs	5.0	6.1
	427972	AA864870	Hs.181304	putative gene product	4.9	6.7
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9	5.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.9	2.8
75	408936	AL138043	Hs.293549	ESTs	4.8	3.7
	414943	D80647	Hs.124193	ESTs	4.8	6.6
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8	3.1
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (I	4.8	2.3
	416577	BE063207	Hs.79381	grancalcin	4.8	9.1
80	420480	AL137361	Hs.98173	hypothetical protein	4.7	2.2
	404793				4.7	2.8
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6	2.2
	438571	AW020775	Hs.56022	ESTs	4.6	7.4
	444585	AW170015	Hs.6594	ESTs	4.6	5.4
					4.6	6.0

5	414272	AI651603	Hs.46988	ESTs	4.5	2.2
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5	30.9
	423449	AI497900	Hs.33067	ESTs	4.5	20.8
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4	19.2
10	429726	AW628326	Hs.27151	ESTs	4.4	10.2
	449093	AB035356	Hs.22998	neurexin 1	4.4	9.4
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4	15.1
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4	8.2
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4	2.4
15	435078	AIW518888	Hs.40937	ESTs	4.4	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3	5.9
	426867	AA460967	Hs.22668	ESTs	4.3	6.0
	412112	BE180342		gb:RC3-HT0622-130400-012-s07 HT0622 Homo	4.3	3.2
	410171	H07892	Hs.12431	ESTs	4.3	5.3
20	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2	5.0
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5'/3'	4.2	3.5
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2	3.9
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin 1	4.1	7.0
25	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypothe	4.1	3.9
	408496	AI683802	Hs.136182	ESTs	4.1	4.7
	434101	AA625205	Hs.259599	KIAA1622 protein	4.1	6.3
	430212	AA469153		gb:nc6704.s1 NCL_CGAP_Pr1 Homo sapiens	4.0	2.5
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0	7.4
30	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0	32.3
	429628	H09604	Hs.13268	ESTs	4.0	4.5
	410087	F12079	Hs.332579	ESTs	4.0	6.9
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.0	2.6
35	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9	21.7
	412677	AW029608	Hs.17384	ESTs	3.9	2.2
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9	7.2
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9	2.2
	414666	NM_004466	Hs.76828	glypican 5	3.8	6.2
40	418217	AI910647	Hs.13442	ESTs	3.8	3.2
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	ESTs	3.8	10.7
	433629	R13140	Hs.13359	ESTs	3.7	2.7
	424738	AI963740	Hs.46826	ESTs	3.7	2.1
45	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7	5.3
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.7	53.7
	423135	N67655	Hs.26411	ESTs	3.7	21.7
	446818	AI342668	Hs.279765	ESTs	3.7	2.6
	427562	R56424	Hs.26534	ESTs	3.6	3.6
50	439274	AF086092	Hs.48372	ESTs	3.6	34.5
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6	6.0
	422897	AA679784	Hs.4290	ESTs	3.6	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6	24.6
	417154	AI674701	Hs.21388	ESTs	3.6	5.8
55	447176	Z42549	Hs.160893	ESTs	3.6	6.4
	405977				3.6	3.9
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fs, clone C	3.6	5.4
	426775	AA384564	Hs.108829	ESTs	3.6	3.4
60	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6	2.8
	425153	AW023193	Hs.27046	ESTs	3.6	4.9
	446495	D60923	Hs.153460	ESTs	3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
65	418207	C14685	Hs.34772	ESTs	3.5	16.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5	6.2
	417027	AA192306	Hs.23926	triadin	3.5	2.5
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothe	3.5	5.5
70	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5	23.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5	42.3
	433803	AI823593	Hs.27688	ESTs	3.4	3.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4	9.8
75	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4	4.7
	427173	BE255017	Hs.97540	ESTs	3.4	2.4
	446092	N33522	Hs.145894	ESTs	3.4	3.5
	416868	AI656856	Hs.292597	ESTs	3.4	4.5
	458234	BE551408	Hs.127196	ESTs	3.4	4.5
80	434053	AW445136	Hs.134946	ESTs	3.4	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.3	42.3
	410366	AI267589	Hs.302689	hypothetical protein	3.3	14.4
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3	4.6
	434998	AW975157	Hs.26037	ESTs	3.3	4.7
	456359	AI967991	Hs.93574	homeo box D3	3.3	4.4
	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type 1, b	3.3	5.2
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3	9.0

5	419875	AA853410	Hs.93557	proenkephalin		
	444612	AW138111	Hs.22902	ESTs	3.3	3.6
	415242	R45986	Hs.295014	ESTs	3.3	3.0
	421640	AW96652		gb:EST378726 MAGE resequences, MAGI Homo	3.2	2.2
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2	3.8
10	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2	2.4
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2	3.2
	403092				3.2	2.2
	452971	AI873878	Hs.91789	ESTs	3.2	2.9
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2	4.5
15	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2	2.7
	421200	AA284811	Hs.264433	ESTs	3.2	2.8
	440827	AI733110	Hs.128128	ESTs	3.2	2.7
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2	2.1
	420156	AW449258	Hs.6187	ESTs	3.2	4.3
20	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2	19.0
	419956	AL137939	Hs.40096	ESTs	3.2	2.0
	423930	AA332697	Hs.42721	ESTs	3.1	8.7
	417868	AI078534	Hs.122592	ESTs	3.1	2.7
	423346	AI267677	Hs.127416	synaplojanin 1	3.1	12.6
25	441921	AI733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1	12.0
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1	4.3
	408217	AI433201	Hs.279860	tumor protein, translationally-controlled	3.1	5.3
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	7.1
	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	6.3
30	429608	U49250	Hs.210862	T-box, brain, 1	3.1	30.1
	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1	2.2
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1	3.0
	427865	AA416931	Hs.126065	ESTs	3.1	10.9
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1	7.5
35	451829	AW964081	Hs.247377	ESTs	3.1	3.4
	405911				3.0	6.2
	418808	AI821836	Hs.10359	ESTs	3.0	2.4
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0	6.2
	423952	AW877787	Hs.136102	KIAA0853 protein	3.0	5.1
40	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0	2.1
	405793				3.0	2.1
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	2.7
	427071	AA397958	Hs.192719	ESTs	3.0	14.3
	453534	NM_014796	Hs.33187	KIAA0748 gene product	3.0	2.1
45	413903	AA496493	Hs.23136	ESTs	3.0	14.5
	426866	U02330	Hs.172816	neuregulin 1	3.0	2.2
	434945	AB033065	Hs.4280	KJAA1239 protein	3.0	11.3
	412639	AW961284	Hs.296235	ESTs	3.0	3.5
	453590	AF150278	Hs.33578	KIAA0820 protein	2.9	4.9
50	414502	AL133721	Hs.224680	ESTs	2.9	33.1
	434367	AB020700	Hs.3830	KIAA0893 protein	2.9	2.3
	425121	AI797511	Hs.154679	synaptotagmin I	2.9	23.1
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.9	8.1
	401213				2.9	20.8
55	401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9	3.2
	415191	AA190381	Hs.120810	ESTs	2.9	3.4
	449275	AW450848	Hs.205457	periaxin	2.9	3.0
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.9	5.6
	411421	BE272110	Hs.21177	ESTs	2.9	35.0
60	430865	AI073424	Hs.5232	HSPC125 protein	2.9	2.0
	437486	AW952089	Hs.5636	RABGA, member RAS oncogene family	2.9	11.4
	442357	AI458586	Hs.135706	ESTs	2.9	2.2
	408274	R17315		gb:yg12g11.1 Soares infant brain 1N1B H	2.9	6.0
	444185	AW298350	Hs.66020	ESTs	2.9	2.2
65	420173	AA256151	Hs.22999	ESTs	2.8	5.0
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.8	5.1
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	2.8	7.0
	440260	AI972867	Hs.7130	copine IV	2.8	4.4
	417084	H08370	Hs.33067	ESTs	2.8	10.6
70	438257	AW474419	Hs.224794	ESTs	2.8	8.4
	441934	T23939	Hs.7344	ESTs	2.8	2.8
	447885	F11528	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	2.8	6.2
	423552	AF107028	Hs.129783	sodium channel, voltage-gated, type II,	2.8	3.5
	450940	AI744943	Hs.143209	ESTs, Weakly similar to I38022 hypothesi	2.8	3.4
75	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.8	14.4
	445887	AI263105	Hs.145597	ESTs	2.8	21.7
	425494	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr	2.8	5.1
	438202	AW169287	Hs.22588	ESTs	2.8	2.4
	436199	R38946	Hs.127951	hypothetical protein FLJ14503	2.8	11.9
80	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.8	6.0
	415462	R52692	Hs.12698	ESTs	2.8	2.4
	418070	NM_000844	Hs.83407	glutamate receptor, metabotropic 7	2.8	3.4
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.8	4.5
	430371	D87466	Hs.240112	KIAA0276 protein	2.8	9.5
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp762Q2215 (f	2.7	7.0
	415838	R44336	Hs.7093	ESTs	2.7	2.5
	438675	AA813725	Hs.213568	ESTs	2.7	3.6
					2.7	2.5

	419558	AW953679		gb:EST365749 MAGE resequences, MAGC Homo	2.7	3.1
	446318	AI949389	Hs.18067	ESTs	2.7	4.1
	445183	AB007877	Hs.12385	KIAA0417 gene product	2.7	5.3
	457012	R41480	Hs.127630	ESTs	2.7	19.0
5	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	7.2
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.7	2.8
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.7	3.8
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.7	6.9
	434731	AA648049	Hs.121518	ESTs	2.7	5.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
	407709	AA456135	Hs.23023	ESTs	2.7	2.5
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	2.7	3.3
	443305	AI050693	Hs.133318	ESTs	2.7	5.9
	435648	H24347	Hs.27524	ESTs	2.7	15.0
15	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.7	2.7
	436771	AW975687	Hs.292979	ESTs	2.7	6.0
	428689	NM_014351	Hs.189810	sulfotransferase family 4A, member 1	2.7	4.8
	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamma	2.7	4.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.7	3.1
20	410330	AW023630	Hs.46786	ESTs	2.6	29.5
	434398	AA121098	Hs.3838	serum-inducible kinase	2.6	2.6
	438831	BE263273	Hs.6439	synapsin II	2.6	7.8
	419066	Z98492	Hs.6975	PRO1073 protein	2.6	3.4
	412643	AW971239	Hs.293982	ESTs	2.6	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	2.6	17.9
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6	2.9
	401421				2.6	2.0
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	2.6	3.8
30	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583	AW994403	Hs.100861	hypothetical protein FLJ14600	2.6	3.7
	417919	AI928203	Hs.86379	ESTs	2.6	3.0
	434293	NM_004445	Hs.3796	EphB6	2.6	3.2
35	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6	6.4
	443037	AW500305	Hs.299166	syntaxin 7	2.6	2.2
	440736	D56919	Hs.265848	myomegalin	2.6	7.1
	404548				2.6	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
40	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.6	3.9
	441190	H09073	Hs.25046	ESTs	2.6	3.1
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.6	2.9
	442731	AI868167	Hs.131044	ESTs	2.6	4.1
	416836	D54745	Hs.80247	cholecystokinin	2.6	14.9
45	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
	436321	AA709133	Hs.180144	ESTs	2.5	2.8
	439693	AI741816	Hs.125897	ESTs	2.5	3.6
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664	Homo sapiens mRNA; cDNA DKFZp434A1627 (f	2.5	3.8
50	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	2.5	3.1
	443992	AW022228	Hs.322922	ESTs	2.5	27.9
	444124	R43097	Hs.6818	ESTs	2.5	5.3
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.5	38.0
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	2.5	3.8
55	446277	AI284218	Hs.159204	ESTs	2.5	2.2
	410111	AI620206	Hs.189647	ESTs	2.5	3.5
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	2.5	4.8
	410718	AI920783	Hs.191435	ESTs	2.5	4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
60	420274	AW968000	Hs.143389	ESTs, Weakly similar to T14318 ubiquitin	2.5	2.8
	433496	AF064254	Hs.49765	VLCS-H1 protein	2.5	4.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	2.5	3.3
	437368	AI471969	Hs.182606	ESTs	2.5	3.0
65	441985	BE047625	Hs.169815	ESTs	2.5	3.6
	410025	BE220489	Hs.113592	ESTs, Moderately similar to I54374 gene	2.5	9.2
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.5	3.6
	429956	AI374651	Hs.22542	ESTs	2.5	23.9
	429028	AA443439	Hs.48797	ESTs	2.5	2.8
	438109	AI076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.5	2.3
	440888	N45600	Hs.326880	ESTs	2.5	3.9
	445246	AI217713	Hs.147586	ESTs	2.5	2.6
	440152	AB002376	Hs.7006	KIAA0378 protein	2.4	23.6
	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	2.4	2.1
75	415122	D60708	Hs.22245	ESTs	2.4	3.9
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	2.4	9.8
	437948	AA772920	Hs.303527	ESTs	2.4	9.8
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-b	2.4	2.8
	427115	AW972853	Hs.112237	ESTs	2.4	2.2
80	452074	BE299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4	10.0
	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-activat	2.4	3.5
	434520	AA205273	Hs.177011	hypothetical protein	2.4	3.1
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.4	3.0

5	442272	AA988302	Hs.129172	ESTs		
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.4	2.1
	444647	H14718	Hs.11506	Human clone Z3589 mRNA sequence	2.4	2.7
	415827	H17462	Hs.23079	ESTs	2.4	2.8
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.4	15.0
10	445200	AA084460	Hs.12409	somatostatin	2.4	3.9
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	2.4	3.7
	420328	Y19062	Hs.96870	staurin (Drosophila, RNA-binding protein	2.4	2.4
	432122	AA526514		gb:n160f02.s1 NCL_CGAP_Ov2 Homo sapiens	2.4	4.3
	444125	AI124882	Hs.118121	ESTs	2.4	4.3
15	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.4	3.5
	457519	X69438	Hs.3052	early growth response 4	2.4	10.8
	409371	R51736	Hs.12381	ESTs	2.4	2.4
	456303	AA224872	Hs.115088	ESTs	2.4	2.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.4	3.2
20	400979				2.4	23.4
	435296	R49685	Hs.24980	ESTs	2.4	4.1
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4	6.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	18.5
	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.4	2.2
25	408974	AW015458	Hs.297017	ESTs	2.4	2.7
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	2.4	2.5
	413153	N94205		gb:za27a08.r1 Soares fetal liver spleen	2.4	2.8
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	2.5
	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.4	2.6
30	424940	AA985308	Hs.194327	ESTs	2.3	3.0
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	2.3	6.3
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	2.3	4.1
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.3	2.9
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.3	8.7
35	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.3	3.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	2.3	5.2
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	2.3	54.7
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	9.1
	414828	AA156651		gb:z105h05.r1 Soares_pregnant_uterus_NbH	2.3	5.0
40	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3	2.4
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	2.3	8.5
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	2.3	26.3
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	2.3	2.5
	439450	R51613	Hs.125304	ESTs	2.3	7.6
45	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	2.3	26.3
	447179	AW015633	Hs.157299	ESTs	2.3	2.2
	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	2.3	3.8
	433449	AW772282		gb:hn71b05.x1 NCL_CGAP_Kid11 Homo sapien	2.3	2.3
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.8
50	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.3	2.5
	425130	AA448208	Hs.99163	ESTs	2.3	7.8
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	4.1
	438283	AA58931	Hs.37282	ESTs	2.3	2.5
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.3	4.2
55	412100	AW892731		gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.0
	448981	AI968719	Hs.195387	ESTs	2.3	3.7
	416101	R24854	Hs.268806	ESTs	2.3	3.2
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	2.3	6.5
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	17.8
60	424596	AB020639	Hs.151017	estrogen-related receptor gamma	2.3	40.1
	420230	AL034344	Hs.284186	forkhead box C1	2.3	2.9
	451559	AL119980	Hs.20935	hypothetical protein DKFZp761D221	2.3	2.4
	404835				2.3	5.7
	456765	AI497900	Hs.33067	ESTs	2.3	2.1
65	455517	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	2.3	4.1
	408206	AF041853	Hs.43670	kinesin family member 3A	2.3	2.4
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.2	18.5
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	2.2	3.9
	458694	F12832	Hs.13298	ESTs	2.2	2.6
70	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.9
	439642	W81441	Hs.153967	ESTs	2.2	4.4
	450138	AW152104	Hs.200879	ESTs	2.2	2.4
	454222	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	2.2	4.9
	405326				2.2	3.7
75	431342	AW971018	Hs.21659	ESTs	2.2	2.7
	453101	AW952776	Hs.94943	ESTs	2.2	5.2
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	2.2	3.3
	451398	AI793124	Hs.144479	ESTs	2.2	2.8
	438208	AL041224	Hs.65379	ESTs	2.2	4.6
80	408449	NM_004408	Hs.166161	dynamitin 1	2.2	10.4
	414130	AI670831	Hs.71592	Homo sapiens cDNA: FLJ21893 fis, clone H	2.2	6.1
	445016	U79716	Hs.12246	retin	2.2	3.1
	424375	AF070547	Hs.146312	Homo sapiens clone 24820 mRNA sequence	2.2	3.9
	424645	NM_014682	Hs.151449	KIAA0535 gene product	2.2	2.3
	409729	D51315	Hs.106289	ESTs	2.2	11.7
	432809	AA565509	Hs.131703	ESTs	2.2	4.9
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.2	19.9
					2.2	10.4

	428532	AF157326	Hs.184786	TBP-interacting protein	2.2	6.5
	413074	AI871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
	452768	AW069459	Hs.61539	ESTs	2.2	2.0
5	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.2	3.2
	426281	AK000987	Hs.169111	oxidation resistance 1	2.2	2.3
	428411	AW291464	Hs.10338	ESTs	2.2	2.3
	413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	2.2	3.1
10	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	7.9
	405385				2.2	2.4
	447285	AI371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	452667	T87219	Hs.13219	ESTs	2.2	3.1
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	2.1	8.3
15	410339	AI916499	Hs.298258	ESTs	2.1	3.2
	413231	D87461	Hs.75244	BCL2-like 2	2.1	4.5
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	2.1	2.2
	451952	AL120173	Hs.301663	ESTs	2.1	36.5
	415841	Z45637	Hs.7093	ESTs	2.1	2.4
20	441086	AI928489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1	2.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.1	5.3
	449712	R56545	Hs.6100	ESTs	2.1	4.5
25	409660	AW452065	Hs.258905	ESTs	2.1	2.1
	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1	5.4
	434138	AA625804		gbzu86h01.s1 Soares_testis_NHT Homo sap	2.1	3.0
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	2.1	4.8
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.1	2.9
30	414876	AW950925	Hs.924	crystallin, mu	2.1	3.4
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.7
	451249	AA016227	Hs.27280	ESTs	2.1	4.1
	451475	T19093	Hs.26450	KIAA0725 protein	2.1	2.1
	448743	AB032962	Hs.21896	KIAA1136 protein	2.1	29.7
	430814	U89336	Hs.247993	NG5 protein	2.1	2.7
35	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.1	2.3
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	G antigen 7B	2.1	2.2
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	2.1	2.3
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	2.1	5.9
40	446383	T05816	Hs.92511	ESTs	2.1	2.9
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	2.1	2.1
	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111	R39039	Hs.328455	EST	2.1	3.3
	452238	F01811	Hs.187931	ESTs	2.1	4.9
45	445279	R41900	Hs.22245	ESTs	2.1	9.8
	448799	AI937094	Hs.179080	ESTs	2.1	3.1
	418338	NM_002522	Hs.84154	neuronal pentraxin I	2.1	8.3
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	4.1
50	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
	429954	AI918130	Hs.21374	ESTs	2.1	7.2
	415292	H29016	Hs.200576	ESTs	2.1	3.9
	423563	R34734	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.1	3.1
55	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	2.1	4.7
	459309	AA040620	Hs.5672	hypothetical protein AF140225	2.1	2.2
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	2.1	5.4
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin	2.1	6.6
60	448792	R42550	Hs.12826	ESTs	2.1	4.1
	449500	AW956345	Hs.12926	ESTs	2.1	2.4
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	2.1	5.8
	433361	AW469373	Hs.300141	ribosomal protein L39	2.1	2.7
	452946	X95425	Hs.31092	EphA5	2.1	5.0
65	426167	AF039023	Hs.167496	RAN binding protein 6	2.0	2.2
	453666	AW015681	Hs.135229	ESTs, Weakly similar to A2BP_HUMAN ATAXI	2.0	3.1
	424632	AB014523	Hs.151406	KIAA0623 gene product	2.0	3.5
	448589	AF017090	Hs.21554	KIAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
70	445627	AW618475	Hs.7363	ESTs	2.0	2.1
	417092	H97508	Hs.181165	eukaryotic translation elongation factor	2.0	2.5
	453653	AW505554	Hs.144559	ESTs	2.0	4.7
	435850	AF250847	Hs.283514	mitochondrial ceramidase	2.0	3.7
	435086	AW975243	Hs.122596	ESTs	2.0	2.1
75	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.0	2.8
	431645	AF078849	Hs.266483	dynein light chain-A	2.0	2.5
	429834	AI929645	Hs.225936	synapsin I	2.0	3.6
	439607	BE540565	Hs.159460	ESTs	2.0	17.5
80	408033	AW138045	Hs.242256	ESTs	2.0	4.0
	430317	AB020645	Hs.239189	glutaminase	2.0	2.7
	419631	AW188117	Hs.303154	popeye protein 3	2.0	2.6
	432660	AI288430	Hs.64004	ESTs	2.0	2.3
	454048	H05626	Hs.6921	ESTs	2.0	15.9

5	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0	3.1
	423246	AL119114	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alp	2.0	2.9
	415989	AI267700	Hs.317584	ESTs	2.0	4.8
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORTI	2.0	5.1
	424983	AI742434	Hs.169911	ESTs	2.0	15.9
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.0	2.7
	450006	AI241555	Hs.60171	ESTs	2.0	3.5

TABLE 11B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

15	Pkey	CAT Number	Accession
	408274	104999_1	R17315 Z43964 AA053547
	412100	1277224_1	AW892731 H08502 Z45826
20	412112	1277883_1	BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 AW893614 AW893615 H85799 H83501 BE180220
	413153	1350849_1	N94205 BE067565 BE067556
	413510	1374377_1	F13044 T77009 BE145525 BE145493
25	414828	149563_1	AA156651 AA156622 R14472
	418948	180806_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	419558	185904_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
30	421249	200649_1	AA285362 AW752386 AW847156 AA285373 AW879575 AW879558
	421640	204833_1	AW966652 AW966653 AA294989 AA385977
	429995	311738_1	AA463571 AI277645 AL118763
35	430212	314437_1	AA469153 AI718503 AA469225
	432122	341756_1	AA526514 AW973343 AA554293
	433449	366532_1	AW772282 AA592974
40	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	437483	43756_1	AL390174 AW898817
	439780	47673_1	AL109688 R23665 R26578
45	452502	919733_1	AI904296 BE007223 R30687
	455517	1321782_1	AW984068 AW984072 AW984077
	456407	184986_1	AW98614 AA243209 AA281411

TABLE 11C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	Nt_position
	400979	8072554	Plus	160842-161028
	401213	9858408	Plus	98243-98380,98489-98619
50	401421	7452889	Minus	142291-142461
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	404648	9796894	Minus	115334-116020
55	404793	7232206	Minus	61087-61590
	404835	6970743	Plus	85462-85684,88139-88287,90338-91018,94827-94990
	405326	4375975	Plus	10633-10709,30805-30893,38078-38253,55112-55327,57718-57818,66696-66841
60	405385	6552772	Plus	48332-48454
	405793	1405887	Minus	89197-89453
	405911	6758795	Plus	101008-101643
65	405977	8247789	Minus	135548-136177

TABLE 12A: ABOUT 678 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 12A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 2.5. The "average" LGG level was set to the 85th percentile amongst various LGG tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of LOWER GRADE GLIOBLASTOMA to normal CNS

75	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	20.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	19.5
80	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	18.5
	402604			Target Exon	16.9
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	15.0
85	409638	AW450420	Hs.21335	ESTs	14.0
	443731	AI083928	Hs.145418	ESTs	14.0
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	13.6
90	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.2
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	10.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	9.5

	425187	AW014486	Hs.22509	ESTs	9.0
	440210	AW674562	Hs.125296	ESTs	8.8
	448769	N68037	Hs.38173	ESTs	8.4
5	437034	AA742643	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens		8.2
	449539	W80363	Hs.58446	ESTs	8.1
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.0
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	7.8
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	7.7
10	449300	AI656959	Hs.346514	ESTs	7.6
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	7.5
	452372	AI885742	Hs.228474	ESTs	7.2
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi)	7.2
	417308	H60720	Hs.81892	KIAAD101 gene product	7.2
	447004	AW296968	Hs.157539	ESTs	7.1
15	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.1
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	7.1
	406478			Target Exon	7.1
	428728	NM_016625	Hs.191381	hypothetical protein	6.9
20	414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	6.9
	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7
	423343	AA324643	Hs.246106	ESTs	6.7
	418097	R45137	Hs.21868	ESTs	6.7
	431553	X78075	Hs.2799	cartilage linking protein 1	6.6
25	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.6
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.4
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheri	6.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.4
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
30	402855			NM_001839: Homo sapiens calponin 3, acid	6.2
	424009	F11690		gb:HSC30D041 normalized infant brain cDN	6.2
	400419	AF084545		Target	6.2
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	6.0
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	6.0
35	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	5.9
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	5.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.8
	405238			Target Exon	5.7
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	5.7
40	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	5.6
	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	5.4
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	5.3
	403349	NM_001406		ephrin-B3	5.3
	453941	U39817	Hs.36820	Bloom syndrome	5.2
45	429139	F09092	Hs.66087	ESTs	5.2
	454860	AW835767		gb:OV4-LT0016-240200-110-b08 LT0016 Homo	5.2
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.1
	418030	BE207573	Hs.83321	neuromedin B	5.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
50	450639	AI703186	Hs.277174	ESTs	5.1
	412811	H06382		ESTs	5.1
	442832	AW206560	Hs.253569	ESTs	5.1
	436608	AA628980		down syndrome critical region protein DS	5.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	5.1
55	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.1
	447497	AW167254	Hs.205722	ESTs	5.0
	450811	AI739486	Hs.245497	ESTs	5.0
	433244	AB040943	Hs.271285	KIAA1510 protein	4.9
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.9
60	438456	AA913381	Hs.20594	ESTs	4.9
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	4.9
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.9
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.9
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.8
65	402274			C19000498:gi4567179 gb AAD23607.1 AC00	4.8
	420092	AA814043	Hs.88045	ESTs	4.8
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.8
	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	4.8
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	4.8
70	403961			Target Exon	4.8
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	4.8
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	4.8
	447891	R41754	Hs.6496	ESTs	4.7
	423529	T87318	Hs.120411	ESTs	4.7
75	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.7
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.6
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	4.6
	403481			Target Exon	4.6
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.6
80	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.6
	416379	N38857	Hs.203933	ESTs	4.6
	406481			Target Exon	4.5
	456052	BE311901	Hs.28935	gb:601142614F1 NIH_MGC_14 Homo sapiens c	4.5
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5

5	411642	NM_014932	Hs.71132	neurofigin 1	4.5
	428282	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	4.5
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	4.5
	452994	AW962597	Hs.31305	KIAA1547 protein	4.5
	449961	AW265634	Hs.133100	ESTs	4.4
10	401454			NM_014226*:Homo sapiens renal tumor anti	4.4
	406395			Target Exon	4.4
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	4.4
	453792	AL134539	Hs.254129	KIAA1678	4.4
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	4.4
15	437695	AA769202	Hs.192142	ESTs	4.4
	422081	AW136820	Hs.196011	ESTs	4.4
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.3
	433323	AA805132	Hs.159142	ESTs	4.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3
20	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.3
	441035	AI694309	Hs.126458	ESTs	4.3
	443836	BE221613	Hs.140553	ESTs	4.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.3
	450166	AA429504		ESTs	4.3
25	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	4.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	451254	AI571016	Hs.172967	ESTs	4.2
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	4.2
	445118	AI208762	Hs.345572	ESTs	4.2
30	444326	AI939357	Hs.270710	ESTs	4.2
	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	4.2
	404120			C5000537*:gi3298595(gb)AAC41376.1} (AF0	4.2
	436899	AA764852	Hs.291567	ESTs	4.1
	407624	AW157431	Hs.248941	ESTs	4.1
35	453361	AA035197	Hs.107375	ESTs	4.1
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.1
	438372	AI140189	Hs.123191	ESTs	4.1
	438624	AA889055	Hs.123468	ESTs	4.1
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	4.1
40	406872	AI760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.1
	425295	AA431366	Hs.37251	ESTs	4.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	4.1
	434206	AW136973	Hs.180479	ESTs, Weakly similar to S69890 mitogen i	4.0
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	4.0
45	400645			Target Exon	4.0
	456306	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	4.0
	419326	W94915	Hs.42419	ESTs	4.0
	414948	C15240	Hs.182155	ESTs	4.0
	423198	M81933	Hs.1634	cell division cycle 25A	4.0
50	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	4.0
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.9
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE	3.9
55	449932	AI675444	Hs.263024	ESTs	3.9
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
	434784	AA649051	Hs.164007	ESTs	3.9
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	3.9
	428538	AA446440	Hs.98643	ESTs	3.9
60	443318	AI051603	Hs.133141	ESTs	3.9
	416857	AA188775	Hs.292453	ESTs	3.9
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	3.9
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	3.9
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.8
65	403696			C4001100*:gi35852342(gb)AAD54015.1} (AF0	3.8
	415884	H22966	Hs.13471	ESTs	3.8
	432646	AW753310		gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	447057	AI423407	Hs.157697	ESTs	3.8
	400814			Target Exon	3.8
70	441329	AI203575	Hs.46821	hypothetical protein FLJ20086	3.8
	416664	H72780	Hs.20289	ESTs	3.8
	426044	AA502490	Hs.170290	ESTs	3.8
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.8
	419043	T19167	Hs.89566	els variant gene 1	3.8
75	445075	AI651827	Hs.344767	ESTs	3.8
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.8
	420004	AW975532	Hs.164039	ESTs, Moderately similar to I38022 hypot	3.8
	428060	AA420616	Hs.249483	ESTs	3.7
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	3.7
80	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.7
	404584			Target Exon	3.7
	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	3.7
	453438	AI469935	Hs.22792	ESTs	3.7
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.7
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.7
	459660	M79082		ESTs	3.7
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.7

	430744	AA485229	Hs.105649	ESTs	3.7
	454392	BE260893	Hs.236131	homeodomain-interacting protein kinase 2	3.7
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	3.7
	435095	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	3.7
5	438206	AA780385	Hs.187885	ESTs	3.7
	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.7
	427809	M26380	Hs.180878	lipoprotein lipase	3.7
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	3.7
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	3.7
10	438898	AI819863	Hs.106243	ESTs	3.7
	418483	W26076	Hs.221847	ESTs	3.7
	415849	R20529	Hs.6806	ESTs	3.6
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.6
	440296	D30829	Hs.180610	splicing factor proline/glutamine rich (3.6
15	438025	AW501360	Hs.258910	ESTs	3.6
	458970	AW246119	Hs.25300	phosphatidylinositol 4-kinase type II	3.6
	448002	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.6
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
20	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	404185			Target Exon	3.6
	427517	AA644142	Hs.7107	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
25	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.6
	440388	AI693520	Hs.223000	ESTs	3.6
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	3.6
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	3.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.6
30	451826	AA020741	Hs.171611	ESTs	3.6
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	3.6
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.6
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	3.6
	418400	BE243026	Hs.301989	KIAA0246 protein	3.6
35	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	3.5
	407013	U35637		gb:Human nebulin mRNA, partial cds	3.5
	403108			ENSP00000241415: Hypothetical 67.7 kDa p	3.5
	422564	AI148006	Hs.222120	ESTs	3.5
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
40	436338	W92147	Hs.118394	ESTs	3.5
	447458	AI741082	Hs.158961	ESTs	3.5
	457364	AW971037		gb:EST383123 MAGE resequences, MAGK Homo	3.5
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.5
	441701	AW339828	Hs.127497	ESTs	3.5
45	405558			Target Exon	3.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.5
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.5
	443282	T47764	Hs.132917	ESTs	3.5
	405183			NM_016358: Homo sapiens iroquois homeobo	3.5
50	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	3.5
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	3.5
	404272			Target Exon	3.5
	428808	AA436007	Hs.188780	ESTs	3.5
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.5
55	450475	AW805634	Hs.205015	ESTs	3.4
	454451	AW846706		gb:QV3-CT0192-211099-008-g02 CT0192 Homo	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	440948	AW188311	Hs.128619	ESTs	3.4
	449611	AI970394	Hs.197075	ESTs	3.4
60	445666	R59960	Hs.282386	ESTs	3.4
	445828	F05802	Hs.81907	ESTs	3.4
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	3.4
	442927	AI024347	Hs.131519	ESTs	3.4
	451130	AI762250	Hs.345554	ESTs	3.4
65	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo	3.4
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.4
	433791	AA719352	Hs.112718	ESTs	3.4
	444911	U06117	Hs.250	xanthene dehydrogenase	3.4
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.4
70	440933	AI208217	Hs.142879	ESTs	3.4
	447726	AL137638	Hs.19368	matrilin 2	3.4
	403849			Target Exon	3.4
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	3.3
	439533	W76021		gb:zd64cd04.r1 Soares_fetal_heart_NbHH19W	3.3
75	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.3
	441668	AI611973	Hs.136313	ESTs	3.3
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	3.3
	412135	AW895309		gb:QV4-NN0038-300300-155-e07 NN0038 Homo	3.3
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	3.3
80	447854	AW138454	Hs.11594	ESTs	3.3
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.3
	404632			NM_022490: Homo sapiens hypothetical prot	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3

	436267	AW450938	Hs.180115	ESTs	3.3
	426625	T78300	Hs.300642	serologically defined colon cancer antig	3.3
	401272			C9000559:gi 12314195 emb CAB99338.1 (A	3.3
5	433128	AB021923	Hs.23367	EST-YD1 protein	3.3
	401702			NM_001171*:Homo sapiens ATP-binding cass	3.3
	454363	AW816274	Hs.250154	hypothetical protein FLJ12973	3.3
	440332	AI218517	Hs.188051	ESTs	3.3
	454177	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	3.3
10	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.3
	440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	3.3
	410267	AW978005	Hs.12600	N-ethylmaleimide-sensitive factor attach	3.3
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.2
15	451597	AW295250	Hs.207536	ESTs	3.2
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	3.2
	421353	AW292857	Hs.255130	ESTs	3.2
	442710	AI015631	Hs.23210	ESTs	3.2
	420560	AW207748	Hs.59115	ESTs	3.2
20	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2
	437834	AA769294	Hs.283854	gb:uz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.2
	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	3.2
	443431	AI056847	Hs.20654	ESTs	3.2
25	445774	AI254165	Hs.339968	ESTs	3.2
	413335	AI613318	Hs.48442	ESTs	3.2
	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.2
	411671	BE049094		ESTs	3.2
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	3.2
30	402747			Target Exon	3.2
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.2
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.2
	445347	AF035318	Hs.12533	Homo sapiens clone Z3705 mRNA sequence	3.2
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.2
35	442314	AI311854	Hs.129220	ESTs	3.2
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	3.2
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	3.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.2
	403291			Target Exon	3.2
40	436210	AI825420	Hs.197824	ESTs	3.2
	418079	R40058	Hs.6911	ESTs	3.2
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	3.2
	435828	AA700705	Hs.13852	ESTs	3.2
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	3.2
45	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.2
	405046			C3000978:gi 9280045 dbj BAB01579.1 (AB0	3.1
	444315	R07860	Hs.20039	ESTs	3.1
	453096	AW294631	Hs.11325	ESTs	3.1
50	433835	AI806185		gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.1
	430608	R45584	Hs.23025	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.1
	453324	W26592	Hs.232089	ESTs	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	446862	AV660697	Hs.282700	ESTs	3.1
55	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	3.1
	416486	H81336	Hs.37560	ESTs	3.1
	429940	W25215		gb:zb87a09.r1 Soares_senescent_fibroblas	3.1
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1
	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
60	437083	AW082597	Hs.244862	ESTs	3.1
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.1
	458810	BE407125	Hs.231510	ESTs	3.1
	443484	AI091458	Hs.134559	ESTs	3.1
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.1
65	444016	AA448154		gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.1
	403288			C1001737:gi 7511201 pir JT27904 hypothe	3.1
	450125	AA005418	Hs.158186	ESTs	3.1
	438138	R98299	Hs.177502	ESTs	3.1
70	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	3.1
	443433	R44743	Hs.301667	ESTs	3.1
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.1
	432044	AW972727		gb:EST384819 MAGE resequences, MAGL Homo	3.1
	405760			Target Exon	3.1
75	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	3.1
	411605	AW006831	Hs.177530	ESTs	3.1
	417893	AA290605	Hs.190002	ESTs	3.1
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	3.1
	429528	AI985303	Hs.99361	ESTs	3.1
	456645	AF227156	Hs.110103	RNA polymerase I transcription factor RR	3.1
80	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.1
	421679	AI475110	Hs.203933	ESTs	3.1
	434503	T96231	Hs.17762	ESTs	3.1
	450756	AI733488	Hs.144062	ESTs	3.1
	415293	R49462	Hs.106541	ESTs	3.0

	403212		NM_019595:Homo sapiens intersectin 2 (IT	3.0
	422757	AI909935	Hs.65551 Homo sapiens. Similar to DNA segment, Ch	3.0
	427624	AA406245	Hs.24895 ESTs	3.0
5	449256	AA059050	Hs.59847 ESTs	3.0
	411543	AW851248	gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	409112	BE243971	Hs.50649 quinone oxidoreductase homolog	3.0
	414403	AW969551	Hs.76064 ribosomal protein L27a	3.0
	427418	AA402587	Hs.325520 LAT1-3TM protein	3.0
10	455481	AW948317	gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	444396	T65213	Hs.4257 ESTs	3.0
	407235	D20569	Hs.169407 SAC2 (suppressor of actin mutations 2, y	3.0
	431431	AL096711	Hs.252953 Human DNA sequence from clone RP3-403A15	3.0
	451391	AA017410	Hs.40568 ESTs	3.0
15	430251	AA609246	Hs.181451 ESTs	3.0
	420658	AW965215	Hs.130707 ESTs	3.0
	442786	H50733	Hs.256261 ESTs, Moderately similar to ALU8_HUMAN A	3.0
	440897	AW104275	Hs.148348 ESTs	3.0
	444609	AW571659	Hs.278081 ESTs	3.0
20	433062	AK001757	Hs.281348 hypothetical protein FLJ10895	3.0
	408523	AW833259	Hs.314287 ESTs	3.0
	443477	R32325	Hs.221794 ESTs	3.0
	423869	BE409301	Hs.134012 C1q-related factor	3.0
	405488		ENSP00000220888*:ZINC FINGER TRANSCRIPTI	3.0
25	414988	C17535	gb:C17535 Human placenta cDNA (TFujwara	3.0
	440471	AA886146	Hs.307944 ESTs	3.0
	416355	H49875	Hs.268906 ESTs	3.0
	408926	AF217525	Hs.49002 Down syndrome cell adhesion molecule	3.0
	424028	AF055084	Hs.153692 Homo sapiens cDNA FLJ14354 fis, clone Y7	2.9
30	438201	AA780243	Hs.54647 ESTs	2.9
	413851	AW897510	Hs.137387 ESTs	2.9
	402229	BE262804	mitochondrial ribosomal protein S2	2.9
	444145	BE153823	Hs.282385 ESTs, Weakly similar to 2004399A chromos	2.9
	423770	AW976766	Hs.132776 Homo sapiens cDNA FLJ10077 fis, clone HE	2.9
35	439627	BE621702	Hs.29076 hypothetical protein FLJ21841	2.9
	414232	W86946	Hs.238246 hypothetical protein FLJ22479	2.9
	400533		ENSP00000209376*:PRED65 protein (Fragmen	2.9
	440483	AI200836	Hs.150386 ESTs	2.9
	443502	AI074528	Hs.133949 ESTs	2.9
40	449667	AB023227	Hs.23860 KIAA1010 protein	2.9
	446809	AW590171	Hs.101413 ESTs	2.9
	408788	AL134947	Hs.213956 Homo sapiens BAC clone RP11-1020S from Y	2.9
	413627	BE182082	Hs.246973 ESTs	2.9
	449655	AI021987	Hs.59970 ESTs	2.9
45	407378	AA299264	Hs.57776 ESTs, Moderately similar to I38022 hypot	2.9
	400090		Eos Control	2.9
	454968	AW849046	gb:IL3-CT0214-150300-085-H06 CT0214 Homo	2.9
	423352	AA324808	Hs.193576 ESTs	2.9
	426197	AA004410	Hs.100009 acyl-Coenzyme A oxidase 1, palmitoyl	2.9
50	452102	U04343	Hs.27954 CD86 antigen (CD28 antigen ligand 2, B7-	2.9
	415346	Z43108	gb:HSC13E071 normalized infant brain cDN	2.9
	436726	AA324975	Hs.198689 ESTs, Weakly similar to T00079 hypotheti	2.9
	442513	AF150207	Hs.207949 ESTs	2.9
	425012	T77666	Hs.92414 Homo sapiens cDNA: FLJ22030 fis, clone H	2.9
55	402322		Target Exon	2.9
	427235	AI126288	Hs.192232 ESTs	2.9
	456412	AW749617	Hs.280776 tankyrase, TRF1-interacting ankyrin-rela	2.9
	431196	AW974436	Hs.154929 ESTs	2.9
	439379	AA835002	Hs.125611 ESTs	2.9
60	423757	AL049337	Hs.132571 Homo sapiens mRNA; cDNA DKFZp564P016 (fr	2.9
	446134	AW161234	Hs.13993 TBP-like 1	2.9
	435645	AI052789	Hs.133263 ESTs	2.9
	449385	AI650471	Hs.347290 ESTs	2.9
	444161	N52543	Hs.142940 ESTs	2.9
65	406635	U07162	gb:Human clone LNA11 autoantibody Ig hea	2.9
	419239	AA468183	Hs.184598 Homo sapiens cDNA: FLJ23241 fis, clone C	2.9
	458760	AI498631	Hs.111334 ferritin, light polypeptide	2.9
	427245	AA421022	Hs.97739 ESTs	2.9
	400658		ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	2.9
70	430701	AI760833	Hs.293971 ESTs	2.9
	435294	T84084	Hs.196008 Homo sapiens cDNA FLJ11723 fis, clone HE	2.9
	429927	NM_001115	Hs.2522 adenylate cyclase 8 (brain)	2.9
	446160	AW392197	Hs.218003 ESTs	2.9
	420674	NM_000055	Hs.1327 butyrylcholinesterase	2.9
75	424330	AW073953	Hs.333396 Homo sapiens cDNA FLJ13596 fis, clone PL	2.9
	418915	AI474778	Hs.118977 ESTs	2.9
	425922	AL157466	Hs.162751 Homo sapiens mRNA; cDNA DKFZp761E2423 (f	2.9
	447512	AW958148	Hs.129454 ESTs	2.9
	449990	AI279010	Hs.48821 ESTs	2.8
80	423779	AW071837	Hs.57971 ESTs	2.8
	427395	AW298741	Hs.97861 ESTs, Moderately similar to I38022 hypot	2.8
	416188	BE157260	Hs.79070 v-myc avian myelocytomatosis viral oncog	2.8
	426746	J03626	Hs.2057 uridine monophosphate synthetase (orolat	2.8
	400362	AF068294	Hs.272414 Homo sapiens HDCMB45P mRNA, partial cds	2.8

	457579	AB030816	Hs.36761	HRAS-like suppressor	2.8
	451059	AW297465	Hs.267150	KIAA1409 protein	2.8
	403903			C5001632*:gij10645308 gb AAG21430.1 AC00	2.8
5	444491	AI151091	Hs.270714	ESTs	2.8
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	2.8
	457292	AI921270	Hs.281462	hypothetical protein FLJ114251	2.8
	428305	AA446628	Hs.2799	cartilage linking protein 1	2.8
	435375	AI733610	Hs.187832	ESTs	2.8
10	409078	AW327515	Hs.346209	ESTs	2.8
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.8
	444656	AI277924	Hs.145199	ESTs	2.8
	426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	2.8
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	2.8
15	438243	AI581311		ESTs	2.8
	434012	AA621425	Hs.186256	ESTs	2.8
	402711			Target Exon	2.8
	442955	AI683534	Hs.131583	ESTs	2.8
20	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.8
	438934	BE220137	Hs.124323	ESTs	2.8
	438689	AW129261	Hs.181672	ESTs	2.8
	420083	AA478847	Hs.42484	hypothetical protein FLJ10618	2.8
	400315	U46120	Hs.193392	Human expressed unknown mRNA	2.8
25	433563	AI732637	Hs.277901	ESTs	2.8
	458093	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	2.8
	409157	AA064631		gb:z77c03.s1 Soares_pineal_gland_N3HPG	2.8
	450597	AI701635	Hs.207077	ESTs	2.8
	425300	AW501773	Hs.270259	ESTs	2.8
	458617	Z25900	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.8
30	418312	AW972468	Hs.170307	Rai guanine nucleotide exchange factor R	2.8
	430335	D80007	Hs.239499	KIAA0185 protein	2.8
	454581	AW809189		gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	419735	AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	2.8
35	436265	AA731331	Hs.190668	ESTs	2.8
	439481	AF086294	Hs.125844	ESTs	2.8
	441964	AA972619	Hs.20506	ESTs, Weakly similar to I38022 hypotheti	2.8
	422648	D86983	Hs.118893	Melanoma associated gene	2.8
	430503	AA533574	Hs.152274	ESTs	2.8
	403942			Target Exon	2.8
40	420565	AI806770	Hs.30258	ESTs	2.8
	439069	H63144	Hs.184178	ESTs, Weakly similar to ALUB_HUMAN !!!	2.8
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	2.8
	408137	AI694131	Hs.29002	KIAA1706 protein	2.8
45	451692	AL137422	Hs.26849	Homo sapiens mRNA; cDNA DKFZp761A1623 (f	2.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.8
	452526	W38537	Hs.280740	hypothetical protein MGC3040	2.8
	414300	AI304870	Hs.188580	ESTs	2.8
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.8
	437933	AI276132	Hs.146155	ESTs	2.7
50	405941			Target Exon	2.7
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.7
	450651	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti	2.7
	426765	AA743603	Hs.172108	nucleoporin 88kD	2.7
55	418886	AA93982	Hs.130858	ESTs	2.7
	429483	AA974832	Hs.128708	ESTs	2.7
	430426	AA478807	Hs.125173	ESTs	2.7
	439019	AF085902	Hs.271737	ESTs	2.7
	400924			Target Exon	2.7
60	458070	AW503578	Hs.209406	ESTs, Weakly similar to I38600 zinc fing	2.7
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	442621	AI004333	Hs.130553	ESTs, Weakly similar to ALUA_HUMAN !!!	2.7
	437643	AL080280		gb:Homo sapiens mRNA full length insert	2.7
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	2.7
65	443392	AI055821	Hs.293420	ESTs	2.7
	429972	AI700846	Hs.234518	ribosomal protein L23	2.7
	438875	AA827640	Hs.189059	ESTs	2.7
	422551	AW967284		gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	446139	H77395	Hs.39749	ESTs	2.7
70	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	2.7
	428612	AA770001	Hs.188778	ESTs	2.7
	439947	AB006627	Hs.6788	aslotactin	2.7
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	438335	AI498421	Hs.243168	ESTs	2.7
75	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	2.7
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	2.7
	438801	AA825971	Hs.124284	ESTs	2.7
	442892	AI038379	Hs.131865	ESTs	2.7
80	432964	AF118395	Hs.279865	trans-prenyltransferase	2.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	2.7
	400335	Y13187	Hs.248068	Homo sapiens drmd gene, intron 11	2.7
	415467	RS0891	Hs.260274	ESTs	2.7
	428715	AW293716	Hs.53126	ESTs	2.7
	457750	AI651474	Hs.163944	ESTs	2.7

	424480	AA341442	Hs.205299	ESTs	2.7
	444822	BE164351	Hs.292767	hypothetical protein FLJ23109	2.7
	432651	AW973744	Hs.293100	ESTs	2.7
	439823	AW665287	Hs.124514	ESTs	2.7
5	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fs, clone H	2.7
	440026	AA861299	Hs.160371	ESTs	2.7
	446960	AW294936	Hs.156762	ESTs	2.7
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	2.7
	458527	AI950256	Hs.224875	ESTs	2.7
	445899	AI263736	Hs.145626	ESTs	2.7
	404254			ENSP00000082468::DJ45P21.3 (butyrophilin	2.7
	402344			Target Exon	2.7
15	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	2.7
	446420	AW015693	Hs.135614	ESTs	2.7
	426914	AA393328	Hs.194303	ESTs	2.7
	407903	AI287341	Hs.154029	bHLH factor Hes4	2.7
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.7
20	403431			Target Exon	2.7
	403290			C10001011::gij4758212[ref]NP_004411.1 d	2.7
	435143	R12375	Hs.194600	ESTs	2.7
	416569	H64891		gb:yr68h03.r1 Soares fetal liver spleen	2.7
	428690	AI948490	Hs.98765	ESTs	2.7
25	425128	BE561929	Hs.154718	tumor protein D52-like 2	2.7
	443361	AI792628	Hs.133273	ESTs	2.7
	404053			Target Exon	2.7
	435113	AA665469	Hs.117136	ESTs	2.6
	405717			CX000838:gil10092633[ref]NP_055314.1 pu	2.6
30	413098	BE065279		gb:RC1-BT0314-030500-016-b09 BT0314 Homo	2.6
	444884	AI201094	Hs.148540	ESTs	2.6
	419015	T79262	Hs.14463	ESTs	2.6
	423234	AA323534	Hs.296162	AD037 protein	2.6
	406871	AA993857	Hs.180842	ribosomal protein L13	2.6
35	428670	AA431682	Hs.134832	ESTs	2.6
	408371	AF161545	Hs.44439	hypothetical protein	2.6
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	2.6
	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	2.6
	419817	AA743434	Hs.193778	ESTs	2.6
40	415788	AW628686	Hs.78851	KIAA0217 protein	2.6
	427388	BE379610	Hs.177592	ribosomal protein, large, P1	2.6
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.6
	405863			Target Exon	2.6
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	2.6
45	430147	R60704	Hs.234434	hair/enhancer-of-split related with YRP	2.6
	425480	AB023198	Hs.158135	KIAA0981 protein	2.6
	407182	AA312551	Hs.230157	ESTs	2.6
	439538	AA837323	Hs.56407	ESTs	2.6
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	2.6
50	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	2.6
	402936			ENSP00000217246::DJ803K15.1 (novel prote	2.6
	420670	AW973577		ESTs	2.6
	455409	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
55	422484	AA568770	Hs.123158	Homo sapiens cDNA FLJ12830 fs, clone NT	2.6
	400780			NM_007325::Homo sapiens glutamate recept	2.6
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.6
	448970	AW138582		gb:UH-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su	2.6
	402615			C1003844::gij6912550[ref]NP_036483.1 of	2.6
60	417099	BE537357	Hs.306995	hypothetical protein MGC5457	2.6
	428397	AA428040		gb:zw50e02.r1 Soares_total_fetus_Nb2HF8_	2.6
	449164	AI632772	Hs.264165	ESTs	2.6
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	2.6
	443635	AI080230	Hs.134214	ESTs	2.6
	402981			Target Exon	2.6
65	433258	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.6
	428917	AA437337	Hs.16689	ESTs	2.6
	418557	BE140602	Hs.246645	ESTs	2.6
	445211	BE045601	Hs.119248	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
70	404423			C800067::gij10432400[emb]CAC10290.1 (A	2.6
	435953	AI767087	Hs.114142	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
	439220	AW295340	Hs.130417	ESTs, Weakly similar to Z195_HUMAN ZINC	2.6
	419597	W73692		gb:zd50c01.s1 Soares_fetal_heart_NbHH19W	2.6
75	436852	AI814817	Hs.269099	ESTs	2.6
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	2.6
	443845	AI590084	Hs.148485	ESTs, Weakly similar to A47161 Mac-2-bin	2.6
	414223	AA954566	Hs.238246	hypothetical protein FLJ22479	2.6
	443770	AW815924		gb:MR3-ST0218-191199-012-a10 ST0218 Homo	2.6
80	450443	AA009847	Hs.120744	ESTs	2.6
	435523	T62849	Hs.11050	membrane-spanning 4-domains, subfamily A	2.6
	400492			C10001573::gij7302749[gb]AAF57827.1 (AE	2.6
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	2.6
	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares fetal liver spleen	2.6

	446423	AW139655	Hs.150120	ESTs	
	447587	AW292139	Hs.115789	ESTs	2.6
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	2.6
5	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	2.6
	432668	AA558601	Hs.43296	ESTs	2.6
	436682	AI590055	Hs.124110	ESTs	2.6
	426894	AI204209	Hs.143911	ESTs	2.6
	402605			Target Exon	2.6
10	457554	AA570111	Hs.155873	ESTs, Weakly similar to ALUE_HUMAN !!!	2.6
	438166	N30158	Hs.122645	ESTs	2.6
	443021	AA368546	Hs.8904	Ig superfamily protein	2.6
	427005	AA394228	Hs.97494	ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.6
15	408603	R25283	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.6
	431019	NM_005249	Hs.2714	forkhead box G1B	2.6
	437287	AA748180	Hs.159346	hypothetical protein FLJ21369	2.5
	458552	AW136139	Hs.245856	ESTs	2.5
	436350	AA713661	Hs.121091	ESTs	2.5
20	421988	AW450481	Hs.161333	ESTs	2.5
	416704	H77795	Hs.39785	ESTs	2.5
	447830	R98920	Hs.164314	ESTs	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.5
	406789	AI041403		ribosomal protein L29	2.5
25	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5
	433523	H29882		ESTs	2.5
	452296	T65535	Hs.111539	ESTs	2.5
	428878	AA436884	Hs.48926	ESTs	2.5
	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	2.5
30	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	2.5
	444422	AI768623	Hs.108264	ESTs	2.5
	420579	AA278449	Hs.137429	ESTs	2.5
	416505	H66470	Hs.16004	ESTs	2.5
	402595			C1001578:gil6759903:gb:AAF28099.1 (AF1	2.5
35	447930	R44574	Hs.107510	ESTs	2.5
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	2.5
	458421	AI279978	Hs.22547	ESTs	2.5
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	2.5
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYTS_HUMAN SYNAP	2.5
40	453362	H14988	Hs.107375	ESTs	2.5
	423600	AI633559	Hs.310359	ESTs	2.5
	433325	AW206986	Hs.143905	ESTs	2.5
	415983	AI436798	Hs.117078	Homo sapiens cDNA: FLJ23028 fis, clone L	2.5
	431198	AL047634	Hs.231913	ESTs	2.5
45	430530	AA480870	Hs.47660	ESTs	2.5
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	2.5
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.5
	422352	AA766296	Hs.99200	ESTs	2.5
	427613	AW273851	Hs.98025	ESTs	2.5
50	453685	AL110309		gb:DKFZp564L0278_r1 564 (synonym: hibr2)	2.5
	450508	R37408	Hs.101654	ESTs	2.5
	436361	AA825814	Hs.149065	ESTs	2.5
	427709	AI631811	Hs.180403	STRIN protein	2.5
	432036	AF224266	Hs.272373	interleukin 20	2.5
55	422752	BE247253	Hs.21263	suppressor of potassium transport defect	2.5
	413786	AW613780	Hs.13500	ESTs	2.5
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.5
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	2.5
	414959	D59968	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	2.5
60	449919	AI674685	Hs.200141	ESTs	2.5
	458891	AI659166	Hs.207144	ESTs	2.5
	427140	AA398487	Hs.97642	ESTs	2.5
	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	2.5
65	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.5
	443753	AW367578	Hs.134749	ESTs	2.5
	432888	T86823		gb:yd81a08.s1 Soares fetal liver spleen	2.5
	445065	AI806657	Hs.302024	glycoprotein beta-Gal 3'-sulfoltransferas	2.5
	431202	AA495824	Hs.188822	ESTs, Weakly similar to A46010 X-linked	2.5
	445658	AI469062	Hs.172660	ESTs	2.5
70	435330	R16769	Hs.173174	Homo sapiens cDNA FLJ14429 fis, clone HE	2.5
	435703	AW630133	Hs.83313	GK003 protein	2.5
	456232	AL040357		gb:DKFZp434O0713_r1 434 (synonym: htes3)	2.5
	421955	AK000160	Hs.121576	Homo sapiens cDNA FLJ20153 fis, clone CO	2.5
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-asso	2.5
75	425428	AL110261	Hs.157211	DKFZP586B0621 protein	2.5
	437627	AW469925	Hs.257837	ESTs	2.5
	408574	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp	2.5
	418733	AA227714	Hs.179703	KIAA0129 gene product	2.5
	440473	BE562314	Hs.98711	Homo sapiens, clone IMAGE:3677165, mRNA,	2.5
80	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	2.5
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	424947	R77952		ESTs, Weakly similar to alternatively sp	2.5
	450831	R37974	Hs.25255	ESTs	2.5

447527	AI702896	Hs.42091	ESTs	2.5
424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	2.5
453385	AW296101	Hs.252806	ESTs	2.5

5

TABLE 12B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

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Pkey	CAT Number	Accession
408292	1050507_1	AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
409157	110363_1	AA064631 AA722000 AA064793
409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119

15

411480	1247089_1	AW848022 AW848704 AW848168 AW848959 AW848476 AW848699 AW848700 AW848761
411537	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
411543	1249127_1	AW851248 AW851425 AW850805 AW851021 AW850905
411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628

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411671	125369_1	BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170
411688	1254076_1	AW953440 T08189 AW857085
412021	1272156_1	AW885592 AW885594 AW885579 AW885651
412135	1279148_1	AW895309 AW895290 AW895307 AW895397 AW895378 AW895402 AW895403 AW895311 AW895298 AW895390 AW895488 AW895468 AW895481

25

412225	1284108_1	AW902042 N77591
412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A1424991 A1693507 A1863108 AA599060 A1091148 AA598689

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413098	1349115_1	R39887 AAB13482 AW016452 H06383 R41807 A1364268 AA620528 A1241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
413986	140720_1	BE065279 BE065306 BE065164 BE065389
414988	1511316_1	Z43567 H24159 AA134240
415131	1523680_1	C17535 D59244 D58878 D79090
415346	1534581_1	D61119 D81508 D81734

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416422	1593811_1	Z43108 F06295 R13085
416569	1601567_1	H60457 H68709 H73528 H54335 R87154
416665	1607797_1	H64891 R93444 R93458 R05590
419597	1863413_1	H72974 W28967

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420352	192979_1	W73692 W73836 W95650
420670	195442_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
422551	217767_1	AW973577 AA553621 AA279187
424009	234177_1	AW967284 AA312192 AA312203

45

424200	236595_1	F11690 AW965370 AA333586 D30830
424686	242486_1	AA337221 AA336756 AW966196
424947	245247_1	AA345504 AA345251 AW963243
425146	247244_1	R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973
425331	250199_1	AW954627 AW954629 AA351258 R25935

50

426503	268283_1	AW962128 AA355353 AA427363
428397	290994_1	AA380153 AA380233 AW963529
429258	301917_1	AA428040 AW889864 AA836434
429940	310884_1	AA448765 C04967 C03045 AA658293
430183	31412_2	W25215 AA461079 AA461391

55

430535	319643_1	BE010038 AA676833 A1311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039909
432044	340773_1	AW968485 AW968670 AA480922 BE350425
432646	351909_1	AW972727 AA524829 AW972733
432888	355780_1	AW753310 AW974000 AA557840 AA558570 AW751539

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433009	357371_1	T86823 A1821425 A1732232 AA569589 AA570737
433523	368873_1	AA761668 AA573621 R92814 R09670
433835	374758_1	H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
434589	38929_1	A1806185 AA610063 A1693089 A1693075
436608	42361_3	AF147363 T47219 T47218

65

437034	431713_1	AA628980 A126603 BE504035
437643	43998_1	AA742643 AA808575 AW976668
438243	453072_1	AL080280 T73124 H02689 AL080281
438458	457837_1	A1581311 AA781682 AA781678
439533	47349_1	AW975186 AA807807 D29548

70

442476	543547_1	W76021 AF088052 W72465
443770	579849_1	AF069475 AF069477 AF069476
444016	58899_1	AW815924 AW815926 A1085174
448970	791254_1	AA448154 AV647571
450166	82677_1	AW138582 A1638298 A1631640 A1963868 A1611082

75

453685	977734_1	AA429504 R41904 AA279467 H09648 AA007236
454037	996287_1	AL110309 AW088119 H22881
454177	1049351_1	AW998716 AW022148 N68020
454451	1206502_1	AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942

80

454457	1207274_1	AW807178 AW807167 AW807398 AW807320 AW807306 AW845866
454581	1225710_1	AW846706 AW846703 AW752167 AW846700 AW846699 AW752176 AW846694
454765	1233905_1	AW753456 AW753036 AW854868 AW854862
454860	1237732_1	AW809189 AW809219 AW813574
454958	1247029_1	AW819629 AW854320
455104	1253737_1	AW835767 AW835537 BE160187

	455409	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW9
5	455481	1293182_1	AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
	455899	1381547_1	BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
	456232	168294_1	AL040357 AA883621 AA203230
10	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457364	328154_1	AW971037 AA508019 AA492345

TABLE 12C:

15	Key:	Unique Eos probeset identifier number
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

	Key	Ref	Strand	Nt_position
20	400492	9213749	Minus	123881-124090
	400533	6981826	Minus	277132-277595
	400645	8117693	Minus	58471-58716
	400658	8118459	Minus	73525-73644
25	400780	8131663	Minus	118372-118619
	400814	8569925	Minus	72840-72924,74761-74849
	400924	7107613	Minus	30309-30498
	401272	9797373	Minus	98374-98509
	401454	9186923	Minus	114659-114832
30	401702	1871197	Minus	68182-68325
	402229	9965022	Minus	15739-15951,16166-16779
	402274	2935596	Plus	5604-6527
	402322	7630359	Minus	75078-75203
	402344	8099256	Minus	76812-79040
35	402595	7705171	Plus	37870-37923,39664-39717,71711-71764
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973
	402615	9926801	Plus	131390-132157
	402711	8901247	Minus	114306-115418
40	402747	9212492	Minus	7105-7357
	402855	9662953	Minus	59763-59909
	402936	8894303	Plus	51655-51771
	402981	9944246	Minus	45716-45889
	403108	8980955	Plus	93253-93667
45	403212	7630897	Minus	156037-156210
	403288	8081479	Plus	133763-133899,135813-135958
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403349	8569773	Minus	167815-168374
50	403431	7139839	Plus	56509-56860
	403481	9965004	Plus	93496-93633
	403696	3135242	Minus	143467-143634
	403790	8084957	Minus	87826-87947,89835-90002
	403849	7708855	Plus	95043-96519
55	403903	7710671	Minus	101165-102597
	403942	7711825	Minus	99606-99757
	403961	7596976	Minus	110393-110603
	404053	3548785	Plus	61797-64205
	404120	7342152	Plus	135775-136000
60	404185	4572584	Minus	129171-129327
	404254	9367203	Plus	129350-129873
	404272	9885189	Plus	83207-83355,84358-84496,90519-90720,91371-91447
	404423	7407959	Plus	34438-34618
	404584	9857511	Plus	138651-139153
65	404592	9943965	Minus	39067-39225
	404632	9796668	Plus	45096-45229
	405046	7596829	Minus	4373-4528
	405183	7209940	Plus	12335-12653
	405238	7249119	Minus	51728-51836
70	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
	405348	2914717	Minus	43310-43462
	405488	7131455	Minus	75771-75883,105295-105398,134754-134875
	405558	1621110	Plus	4502-4644,5983-6083
	405717	9588573	Plus	11275-11973
75	405760	6066938	Minus	37424-38045
	405863	7657810	Plus	49410-49620
	405941	6758796	Plus	2798-3444
	406395	9256242	Minus	20805-20960
	406478	9857502	Plus	68314-68523,68853-68950
80	406481	9864741	Minus	91439-91579

TABLE 13A: 964 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG level was set to the 85th

percentile amongst various LGG tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of LOWER GRADE GLIOBLASTOMA to NORMAL ADULT TISSUES			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	67.6
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	58.2
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.8
	431917	D16181	Hs.2868	peripheral myelin protein 2	50.6
15	428321	AI699994	Hs.2868	peripheral myelin protein 2	48.3
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	44.3
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	44.2
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	43.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	40.8
20	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	40.1
	417183	R52089	Hs.172717	ESTs	38.8
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	36.8
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	34.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	34.4
25	429276	AF056085	Hs.198612	G protein-coupled receptor 51	34.2
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	33.9
	450133	AW969769	Hs.105201	ESTs	33.8
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	32.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
30	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	31.3
	402604			Target Exon	30.3
	412733	AA984472	Hs.74554	KIAA0080 protein	28.8
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	28.2
	439239	AI031540	Hs.235331	ESTs	27.9
35	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	27.1
	439415	F05538	Hs.4273	ESTs	26.2
	425048	H05468	Hs.164502	ESTs	25.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	25.3
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	24.0
40	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	23.5
	447359	NM_012093	Hs.18268	adenylate kinase 5	23.5
	425842	AI587490	Hs.159523	NK-2 (Drosophila) homolog B	23.2
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	23.2
	435708	AI362949	Hs.75169	ESTs	22.9
45	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	21.6
	409395	U46745	Hs.336678	dystrobrevin, alpha	21.1
	441285	NM_002374	Hs.167	microtubule-associated protein 2	20.4
	422656	AI870435	Hs.1569	LIM homeobox protein 2	20.0
50	425523	AB007948	Hs.158244	KIAA0479 protein	19.7
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
	441497	R51064	Hs.23172	ESTs	19.3
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.1
	408604	D51408	Hs.21925	ESTs	18.9
55	413597	AW302885	Hs.117183	ESTs	18.8
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	18.8
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	18.6
	429466	M85835	Hs.12827	ESTs	18.2
60	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	18.2
	439199	R40373	Hs.26299	ESTs	17.4
	448743	AB032962	Hs.21896	KIAA1136 protein	17.4
	418338	NM_002522	Hs.84154	neuronal pentraxin I	17.3
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	17.2
65	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	17.1
	447004	AW296968	Hs.157539	ESTs	16.8
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	16.5
	448672	AI955511	Hs.225106	ESTs	16.1
	452372	AI885742	Hs.228474	ESTs	15.8
70	424120	T80579	Hs.290270	ESTs	15.7
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	15.6
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	15.4
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	15.2
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	15.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	14.9
75	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	14.7
	441440	AI807981	Hs.30495	ESTs	14.6
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	14.6
	415849	R20529	Hs.6806	ESTs	14.4
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	14.2
80	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	14.0
	409638	AW450420	Hs.21335	ESTs	14.0
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	13.9
	415734	NM_014747	Hs.78748	KIAA0237 gene product	13.7

	424945	AI221919		hypothetical protein FLJ10582	13.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	13.4
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	13.3
5	429946	R49390	Hs.254129	KIAA1678	13.3
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypothe	13.3
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	13.2
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	13.2
	412266	N59006	Hs.26133	ESTs	13.2
10	436878	BE465204	Hs.47448	ESTs	13.1
	428536	AI143139	Hs.2288	visinin-like 1	13.1
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	13.1
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.0
	437948	AA772920	Hs.303527	ESTs	13.0
15	444124	R43097	Hs.6818	ESTs	12.9
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	12.7
	412959	D87458	Hs.75090	KIAA0282 protein	12.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	12.6
20	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	12.6
	431019	NM_005249	Hs.2714	forkhead box G1B	12.4
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	12.4
	430091	AB032958	Hs.233023	KIAA1132 protein	12.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	12.2
25	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	12.2
	409049	AI423132	Hs.146343	ESTs	12.0
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	11.9
	451952	AL120173	Hs.301663	ESTs	11.9
	411305	BE241596	Hs.69547	myelin basic protein	11.8
30	433551	AI985544	Hs.12450	protocadherin 9	11.6
	431988	AC002302	Hs.77202	protein kinase C, beta 1	11.6
	415170	R44386	Hs.164578	ESTs	11.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	11.4
	435501	AW051819	Hs.129908	KIAA0591 protein	11.4
35	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	11.1
	423419	R55336	Hs.23539	ESTs	11.1
	424432	AB037821	Hs.146858	protocadherin 10	10.9
	433896	AW294729	Hs.274461	ESTs	10.9
	415293	R49462	Hs.106541	ESTs	10.9
40	447101	N72185	Hs.44189	ESTs	10.9
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	10.9
	438054	AA776626	Hs.169309	ESTs	10.8
	433597	AA708205	Hs.100343	ESTs	10.7
	421659	NM_014459	Hs.106511	protocadherin 17	10.6
45	445102	AW204610	Hs.22270	ESTs	10.6
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	10.6
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	10.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.6
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	10.5
50	407886	AW969688	Hs.100826	ESTs	10.4
	420345	AW295230	Hs.25231	ESTs	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.3
	424997	AL138167	Hs.96920	ESTs	10.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	10.2
55	419078	M93119	Hs.89584	insulinoma-associated 1	10.2
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypothe	10.1
	416857	AA188775	Hs.292453	ESTs	10.0
	445041	T64183	Hs.282982	solute carrier	10.0
	419271	N34901	Hs.238532	ESTs	9.8
60	446711	AF169692	Hs.12450	protocadherin 9	9.8
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	9.7
	427304	AA761526	Hs.163853	ESTs	9.7
	418097	R45137	Hs.21868	ESTs	9.7
	449300	AI656959	Hs.346514	ESTs	9.7
65	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.s.a	9.7
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	9.5
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	9.5
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	9.5
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.4
70	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	9.4
	419683	AA248897	Hs.48784	ESTs	9.4
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	9.2
	400292	AA250737	Hs.72472	BMP-R1B	9.2
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	9.2
75	454048	H05626	Hs.6921	ESTs	9.2
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.1
	441016	AW138653	Hs.25845	ESTs	9.0
	425187	AW014486	Hs.22509	ESTs	9.0
	445568	H00918	Hs.268744	KIAA1796 protein	8.9
80	453941	U39817	Hs.36820	Bloom syndrome	8.9
	422411	AW749443	Hs.22511	ESTs	8.8
	447350	AI375572	Hs.172634	ESTs	8.8
	424481	R19453	Hs.1787	proteolipid protein 1 (Pefizeus-Merzbac	8.7
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	8.7

	448986	H42169	Hs.347310	hypothetical protein FLJ14627	8.6
	423135	N67655	Hs.26411	ESTs	8.5
	418030	BE207573	Hs.83321	neuromedin B	8.4
5	448769	N68037	Hs.38173	ESTs	8.4
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	8.3
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	8.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	8.2
	451516	AI800515	Hs.12024	ESTs	8.2
10	419629	AB020695	Hs.91662	KIAA0888 protein	8.2
	437034	AA742643		gb:ny91c01.s1 NC1_CGAP_GCB1 Homo sapiens	8.2
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	8.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	8.1
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	8.1
15	422864	AA318323	Hs.12627	gb:EST20390 Retina II Homo sapiens cDNA	8.1
	452526	W38537	Hs.280740	hypothetical protein MGC3040	8.0
	435793	AB037734	Hs.4993	KIAA1313 protein	7.9
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	7.9
	407168	R45175	Hs.117183	ESTs	7.9
20	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.8
	442710	AI015631	Hs.23210	ESTs	7.8
	416836	D54745	Hs.80247	cholecystokinin	7.8
	419721	NM_001650	Hs.288650	aquaporin 4	7.7
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN !!!!	7.7
25	436109	AA922153	Hs.132760	hypothetical protein MGC15729	7.7
	428845	AL157579	Hs.153610	KIAA0751 gene product	7.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.7
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	7.6
	443392	AI055821	Hs.293420	ESTs	7.6
30	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	7.5
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	447198	D61523	Hs.283435	ESTs	7.5
	448555	AI536697	Hs.159863	ESTs	7.5
35	458332	AI000341	Hs.220491	ESTs	7.4
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	7.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	7.4
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	7.4
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	7.4
40	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	7.4
	449078	AK001256	Hs.22975	KIAA1576 protein	7.3
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	7.2
	425741	AF052152	Hs.159412	Homo sapiens clone 24528 mRNA sequence	7.2
	440210	AW674562	Hs.125296	ESTs	7.2
45	415651	AI207162	Hs.3815	slathmin-like-protein RB3	7.2
	428409	AW117207	Hs.98523	ESTs	7.1
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	443992	AW022228	Hs.322922	ESTs	7.1
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	7.1
50	427540	R12014	Hs.20976	ESTs	7.0
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	7.0
	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	7.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0
55	440152	AB002376	Hs.7006	KIAA0378 protein	7.0
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	7.0
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	7.0
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.0
60	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.9
	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	6.9
	449605	AW138581	Hs.198416	ESTs	6.9
	444396	T65213	Hs.4257	ESTs	6.9
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	6.9
65	414245	BE148072	Hs.75850	WAS protein family, member 1	6.9
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.9
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	6.9
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.9
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	6.9
70	446782	AI653048	Hs.144006	ESTs	6.8
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.8
	423346	AI267677	Hs.127416	synaptotagmin 1	6.8
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	6.8
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	6.8
75	410037	AB020725	Hs.58009	KIAA0918 protein	6.8
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	6.8
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	6.8
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	6.8
	421141	AW117261	Hs.125914	ESTs	6.7
80	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	6.7
	441916	AA993571	Hs.129075	ESTs	6.7
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	6.7
	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7
	423343	AA324643	Hs.246106	ESTs	6.7

	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.7
	434811	AW971205	Hs.114280	ESTs	6.7
5	424922	BE386547	Hs.217112	hypothetical protein MGC10825	6.7
	449328	AI962493	Hs.345303	ESTs	6.6
	431553	X78075	Hs.2799	cartilage linking protein 1	6.6
	420156	AW449258	Hs.6187	ESTs	6.6
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.6
10	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	6.6
	429239	AA448419	Hs.45209	ESTs	6.5
	453924	R49295	Hs.24886	ESTs	6.5
	433929	AI375499	Hs.27379	ESTs	6.5
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	6.5
	414683	S78296	Hs.76888	hypothetical protein MGC12702	6.4
15	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	6.4
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothesi	6.4
	453590	AF150278	Hs.33578	KIAA0820 protein	6.4
	422263	AA307639	Hs.129908	KIAA0591 protein	6.4
20	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	6.4
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	6.3
	425588	F07396	Hs.46627	ESTs	6.3
	410366	AI267589	Hs.302689	hypothetical protein	6.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	6.3
25	446997	AA383439	Hs.16758	Spir-1 protein	6.3
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.3
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	6.3
	452834	AI638627	Hs.105685	KIAA1688 protein	6.3
30	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	6.3
	418512	AW489874		diacylglycerol kinase, zeta (104kD)	6.2
	410099	AA081630		KIAA0036 gene product	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	6.2
35	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.2
	439274	AF086092	Hs.48372	ESTs	6.2
	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	6.2
	439607	BE540565	Hs.159460	ESTs	6.2
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	6.2
40	412709	AL022327	Hs.74518	KIAA0027 protein	6.2
	435624	AF218942	Hs.24889	formin 2	6.1
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1
	420077	AW512260	Hs.87767	ESTs	6.1
	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	6.1
45	440471	AA886146	Hs.307944	ESTs	6.1
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	6.1
	438624	AA889055	Hs.123468	ESTs	6.1
	452752	AW044058	Hs.33578	KIAA0820 protein	6.1
	438208	AL041224	Hs.65379	ESTs	6.1
50	416072	AL110370	Hs.79000	growth associated protein 43	6.1
	407808	AA663559	Hs.279789	histone deacetylase 3	6.1
	433701	AW445023	Hs.15155	ESTs	6.1
	419704	AA429104	Hs.45067	ESTs	6.1
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.1
55	433244	AB040943	Hs.271285	KIAA1510 protein	6.0
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.0
	420133	AA426117	Hs.155543	ESTs	6.0
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	6.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	6.0
60	415257	F03016	Hs.27513	ESTs	5.9
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.9
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.9
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	5.9
65	433523	H29882		ESTs	5.9
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.9
	427317	AB028955	Hs.175780	KIAA1032 protein	5.9
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	5.9
	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	5.8
70	459516	AI049662	Hs.246858	EST	5.8
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T15326 hypothesi	5.8
	414737	AI160386	Hs.125087	ESTs	5.8
	424332	AA338919	Hs.101615	ESTs	5.8
	403142			NM_002706; Homo sapiens protein phosphat	5.8
75	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens	5.8
	450813	AI739625	Hs.203376	ESTs	5.8
	402145			Target Exon	5.8
	434792	AA649253	Hs.132458	ESTs	5.8
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	5.8
80	445745	AB007924	Hs.13245	KIAA0455 gene product	5.8
	420608	BE548277	Hs.103104	ESTs	5.8
	451407	AA131376	Hs.343809	fibroblast growth factor 12B	5.7
	441102	AA973905		intermediate filament protein syncoitin	5.7
	424560	AA158727	Hs.150555	protein predicted by clone 23733	5.7

	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.7
	405238			Target Exon	5.7
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	5.7
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.7
5	413492	D87470	Hs.75400	KIAA0280 protein	5.7
	427624	AA406245	Hs.24895	ESTs	5.7
	418079	R40058	Hs.6911	ESTs	5.6
	424458	M29273	Hs.1780	myelin associated glycoprotein	5.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.6
10	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	5.6
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypothe	5.6
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	5.6
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	5.6
	452898	AA814497	Hs.78792	ESTs	5.6
15	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.6
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	5.5
	412190	R16180	Hs.274461	ESTs	5.5
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	5.5
20	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.5
	423449	AI497900	Hs.33067	ESTs	5.5
	440866	AI703103	Hs.271360	hypothetical protein MGC16275	5.5
	432154	AI701523	Hs.112577	ESTs	5.4
	423476	AL035633		Human DNA sequence from clone RPS-1046G1	5.4
25	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.4
	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	5.4
	436936	AL134451	Hs.197478	ESTs	5.4
	427250	R35941	Hs.25418	ESTs	5.4
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	5.4
30	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	5.4
	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	5.4
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	5.4
	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	5.4
	438330	AW450572	Hs.257316	ESTs	5.3
35	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.3
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	5.3
	445225	AI216555	Hs.202398	ESTs	5.3
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	5.3
40	418759	AA227879	Hs.187621	ESTs	5.3
	402605			Target Exon	5.3
	412046	Y07847	Hs.73088	RAS-related on chromosome 22	5.3
	423869	BE409301	Hs.134012	C1q-related factor	5.2
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
45	453096	AW294631	Hs.11325	ESTs	5.2
	450475	AW805634	Hs.205015	ESTs	5.2
	429139	F09092	Hs.66087	ESTs	5.2
	451783	R42554	Hs.210862	T-box, brain, 1	5.2
	436568	H12049	Hs.91564	ESTs	5.2
50	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	5.2
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	5.2
	447499	AW262580	Hs.147674	protocadherin beta 16	5.2
	402855			NM_001839: Homo sapiens calponin 3, acid	5.2
	420805	L10333	Hs.99947	reticulon 1	5.2
55	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	5.2
	417355	D13168	Hs.82002	endothelin receptor type B	5.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
	450639	AI703186	Hs.277174	ESTs	5.1
	412811	H06382		ESTs	5.1
60	400379	NM_018432		Homo sapiens ovarian cancer related prot	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	5.1
	442832	AW206560	Hs.253569	ESTs	5.1
	422709	AA315331	Hs.153485	ESTs	5.1
	411555	AF113537	Hs.70669	HMP19 protein	5.1
65	419043	T19167	Hs.89566	ets variant gene 1	5.0
	430979	AI479755	Hs.129010	ESTs	5.0
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	5.0
	423678	AW963357	Hs.7847	ESTs	5.0
	429918	AW873986	Hs.119383	ESTs	5.0
70	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	5.0
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	5.0
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	5.0
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	5.0
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.0
75	439108	AW163034	Hs.6467	synaptogyrin 3	5.0
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	5.0
	451752	AB032997	Hs.26966	KIAA1171 protein	5.0
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.9
80	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (I	4.9
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.9
	445133	AW157646	Hs.198689	ESTs	4.9
	410359	R38624	Hs.106313	ESTs	4.9
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	4.9
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.9

	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.9
	409100	H98216	Hs.42245	ESTs, Moderately similar to I38022 hypot	4.9
	437117	AL049256	Hs.122593	ESTs	4.9
	415101	R45531	Hs.144534	ESTs	4.9
5	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.9
	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	4.9
	438283	AI458931	Hs.37282	ESTs	4.9
	449714	AB033015	Hs.23941	KIAA1189 protein	4.9
10	420871	AA702972	Hs.65300	ESTs	4.9
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.9
	424001	W67883	Hs.137476	paternally expressed 10	4.9
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	4.9
	446727	AB011095	Hs.16032	KIAA0523 protein	4.8
15	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	4.8
	428189	AA424030	Hs.46627	ESTs	4.8
	420092	AA814043	Hs.88045	ESTs	4.8
	410631	AA086469	Hs.47171	ESTs	4.8
	449277	AA001064	Hs.43670	ESTs	4.8
20	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.8
	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
	438703	AI803373	Hs.31599	ESTs	4.8
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.8
	445890	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence	4.8
25	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	4.7
	408177	AI241733	Hs.43871	ESTs	4.7
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	4.7
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.7
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.7
30	409172	Z99399	Hs.122593	ESTs	4.7
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.7
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	4.7
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.7
35	447891	R41754	Hs.6496	ESTs	4.7
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	4.7
	404819			NM_002688: Homo sapiens peanut (Drosophi	4.7
	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7
40	437762	T78028	Hs.154679	synaptotagmin I	4.7
	441668	AI611973	Hs.136313	ESTs	4.7
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	4.7
	429269	AA449013	Hs.99203	ESTs	4.6
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	4.6
45	416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.6
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	4.6
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	4.6
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	4.6
50	445813	Z42023	Hs.106576	alanine-glyoxylate aminotransferase 2-li	4.6
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	4.6
	448765	R15337	Hs.21958	Homo sapiens mRNA: cDNA DKFZp547D086 (fr	4.6
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	4.6
	424282	R76421	Hs.135694	ESTs	4.6
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	4.6
55	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.6
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	4.5
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.5
	443731	AI083928	Hs.145418	ESTs	4.5
	449539	W80363	Hs.58446	ESTs	4.5
60	420362	U79734	Hs.97206	huntingtin interacting protein 1	4.5
	443301	AI733614	Hs.220587	ESTs, Moderately similar to ALU5_HUMAN A	4.5
	423178	AI033140	Hs.124983	Homo sapiens mRNA: cDNA DKFZp564C142 (fr	4.5
	437933	AI276132	Hs.146155	ESTs	4.5
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	4.5
65	411642	NM_014932	Hs.71132	neurotigin 1	4.5
	428282	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	4.5
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	4.5
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.5
	436637	AI783629	Hs.26766	ESTs	4.5
70	438456	AA913381	Hs.20594	ESTs	4.5
	400533			ENSP00000209376: PRED65 protein (Fragmen	4.4
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.4
	417632	R20855	Hs.5422	glycoprotein M6B	4.4
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	4.4
75	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.4
	413812	AW188687	Hs.44748	ESTs	4.4
	448451	AW015994	Hs.345433	gb:U1-H-B10p-abh-g-09-0-U1.s1 NCI_CGAP_S	4.4
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	4.4
	458760	AI498631	Hs.111334	ferritin, light polypeptide	4.4
80	405819			NM_002578: Homo sapiens p21 (CDKN1A)-acti	4.4
	447877	AI435184	Hs.164252	ESTs	4.4
	431342	AW971018	Hs.21659	ESTs	4.4
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	4.4

	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.4
	419088	AI538323	Hs.52620	integrin, beta 8	4.4
	428305	AAA46628	Hs.2799	cartilage linking protein 1	4.4
5	410768	AF038185	Hs.66187	Homo sapiens clone Z3700 mRNA sequence	4.4
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.4
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	4.4
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.3
	433932	AW954599	Hs.169330	neuronal protein	4.3
	439935	S75105	Hs.8358	glutamate receptor, ionotropic, kainate	4.3
10	436039	AW023323	Hs.121070	ESTs	4.3
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.3
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.3
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	4.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3
15	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	4.3
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.3
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.3
	436391	AJ227892	Hs.146274	ESTs	4.3
	452106	AI141031	Hs.21342	ESTs	4.3
20	422465	AF073710	Hs.117149	regulator of G-protein signalling 9	4.3
	439285	AL133916		hypothetical protein FLJ20093	4.3
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.3
	424572	M19650		Z,3'-cyclic nucleotide 3' phosphodiester	4.3
25	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	409182	AA064970	Hs.122593	ESTs	4.3
	444600	R41398	Hs.6996	ESTs	4.3
	408838	AI669535	Hs.40369	ESTs	4.3
	410592	R94088	Hs.43569	ESTs	4.3
	440168	AA868507	Hs.126141	ESTs	4.2
30	445078	AI869975	Hs.4775	junctophilin 3	4.2
	428670	AA431682	Hs.134832	ESTs	4.2
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	4.2
	412505	AA974491	Hs.21734	ESTs	4.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.2
35	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	4.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	448243	AW369771	Hs.52620	integrin, beta 8	4.2
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypothe	4.2
40	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (4.2
	404584			Target Exon	4.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	451254	AI571016	Hs.172967	ESTs	4.2
	428585	AB007863	Hs.185140	KIAA0403 protein	4.2
45	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	4.2
	425790	AW136286	Hs.288446	ESTs	4.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4.2
	425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	4.2
50	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	4.1
	400777			NM_007325*:Homo sapiens glutamate recept	4.1
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.1
	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	4.1
55	438461	AW075485	Hs.286049	phosphoserine aminotransferase	4.1
	421268	AI126821	Hs.30514	ESTs	4.1
	416439	AA180363	Hs.118769	ESTs	4.1
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	4.1
	435040	AI932350	Hs.152825	ESTs	4.1
60	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	4.1
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypothe	4.1
	410320	AA084071	Hs.93816	Homo sapiens mRNA; cDNA DKFZp547N093 (fr	4.1
	436899	AA764852	Hs.291567	ESTs	4.1
	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	4.1
65	453118	AW195849	Hs.252757	ESTs	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	444185	AW298350	Hs.66020	ESTs	4.1
	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
70	430147	R60704	Hs.234434	hair/enhancer-of-split related with YRP	4.1
	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	4.1
	433819	AW511097	Hs.112765	ESTs	4.1
	415827	H17462	Hs.23079	ESTs	4.1
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	4.1
	441390	AI692560	Hs.131175	ESTs	4.1
75	440483	AI200836	Hs.150386	ESTs	4.0
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	4.0
	447397	BE247676	Hs.18442	E-1 enzyme	4.0
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	4.0
80	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	4.0
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	4.0
	408081	AW451597	Hs.167409	ESTs	4.0
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	4.0
	436511	AA721252	Hs.291502	ESTs	4.0

	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	4.0
	419412	AW161058	Hs.90297	synuclein, beta	4.0
	409091	AW970386	Hs.269423	ESTs	4.0
5	453438	AJ469935	Hs.22792	ESTs	4.0
	450582	AJ339732		G-rich RNA sequence binding factor 1	4.0
	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	4.0
	437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKFZp762G113 (fr	4.0
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
10	439450	R51613	Hs.125304	ESTs	4.0
	453792	AL134539	Hs.254129	KIAA1678	4.0
	459080	AW192083	Hs.290855	ESTs	4.0
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	4.0
	446233	AI282028	Hs.25205	ESTs	4.0
15	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	4.0
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.0
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	3.9
20	410126	BE169274		KIAA0036 gene product	3.9
	431173	AW971198	Hs.294068	ESTs	3.9
	446936	H10207	Hs.47314	ESTs	3.9
	424899	AL119387	Hs.119062	ESTs	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
25	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	3.9
	438142	T90309	Hs.269651	ESTs	3.9
	412659	AW753865	Hs.74376	otactomedin related ER localized protei	3.9
	412788	AA120960	Hs.198416	ESTs	3.9
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	3.9
30	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
	432809	AA565509	Hs.131703	ESTs	3.9
	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE	3.9
	425480	AB023198	Hs.158135	KIAA0981 protein	3.9
	449932	AI675444	Hs.263024	ESTs	3.9
35	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
	450590	AI701507	Hs.273740	ESTs	3.9
	419586	AI088485	Hs.144759	ESTs, Weakly similar to I38022 hypotheti	3.9
	414040	N58513	Hs.32171	ESTs	3.9
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.9
40	443210	AI692649	Hs.9451	hypothetical protein MGC13168	3.9
	448448	NM_014954	Hs.21239	KIAA0985 protein	3.9
	447067	R42098	Hs.21964	ESTs	3.9
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.9
	429421	AL031658		Human DNA sequence from clone RP1-310Q13	3.9
45	415795	R87548	Hs.78854	ATPase, Na ⁺ transporting, beta 2 polypep	3.8
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.8
	418771	AA807881	Hs.25329	ESTs	3.8
	417565	AI203405	Hs.47831	ESTs	3.8
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.8
50	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	3.8
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.8
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	3.8
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	3.8
	459079	AI821122		gb:ns91g10.y5 NCI_CGAP_Pr3 Homo sapiens	3.8
55	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	3.8
	437756	AA767537	Hs.197096	ESTs	3.8
	403696			C4001100:gi5852342[gb]AAD54015.1[AF0	3.8
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.8
60	441732	AW298818	Hs.127341	ESTs	3.8
	415884	H22966	Hs.13471	ESTs	3.8
	432646	AW753310		gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	451059	AW297465	Hs.267150	KIAA1409 protein	3.8
	447057	AI423407	Hs.157697	ESTs	3.8
65	418915	AI474778	Hs.118977	ESTs	3.8
	441111	AI806867	Hs.126594	ESTs	3.8
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.8
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.8
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	3.8
70	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
	428878	AA436884	Hs.48926	ESTs	3.8
	438944	AA302517	Hs.92732	KIAA1444 protein	3.8
	420898	AB002379	Hs.100113	KIAA0381 protein	3.8
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.8
75	427209	H06509	Hs.92423	KIAA1566 protein	3.7
	445319	AF052108	Hs.12513	Homo sapiens clone 23687 mRNA sequence	3.7
	428841	AI418430	Hs.104935	ESTs	3.7
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.7
	443310	BE552018	Hs.133152	ESTs	3.7
80	407728	AW071502	Hs.175931	ESTs	3.7
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.7
	444127	N63620	Hs.13281	ESTs	3.7
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.7
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.7

	459660	M79082		ESTs	3.7
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.7
	437627	AW469925	Hs.257837	ESTs	3.7
	408508	AI806109	Hs.135736	KIAA1580 protein	3.7
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	3.7
	410623	AW958932	Hs.293833	ESTs	3.7
	430744	AA485229	Hs.105649	ESTs	3.7
	454392	BE260893	Hs.236131	homeodomain-interacting protein kinase 2	3.7
	453739	AL120266		ESTs	3.7
10	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.7
	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	3.7
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.7
	451027	AW519204	Hs.40808	ESTs	3.7
15	415131	D61119		gb:HUM158C118 Clontech human fetal brain	3.7
	443454	AI057494	Hs.133421	ESTs	3.7
	423779	AW071837	Hs.57971	ESTs	3.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.7
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
20	447028	AI973128	Hs.167257	brain link protein-1	3.6
	452997	N64777	Hs.44656	ESTs	3.6
	408601	U47928	Hs.86122	protein A	3.6
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fs, clone HE	3.6
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.6
25	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.6
	421679	AI475110	Hs.203933	ESTs	3.6
	448985	AA324885	Hs.22777	carbonic anhydrase XI	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	411775	H08342		gb:yf87b09.r1 Soares infant brain 1N1B H	3.6
30	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	3.6
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.6
	423611	AB011163	Hs.129908	KIAA0591 protein	3.6
	453169	AB037815	Hs.32156	KIAA1394 protein	3.6
	436954	AA740151	Hs.130425	ESTs	3.6
35	439249	AF086060	Hs.170053	G-protein coupled receptor 88	3.6
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
40	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.6
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	445105	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
45	446420	AW015693	Hs.135614	ESTs	3.6
	428138	AA773842	Hs.293799	ESTs	3.6
	404185			Target Exon	3.6
	427517	AA644142	Hs.7107	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
	443150	AI034467	Hs.34650	ESTs	3.6
50	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.6
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	3.6
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	3.6
55	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.6
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.6
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.6
	438328	AI492261	Hs.32450	ESTs	3.6
60	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.6
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	3.6
	434784	AA649051	Hs.164007	ESTs	3.5
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.5
	421183	AL135740	Hs.102447	TSC-22-like	3.5
65	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.5
	425870	R13406	Hs.56782	ESTs	3.5
	425115	R44664	Hs.123956	ESTs	3.5
	444471	AB020684	Hs.11217	KIAA0877 protein	3.5
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.5
70	407792	AI077715	Hs.39384	putative secreted ligand homologous to I	3.5
	422564	AI148006	Hs.222120	ESTs	3.5
	433323	AA805132	Hs.159142	ESTs	3.5
	435743	T66861	Hs.12962	ESTs	3.5
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
75	403341			Target Exon	3.5
	443761	AI525743	Hs.345187	ESTs	3.5
	458743	R53169	Hs.80712	KIAA0202 protein	3.5
	447925	AW292271	Hs.250718	ESTs	3.5
	445424	AB028945	Hs.12696	contactin SH3 domain-binding protein	3.5
80	416874	H98752	Hs.42568	ESTs	3.5
	430456	AA314998	Hs.241503	hypothetical protein	3.5
	419647	AA348947	Hs.91816	hypothetical protein	3.5
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fs, clone C	3.5

	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	3.5
	451066	AI758660	Hs.206132	ESTs	3.5
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	3.5
5	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	3.5
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.5
	442118	AA976718	Hs.202242	ESTs	3.5
	421686	AB011156	Hs.106794	KIAA0584 protein	3.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.5
10	444326	AI839357	Hs.270710	ESTs	3.5
	443361	AI792628	Hs.133273	ESTs	3.5
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.4
	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	3.4
	419235	AW470411	Hs.288433	neurotrophin	3.4
15	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4
	417084	H08370	Hs.33067	ESTs	3.4
	432925	AA878324		ESTs	3.4
	439920	H05430	Hs.288433	neurotrophin	3.4
	453710	AL119136	Hs.236131	homeodomain-interacting protein kinase 2	3.4
20	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.4
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.4
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	3.4
	449611	AI970394	Hs.197075	ESTs	3.4
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	3.4
25	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.4
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	3.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.4
	445666	R59960	Hs.282386	ESTs	3.4
	412820	BE001236		gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3.4
30	458912	AI911066		ESTs	3.4
	452449	AW068658	Hs.20943	ESTs	3.4
	437085	AA743935	Hs.202329	ESTs	3.4
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.4
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.4
35	435741	AI240668	Hs.113099	ESTs	3.4
	445828	F05802	Hs.81907	ESTs	3.4
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.4
	431733	AW298410	Hs.21475	ESTs	3.4
	415949	H10562	Hs.21691	ESTs	3.4
40	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	3.4
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	3.4
	442593	R39804	Hs.31961	ESTs	3.4
	442927	AI024347	Hs.131519	ESTs	3.4
	429528	AI985303	Hs.99361	ESTs	3.4
45	450756	AI733488	Hs.144062	ESTs	3.4
	437387	AI198874	Hs.28847	AD026 protein	3.4
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	3.4
	404283			ENSP00000244751*:Copine-like protein KIA	3.4
50	433229	AB040925	Hs.91625	KIAA1492 protein	3.4
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.4
	436114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.4
	439690	AA843868	Hs.190567	ESTs	3.4
	450784	AW246803	Hs.47289	ESTs	3.4
	417868	AI078534	Hs.122592	ESTs	3.3
55	439793	AA018825	Hs.7934	Kruppel-like factor 4 (gut)	3.3
	456209	W60633	Hs.297792	ESTs	3.3
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.3
	438201	AA780243	Hs.54647	ESTs	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
60	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	3.3
	423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
	415539	AI733881	Hs.72472	BMP-R1B	3.3
	450337	AI693256	Hs.202427	ESTs	3.3
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	3.3
65	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp7611224 (f	3.3
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.3
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	3.3
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.3
70	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
	404632			NM_022490:Homo sapiens hypothetical prot	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares fetal liver spleen	3.3
	436267	AW450938	Hs.180115	ESTs	3.3
75	426625	T78300	Hs.300642	serologically defined colon cancer antig	3.3
	401272			C9000559*:gi12314195[emb]CAB99338.1 (A	3.3
	435071	D60683	Hs.35495	ESTs	3.3
	433128	AB021923	Hs.23367	EST-YD1 protein	3.3
	426920	AA393351	Hs.132121	ESTs	3.3
80	423668	Y10148	Hs.131138	neurotensin receptor 2	3.3
	435056	AW023337	Hs.5422	glycoprotein M6B	3.3
	445534	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	445260	AI218133	Hs.147617	ESTs	3.3

	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	3.3
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.3
5	432488	AA551010	Hs.216640	ESTs	3.3
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.3
	412719	AW016610	Hs.816	ESTs	3.3
	420050	AL118615	Hs.94653	neurochondrin	3.3
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.3
10	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.3
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434574	AI424458	Hs.33470	ESTs	3.2
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.2
	426757	AW205640	Hs.158206	ESTs	3.2
15	428167	AA770021	Hs.16332	ESTs	3.2
	451597	AW295250	Hs.207536	ESTs	3.2
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	429550	AW293055	Hs.119357	ESTs	3.2
20	404120			CS000537*gi3298595 gb AAC41376.1 (AF0	3.2
	417123	BE326521	Hs.159450	ESTs	3.2
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	3.2
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	3.2
25	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.2
	415558	AA885143	Hs.125719	ESTs	3.2
	451996	AW514021	Hs.245510	ESTs	3.2
	420560	AW207748	Hs.59115	ESTs	3.2
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	3.2
30	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2
	414300	AI304870	Hs.188680	ESTs	3.2
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCL_CGAP_GCB1 Homo sapiens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.2
	447714	AW296313	Hs.255537	ESTs	3.2
35	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	3.2
	443431	AI056847	Hs.20654	ESTs	3.2
	445774	AI254165	Hs.339968	ESTs	3.2
	431327	AW972220	Hs.105426	ESTs	3.2
	413335	AI613318	Hs.48442	ESTs	3.2
40	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	3.2
	445858	AL133811		solute carrier family 1 (glial high affi	3.2
	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.2
	439039	AI656707	Hs.48713	ESTs	3.2
	401720			NM_014587*:Homo sapiens SRY (sex determi	3.2
45	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 femi	3.2
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.2
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypotheti	3.2
	438138	R98299	Hs.177502	ESTs	3.2
	436338	W92147	Hs.118394	ESTs	3.2
	417169	R13550	Hs.246773	ESTs	3.2
50	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	3.2
	435767	H73505	Hs.117874	ESTs	3.2
	415314	N88802	Hs.5422	glycoprotein M6B	3.2
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.2
55	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.2
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	3.2
	453896	AW293483	Hs.255205	KIAA1853 protein	3.1
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
60	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
	429046	X57436	Hs.194772	oligodendrocyte myelin glycoprotein	3.1
	421896	N52293	Hs.45107	ESTs	3.1
	413995	BE048146	Hs.75671	synlaxin 1A (brain)	3.1
	414734	AA151712	Hs.82572	ESTs	3.1
65	446147	AL133064	Hs.14051	Homo sapiens mRNA; cDNA DKFZp434A2417 (f	3.1
	427712	AI368024	Hs.283696	ESTs	3.1
	406481			Target Exon	3.1
	453204	R10799	Hs.191990	ESTs	3.1
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.1
70	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	3.1
	421030	AW161357		microtubule-associated protein tau	3.1
	423603	AB007880	Hs.129883	Homo sapiens KIAA0420 mRNA, complete cds	3.1
	413985	AI018666	Hs.75667	synaptophysin	3.1
	431721	AB032996	Hs.268044	KIAA1170 protein	3.1
75	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
	429876	AB028977	Hs.225974	KIAA1054 protein	3.1
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.1
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	3.1
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.1
80	453324	W26592	Hs.232089	ESTs	3.1
	424009	F11690		gb:HSC300041 normalized infant brain cDN	3.1
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	446862	AV660697	Hs.282700	ESTs	3.1

5	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	3.1
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	3.1
	415838	R44336	Hs.7093	ESTs	3.1
	451692	AL137422	Hs.26849	Homo sapiens mRNA; cDNA DKFZp761A1623 (f	3.1
	445294	Z45978		Human clone Z3826 mRNA sequence	3.1
	434460	AA478486	Hs.3852	KIAA0368 protein	3.1
	449919	AI674685	Hs.200141	ESTs	3.1
	440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	3.1
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	3.1
	428060	AA420616	Hs.249483	ESTs	3.1
	423597	AL043117	Hs.129872	sperm associated antigen 9	3.1
	452454	AW820480		gb:QV2-ST0298-140200-042410 ST0298 Homo	3.1
	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.1
15	413974	BE208636	Hs.27788	ESTs	3.1
	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	435375	AI733610	Hs.187832	ESTs	3.1
	450661	AW952160	Hs.83849	ESTs	3.1
20	428647	AA830050	Hs.124344	ESTs	3.1
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.0
	443845	AI590084	Hs.148485	ESTs, Weakly similar to A47161 Mac-2-bin	3.0
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
25	437738	AA766914	Hs.203475	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	444772	AW450800	Hs.178859	ESTs	3.0
	453825	AL157475	Hs.35453	Homo sapiens mRNA; cDNA DKFZp761G151 (fr	3.0
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	3.0
	408449	NM_004408	Hs.166161	dynamitin 1	3.0
30	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	3.0
	453657	W23237	Hs.296162	AD037 protein	3.0
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.0
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	3.0
35	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.0
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.0
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.0
	440461	R52728	Hs.7193	KIAA1183 protein	3.0
40	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-link	3.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	447881	BE620886	Hs.75354	GCN1 (general control of amino-acid synt	3.0
	454042	H22570		hypothetical protein FLJ20093	3.0
	429168	AA984682	Hs.146589	ESTs, Weakly similar to JC5238 galactosy	3.0
45	451391	AA017410	Hs.40568	ESTs	3.0
	446377	AW014022	Hs.170953	ESTs	3.0
	430251	AA609246	Hs.181451	ESTs	3.0
	420658	AW965215	Hs.130707	ESTs	3.0
	454119	BE549773	Hs.40510	uncoupling protein 4	3.0
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	3.0
50	435321	R16814	Hs.112062	ESTs	3.0
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.0
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.0
	431242	AA987742	Hs.347534	KIAA1201 protein	3.0
	403022			C21000178*:gii7341207[gb]AAF61215.1[AF22	3.0
55	445899	AI263736	Hs.145626	ESTs	3.0
	440261	M81886	Hs.71117	glutamate receptor, ionotropic, AMPA 1	3.0
	446809	AW590171	Hs.101413	ESTs	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.0
60	448499	BE613280	Hs.77550	hypothetical protein MGC1780	3.0
	432229	AW290976	Hs.143587	ESTs	3.0
	443726	AI083825	Hs.148382	ESTs	3.0

TABLE 13B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
70	408065	103646_1	AW954272 AI003154 AA059300 AA046911
	410099	117647_1	AA081630 T08671 AI174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 AI439658 AA283724 AI805992 AI457096 AA084618 BE467736 AI092635 AI887863 AI697593 AA436618 AI167419 AI418634 T31586 AA436630 AA706191 AI041169 AI422304 T03534 AA211402 AI204899 AI366472 AW827081 AA788593 T32736 AI767935 AA167791 AA747914 AA663870 AI865504
	410126	117761_1	BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880
75	411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
	411775	125757_1	H08342 R52430 Z42067 AA095285
	412021	1272156_1	AW885592 AW885594 AW885579 AW885651
80	412799	132817_1	AI267606 AA121045 AA126521
	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE001236 BE001177 BE001180 BE001234 D61119 D81508 D81734
	412820	1330039_1	
	415131	1523680_1	

418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649
420111	190755_1	AA255652 AA280911 AW967920 AA262684
420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
421030	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454 AI807703 R44253 AA976667 AI985185 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045 Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW204071 AW956110 C15616 D81142 H17038 AW162343 T87230 AI366013 H10064 AI190479 AI093318 AI867923 BE219303 BE048820 AI198397 AA654667 Z39851 F02655 Z28734 F04161 T16575 F10145 AA318815 R40898
423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 AI299437 AL133995 AA057405 N78357 AA917450 AI002692 T09262 T65008 H29290 AI200874 AA894415 AI732887 AI791768 AI733447 AA988785 N62128 T09261 AW956936
424009	234177_1	F11690 AW965370 AA333586 D30830
424572	24097_1	M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303 AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 AI858240 R73218 H30477 H17776 AA659570 BE276750 AI118657 AA375861 AA352427 AW581695 AI141188 N63474 AA654162 H17659 AI120696 T28867 AW498868 AI355918 AA902349 AA569098 AI088231 AI042604 AA555133 AI183611 AI608822 AI275941 AW316805 AA349486 AI355233 R85117 AW613626 R49234 AA458846 N20669 H18693 AA977567 T15423 AW002084 AI824721 N36242 AA17281 AI018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916639 AA872560 F00482 H45184 AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 AI807085 AA808009 AA915914 F00007 AA019749 AL121560 AW675544 AW090233 AW072071 AI810932 AI089733 AW026222 AA770155 AI089647 AI085733 AW516061 AI037635 AL037635 AI863947 H50420 R11203 AA019133 N94772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13146 AA349487 AU077160 BE255671 BE276795 BE250823 AL120301 BE311390 BE252483 AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N29658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665
425331	250199_1	AW962128 AA355353 AA427363
426413	266650_1	AA377823 AW954494 AI022688
426503	268283_1	AA380153 AA380233 AW963529
426919	273507_1	AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601
428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 D80642 AA443145 AL119015 AW904500 AL031658 AI693758 AL040619 AW977914 AA811957 AI352198 AW104364 AA648367 AA897604 AW341668 AI201382 AL040620 BE010038 AA676833 AI311783 T88895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909 AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 AI352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 AW972830 AA527647 AA489820 AA570362 AW753310 AW974000 AA557840 AA558570 AW751539 AA878324 AI863159 AI619686 AA570406 AI014377 AA761668 AA573621 R92814 R09670 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA742643 AA808575 AW976668 AI147061 AA743380 AA765223 AW976398 AI803927 AW975186 AA807807 D29548 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077 AA973905 AI299888 AA917019 H63235 T90771 Z45978 U79248 T77277 R24952 AA361008 AW953678 T10376 AW860579 AW860657 AW364889 AW860635 AW860658 AW905164 W21226 AA448954 W69484 AA993098 AA287413 AA449682 AI961815 W57612 AW271363 R45215 AW136256 AI865103 W69577 AI961826 AA747542 AA173746 AI961816 F07706 R39461 F04829 F05938 AA172385 AI133811 M78538 T07792 AW895859 AW895589 AL119422 T79876 R19494 AF131756 H18570 T08285 F11532 Z42038 AW961964 AA683391 M62092 AL119616 Z21141 AA663820 Z19748 H18462 AL120152 R43841 R37594 AA775980 F09194 AI207884 Z38142 F01555 AA020737 AL120362 AW952737 T04912 Z44514 AI352097 AI803984 AW235923 AI965558 AI954637 AI336983 R36075 AI366546 R36167 AI458682 H24240 R14537 R18426 AW867082 AI339732 AA010300 AW515041 AA768334 Z29860 AA425874 AA425118 AA865829 AW936878 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612 AW820480 AW820288 AI902522 AL120266 AW269469 AW890114 H22570 AW292267 AW137298 AW874199 AI206120 H45263 AA788851 R49056 AW241428 AI921013 AW129293 AI684910 BE466753 AA340613 AW025969 AI202561 AI243913 AW771106 F04969 AI654847 AI494436 AW771447 AW103715 N64350 AA347071 AI431587 AA779107 AA041195 AI358894 AI421678 AI018523 AA707199 AA410309 AI366468 AW020049 AI880103 AL119553 R42410 R55722 T66767 R43035 H17396 H45331 F01659 Z38381 AA708686 AI081305 R53955 AA041432 W27787 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 AI911066 AI933734 AI680888 AJ003599 AI821122 AI821866

TABLE 13C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400658	8118459	Minus	73525-73644
400777	8131663	Plus	70745-71121
401272	9797373	Minus	98374-98509
401720	6468551	Plus	7783-8468
402145	8018280	Plus	113086-114800
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973
402855	9662953	Minus	59763-59909
403022	3132351	Plus	92097-92864
403142	9444521	Plus	89286-90131
403341	8569175	Plus	30699-30910
403696	3135242	Minus	143467-143634
404120	7342152	Plus	135775-136000
404185	4572584	Minus	129171-129327
404283	2276311	Minus	99460-99564
404541	8318559	Plus	103456-103664
404584	9857511	Plus	138651-139153
404632	9796668	Plus	45096-45229
404819	4678240	Plus	16223-16319, 16427-16513, 16736-16859, 16941-17075, 17170-17287, 17389-17529, 18261-18357, 18443-18578
405238	7249119	Minus	51728-51836
405239	7249119	Plus	144345-144464, 144690-144836, 151750-151883, 152407-152484
405348	2914717	Minus	43310-43462
405819	4007557	Plus	2830-2967
405481	9864741	Minus	91439-91579

TABLE 14A: ABOUT 1111 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 14A lists about 1111 genes up-regulated in glioblastoma compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" glioblastoma to "average" CNS tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 65th percentile amongst various brain tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of GLIOBLASTOMA to CNS

Pkey	ExAccn	UnigenelD	Unigene Title	R1
422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	32.8
423961	D13666	Hs.136348	periostin (OSF-2os)	28.0
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	25.3
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	24.3
424800	AL035588	Hs.153203	MyoD family inhibitor	22.6
417308	H60720	Hs.81892	KIAA0101 gene product	22.2
449539	W80363	Hs.58446	ESTs	20.7
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	18.7
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	18.6
444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	17.2
412420	AL035668	Hs.73853	bone morphogenetic protein 2	16.7
417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	16.7
414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	14.3
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	14.3
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.1
446584	U53445	Hs.15432	downregulated in ovarian cancer 1	13.9
422672	X12784	Hs.119129	collagen, type IV, alpha 1	13.6
402604			Target Exon	13.6
424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fs, clone PL	13.0
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.9
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	12.5
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.4
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	12.2
456759	BE259150	Hs.127792	delta (Drosophila)-like 3	12.1
409638	AW450420	Hs.21335	ESTs	11.5
441269	AW015206	Hs.178784	ESTs	10.5
435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	10.5
422163	AF027208	Hs.112360	prominin (mouse)-like 1	10.1
444969	AI203334	Hs.160628	ESTs	10.1
430132	AA204586	Hs.234149	hypothetical protein FLJ20647	9.9
433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	9.4
445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	9.2
413929	BE501689	Hs.75617	collagen, type IV, alpha 2	9.1
425187	AW014486	Hs.22509	ESTs	9.1
449722	BE280074	Hs.23960	cyclin B1	8.9
449611	AI970394	Hs.197075	ESTs	8.9
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.9
419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fs, clone C	8.9
443731	AI083928	Hs.145418	ESTs	8.8
402855			NM_001839*:Homo sapiens catponin 3, acid	8.7

	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.6
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	8.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
	417426	NM_002291	Hs.82124	laminin, beta 1	8.4
5	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	8.3
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.1
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	8.1
	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	8.1
	430691	C14187	Hs.103538	ESTs	8.0
10	447726	AL137638	Hs.19368	matrilin 2	8.0
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	7.9
	447004	AW296968	Hs.157539	ESTs	7.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.8
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	7.8
15	419938	AU076772	Hs.1279	complement component 1, r subcomponent	7.7
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	7.7
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	7.5
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.5
20	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.5
	406972	M32053		gb:Human H19 RNA gene, complete cds.	7.4
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	7.4
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.3
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	7.3
25	409902	AI337658	Hs.156351	ESTs	7.3
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.2
	449961	AW265634	Hs.133100	ESTs	7.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	7.2
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	7.2
30	428728	NM_016625	Hs.191381	hypothetical protein	7.1
	429183	AB014604	Hs.197955	KIAA0704 protein	7.1
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	7.1
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	7.0
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	7.0
35	453941	U39817	Hs.36820	Bloom syndrome	6.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheri	6.9
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.8
	411078	AI222020	Hs.182364	CocoaCrisp	6.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.7
40	448769	N56037	Hs.38173	ESTs	6.7
	418400	BE243026	Hs.301989	KIAA0246 protein	6.6
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	6.6
	440210	AW674562	Hs.125296	ESTs	6.6
	437036	AI571514	Hs.133022	ESTs	6.6
45	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	6.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	6.6
	449300	AI656959	Hs.346514	ESTs	6.5
	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheri	6.5
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.5
50	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.5
	452461	N78223	Hs.108106	transcription factor	6.5
	408243	Y00787	Hs.624	interleukin 8	6.5
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	6.4
	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
	406478			Target Exon	6.4
55	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	6.4
	439710	AF086543		gb:Homo sapiens full length insert cDNA	6.4
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	6.4
	410276	AI554545	Hs.68301	angiopoietin-2	6.4
60	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	6.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	6.3
	436895	AF037335	Hs.5338	carbonic anhydrase XII	6.3
	447458	AI741082	Hs.158961	ESTs	6.3
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	6.3
65	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.3
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	6.2
	440704	M69241	Hs.162	insulin-like growth factor binding prote	6.2
	400419	AF084545		Target	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (ratkines	6.2
70	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.2
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
	430630	AW269920	Hs.2621	cystatin A (stefin A)	6.0
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	6.0
75	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
	413627	BE182082	Hs.246973	ESTs	6.0
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.9
	421899	AJ011895	Hs.109281	Nef-associated factor 1	5.9
	407182	AA312551	Hs.230157	ESTs	5.9
80	410286	AI739159	Hs.61898	DKFZP586N2124 protein	5.9
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	5.9
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	5.8
	418097	R45137	Hs.21868	ESTs	5.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.8

	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	5.7
	421988	AW450481	Hs.161333	ESTs	5.7
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	5.7
5	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
	434846	AW295389	Hs.119768	ESTs	5.7
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	5.7
	452372	AI885742	Hs.228474	ESTs	5.6
	443247	BE614387	Hs.333893	c-Myc target JPO1	5.6
10	423198	M81933	Hs.1634	cell division cycle 25A	5.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.6
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	429447	AW812452	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	5.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	5.6
15	437695	AA769202	Hs.192142	ESTs	5.6
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	5.6
	453361	AA035197	Hs.107375	ESTs	5.5
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	5.5
	405348			C7001664.gi12698061 dbj BAB21849.1 (AB	5.5
20	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	452799	AI948829	Hs.213786	ESTs	5.4
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.4
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.4
25	424009	F11690		gb:HSC300041 normalized infant brain cDN	5.4
	440332	AI218517	Hs.188051	ESTs	5.4
	422094	AF129535	Hs.272027	F-box only protein 5	5.4
	443884	N20617	Hs.194397	leptin receptor	5.4
30	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
	432731	R31178	Hs.287820	fibronectin 1	5.4
	426108	AA622037	Hs.166468	programmed cell death 5	5.3
	407624	AW157431	Hs.248941	ESTs	5.3
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	5.3
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	5.3
35	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.2
	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.2
	413786	AW613780	Hs.13500	ESTs	5.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	5.2
	428037	N47474	Hs.89230	potassium intermediate/small conductance	5.2
40	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	5.1
	416737	AF154335	Hs.79691	LIM domain protein	5.1
	445837	AI261700	Hs.145544	ESTs	5.1
	425882	U83115	Hs.161002	absent in melanoma 1	5.1
	415682	AI347128	Hs.191870	ESTs	5.1
45	414053	BE391635	Hs.75725	transgelin 2	5.1
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	431512	BE270734	Hs.2795	lactate dehydrogenase A	5.1
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	5.0
	433323	AA805132	Hs.159142	ESTs	5.0
50	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.0
	410434	AF051152	Hs.63668	toll-like receptor 2	5.0
	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	5.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.9
	446131	NM_000929	Hs.290	phospholipase A2, group V	4.9
55	412777	AI335773	Hs.270123	ESTs	4.9
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	4.9
	433244	AB040943	Hs.271285	KIAA1510 protein	4.9
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
	445118	AI208762	Hs.345572	ESTs	4.9
60	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
	420092	AA814043	Hs.88045	ESTs	4.9
	412811	H06382		ESTs	4.9
	436607	AW661783	Hs.211061	ESTs	4.9
	438456	AA913381	Hs.20594	ESTs	4.9
65	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	4.9
	431553	X78075	Hs.2799	cartilage linking protein 1	4.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.9
	411252	AB018549	Hs.69328	MD-2 protein	4.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	4.8
70	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	403349	NM_001406		ephrin-B3	4.8
	402274			C19000498.gi4567179 gb AA223607.1 AC00	4.8
	426044	AA502490	Hs.170290	ESTs	4.8
	423600	AI633559	Hs.310359	ESTs	4.8
75	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.8
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	4.7
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	4.7
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.7
80	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	4.7
	435937	AA830893	Hs.119769	ESTs	4.7
	403961			Target Exon	4.7
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	4.6
	408523	AW833259	Hs.314287	ESTs	4.6

	403481		Target Exon	4.6
	423529	T87318	ESTs	4.6
	416847	L43821	enhancer of filamentation 1 (cas-like do	4.6
5	453362	H14988	ESTs	4.6
	407013	U35637	gb:Human nebulin mRNA, partial cds	4.6
	423757	AL049337	Hs.132571 Homo sapiens mRNA; cDNA DKFZp564P016 (fr	4.6
	432363	AA534489	gb:n776g11.s1 NCI_CGAP_Co3 Homo sapiens	4.6
	408380	AF123050	diubiquitin	4.6
10	429149	AW193360	Hs.44532 ESTs, Weakly similar to I38022 hypoteti	4.6
	422170	AI791949	Hs.112432 anti-Mullerian hormone	4.6
	405558		Target Exon	4.6
	410295	AA741357	Hs.5174 nidogen (enactin)	4.6
	450166	AA429504	ESTs	4.6
15	451418	BE387790	Hs.26369 hypothetical protein FLJ20287	4.5
	420075	AF142482	Hs.203846 TEA domain family member 3	4.5
	422158	L10343	Hs.112341 protease inhibitor 3, skin-derived (SKAL	4.5
	457465	AW301344	Hs.122908 DNA replication factor	4.5
	436827	H72187	Hs.5322 guanine nucleotide binding protein (G pr	4.5
20	452620	AA436504	Hs.119286 ESTs	4.5
	424381	AA285249	Hs.146329 protein kinase Chk2	4.5
	444656	AI277924	Hs.145199 ESTs	4.5
	450639	AI703186	Hs.277174 ESTs	4.5
	424247	X14008	Hs.234734 lysozyme (renal amyloidosis)	4.5
25	423178	AJ033140	Hs.124983 Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5
	447072	D61594	Hs.17279 tyrosylprotein sulfotransferase 1	4.5
	447444	AK000318	Hs.18616 hypothetical protein FLJ20311	4.4
	401454		NM_014226*:Homo sapiens renal tumor anti	4.4
	420560	AW207748	Hs.59115 ESTs	4.4
30	409205	AJ952884	Hs.14832 ESTs, Moderately similar to unnamed prot	4.4
	451129	BE072881	gb:RC2-BT0548-200300-012-e09 BT0548 Homo	4.4
	412530	AA766268	Hs.266273 hypothetical protein FLJ13346	4.4
	447752	M73700	Hs.105938 lactotransferrin	4.4
	429083	Y09397	Hs.227817 BCL2-related protein A1	4.4
35	418283	S79895	Hs.83942 cathepsin K (pseudosostosis)	4.3
	424736	AF230877	Hs.152701 microtubule-interacting protein that ass	4.3
	416379	N38857	Hs.203933 ESTs	4.3
	452994	AW962597	Hs.31305 KIAA1547 protein	4.3
40	437834	AA769294	Hs.283854 gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.3
	441035	AI694309	Hs.126458 ESTs	4.3
	425292	NM_005824	Hs.155545 37 kDa leucine-rich repeat (LRR) protein	4.3
	418030	BE207573	Hs.83321 neuromedin B	4.3
	450811	AI739486	Hs.245497 ESTs	4.3
	438458	AW975186	gb:EST387294 MAGE resequences, MAGN Homo	4.3
45	442201	AW516704	Hs.208726 ESTs	4.3
	429732	U20158	Hs.2488 lymphocyte cytosolic protein 2 (SH2 doma	4.3
	435677	AA694142	Hs.293726 ESTs, Weakly similar to TSGA RAT TESTIS	4.3
	442832	AW206560	Hs.253569 ESTs	4.3
	449318	AW236021	Hs.78531 Homo sapiens, Similar to RIKEN cDNA 5730	4.2
50	421027	AA761198	Hs.55254 ESTs	4.2
	414300	AI304870	Hs.188680 ESTs	4.2
	452874	AK001061	Hs.30925 hypothetical protein FLJ10199	4.2
	444161	N52543	Hs.142940 ESTs	4.2
	416908	AA333990	Hs.80424 coagulation factor XIII, A1 polypeptide	4.2
55	418483	W26076	Hs.221847 ESTs	4.2
	443318	AI051603	Hs.133141 ESTs	4.2
	415079	R43179	Hs.22895 hypothetical protein FLJ23548	4.2
	416871	H98716	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	423678	AW963357	Hs.7847 ESTs	4.2
60	429643	AA455889	Hs.167279 FYVE-finger-containing Rab5 effector pro	4.2
	438875	AA827640	Hs.189059 ESTs	4.2
	428600	AW863261	Hs.242413 hypothetical protein DKFZp434K1421	4.2
	430968	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	4.2
	406872	AI760903	gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.2
65	403790		NM_001334*:Homo sapiens cathepsin O (CTS	4.1
	409112	BE243971	Hs.50649 quinone oxidoreductase homolog	4.1
	435703	AW630133	Hs.83313 GK003 protein	4.1
	432625	AI243596	Hs.94830 ESTs, Moderately similar to T03094 A-kin	4.1
	404407		Target Exon	4.1
70	412568	AI878826	Hs.74034 caveolin 1, caveolae protein, 22kD	4.1
	422087	X58968	Hs.111301 matrix metalloproteinase 2 (gelatinase A	4.1
	435143	R12375	Hs.194600 ESTs	4.1
	447497	AW167254	Hs.205722 ESTs	4.1
	456304	AI820973	gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.1
75	427676	AA394062	Hs.300772 tropomyosin 2 (beta)	4.1
	436608	AA628980	down syndrome critical region protein DS	4.1
	453331	AI240665	ESTs	4.0
	420004	AW975532	Hs.164039 ESTs, Moderately similar to I38022 hypot	4.0
	412125	Y17114	Hs.73393 eyes absent (Drosophila) homolog 4	4.0
80	426215	AW963419	Hs.155223 stanniocalcin 2	4.0
	407603	AW955705	Hs.62604 Homo sapiens, clone IMAGE:4299322, mRNA,	4.0
	450581	AF081513	Hs.25195 TGF-beta 4	4.0
	415323	BE269352	Hs.949 neutrophil cytosolic factor 2 (65kD, chr	4.0
	409893	AW247090	Hs.57101 minichromosome maintenance deficient (S.	4.0

	432058	AW665996	Hs. 130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	444609	AW571659	Hs. 278081	ESTs	4.0
	445666	RS9960	Hs. 282386	ESTs	4.0
5	437814	AI088192	Hs. 135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
	414948	C15240	Hs. 182155	ESTs	4.0
	435542	AA687376		ESTs	4.0
	422564	AI148006	Hs. 222120	ESTs	4.0
	449571	AW016812	Hs. 200266	ESTs	4.0
10	433556	W56321	Hs. 111460	calcium/calmodulin-dependent protein kin	4.0
	458946	AA009716	Hs. 42311	ESTs	4.0
	449655	AI021987	Hs. 59970	ESTs	4.0
	426649	AI914936	Hs. 97152	ESTs	4.0
	457292	AI921270	Hs. 281462	hypothetical protein FLJ14251	4.0
15	440435	AL042201	Hs. 21273	transcription factor NYD-sp10	4.0
	456977	AK000252	Hs. 169758	hypothetical protein FLJ20245	4.0
	420649	AI866964	Hs. 124704	ESTs, Moderately similar to S65657 alpha	4.0
	416406	D86961	Hs. 79299	ipoma HMGC fusion partner-like 2	4.0
	446291	BE397753	Hs. 14623	interferon, gamma-inducible protein 30	3.9
20	449256	AA059050	Hs. 59847	ESTs	3.9
	421637	AF035290	Hs. 106300	Homo sapiens clone 23556 mRNA sequence	3.9
	456306	AA225313	Hs. 222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.9
	438372	AI140189	Hs. 123191	ESTs	3.9
	427375	AL035460	Hs. 177536	metallocarboxypeptidase CPX-1	3.9
25	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.9
	439231	AW581935	Hs. 141480	Homo sapiens mRNA: cDNA DKFZp434N079 (fr	3.9
	424998	U58515	Hs. 154138	chitinase 3-like 2	3.9
	433376	AI249361	Hs. 74122	caspase 4, apoptosis-related cysteine pr	3.9
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	3.9
30	443426	AF098158	Hs. 9329	chromosome 20 open reading frame 1	3.9
	419594	AA013051	Hs. 91417	topoisomerase (DNA) II binding protein	3.9
	417576	AA339449	Hs. 82285	phosphoribosylglycinamide formyltransfer	3.9
	416857	AA188775	Hs. 292453	ESTs	3.9
	434784	AA649051	Hs. 164007	ESTs	3.8
35	438898	AI819863	Hs. 106243	ESTs	3.8
	408102	U46351	Hs. 621	lectin, galactoside-binding, soluble, 3	3.8
	422081	AW136820	Hs. 196011	ESTs	3.8
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	3.8
	447343	AA256641	Hs. 236894	ESTs, Highly similar to S02392 alpha-2-m	3.8
40	406395			Target Exon	3.8
	433675	AW977653	Hs. 75319	ribonucleotide reductase M2 polypeptide	3.8
	403696			C4001100*:gil5852342[gb]AAD54015.1] (AF0	3.8
	443740	R56434	Hs. 21062	ESTs	3.8
	413076	U10564	Hs. 75188	wee1 (S. pombe) homolog	3.8
45	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.8
	444326	AI939357	Hs. 270710	ESTs	3.8
	436899	AA764852	Hs. 291567	ESTs	3.8
	445075	AI651827	Hs. 344767	ESTs	3.8
	416892	L24498	Hs. 80409	growth arrest and DNA-damage-inducible,	3.8
50	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	416114	AI695549	Hs. 183868	glucuronidase, beta	3.8
	417018	M16038	Hs. 80887	v-yes-1 Yamaguchi sarcoma viral related	3.8
	446839	BE091926	Hs. 16244	mitotic spindle coiled-coil related prot	3.8
	454117	BE410100	Hs. 40368	adaptor-related protein complex 1, sigma	3.8
55	416664	H72780	Hs. 20289	ESTs	3.8
	449444	AW818436	Hs. 23590	solute carrier family 16 (monocarboxylic	3.8
	419735	AW750056	Hs. 169577	Homo sapiens cDNA FLJ14743 fis, clone NT	3.8
	448275	BE514434	Hs. 20830	kinesin-like 2	3.7
	405141	Y14443		zinc finger protein 200	3.7
60	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.7
	422648	D86983	Hs. 118893	Melanoma associated gene	3.7
	449145	AI632122	Hs. 198408	ESTs	3.7
	428060	AA420616	Hs. 249483	ESTs	3.7
	404584			Target Exon	3.7
65	418596	AW976721	Hs. 293327	ESTs	3.7
	458072	AI890347	Hs. 271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.7
	445908	R13580	Hs. 13436	Homo sapiens clone 24425 mRNA sequence	3.7
	439979	AW600291	Hs. 6823	hypothetical protein FLJ10430	3.7
	431770	BE221880	Hs. 268555	5'-3' exonuclease 2	3.7
70	427809	M26380	Hs. 180878	lipoprotein lipase	3.7
	436674	AA725002	Hs. 272018	low molecular mass ubiquinone-binding pr	3.7
	413450	Z99716	Hs. 75372	N-acetylgalactosaminidase, alpha-	3.7
	434467	BE552368	Hs. 231853	Homo sapiens cDNA FLJ13445 fis, clone PL	3.7
	448048	BE281291	Hs. 170408	ESTs, Moderately similar to A47582 B-cel	3.7
75	422798	RS2347	Hs. 34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	402082			C18000743*:gil6678363[ref]NP_033416.1] t	3.7
	448019	AW947164	Hs. 195641	ESTs, Moderately similar to I38022 hypot	3.7
	428873	AI701609	Hs. 98908	ESTs	3.7
	437323	AA371145	Hs. 194397	leptin receptor	3.7
80	413095	AA494359	Hs. 30715	potassium voltage-gated channel, Isk-rel	3.7
	425139	AW630488	Hs. 25338	protease, serine, 23	3.7
	452279	AA286844	Hs. 61260	hypothetical protein FLJ13164	3.7
	439574	AI469788	Hs. 165190	ESTs	3.7
	408829	NM_006042	Hs. 48384	heparan sulfate (glucosamine) 3-O-sulfot	3.7

	407838	BE146411	Hs.40342	putative nuclear protein	3.7
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	3.6
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.6
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.6
5	453438	AI689935	Hs.22792	ESTs	3.6
	415024	AI983981	Hs.189114	ESTs	3.6
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.6
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	3.6
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	3.6
10	448002	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.6
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.6
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.6
	402239			Target Exon	3.6
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6
15	443715	AI583187	Hs.9700	cyclin E1	3.6
	403011			ENSP00000215330*:Probable serine/threoni	3.6
	428403	AI393048	Hs.326159	leucine rich repeat (in FLJ) interactin	3.6
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
20	453948	AI970797	Hs.64859	ESTs	3.6
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfam	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.6
	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypotheti	3.6
25	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	406481			Target Exon	3.6
	433835	AI806185		gb:w26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.6
	456052	BE311901	Hs.28935	gb:601142614F1 NIH_MGC_14 Homo sapiens c	3.6
30	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.5
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.5
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	419402	Z68155	Hs.90291	laminin, beta 2 (laminin S)	3.5
	403108			ENSP00000241415*:Hypothetical 67.7 kDa p	3.5
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.5
35	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.5
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.5
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.5
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.5
	425212	AW962253	Hs.171618	ESTs	3.5
40	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.5
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.5
45	421247	BE391727	Hs.102910	general transcription factor IIH, polype	3.5
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.5
	453792	AL134539	Hs.254129	KIAA1678	3.5
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.5
50	412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	3.5
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.5
	407729	T40707	Hs.270862	ESTs	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.5
55	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 14	3.5
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.4
	449932	AI675444	Hs.263024	ESTs	3.4
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	3.4
60	403849			Target Exon	3.4
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	3.4
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	3.4
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.4
	403361			NM_002210*:Homo sapiens integrin, alpha	3.4
	420841	AI625251	Hs.94037	hypothetical protein FLJ23053	3.4
65	438206	AA780385	Hs.187885	ESTs	3.4
	425295	AA431366	Hs.37251	ESTs	3.4
	411789	AF245505	Hs.72157	Adicican	3.4
	440948	AW188311	Hs.128619	ESTs	3.4
70	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
	418821	AA436002	Hs.183161	ESTs	3.4
	459650	M79082		ESTs	3.4
	404209			Target Exon	3.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	3.4
75	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4
	425300	AW601773	Hs.270259	ESTs	3.4
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.4
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.4
	444911	U08117	Hs.250	xanthine dehydrogenase	3.4
80	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	3.4
	441287	AW293132	Hs.131373	ESTs	3.4
	446960	AW294936	Hs.156762	ESTs	3.4
	405605			C2001342:gi127814[sp]P26434[NAH4_RAT SO	3.4
	433791	AA719352	Hs.112718	ESTs	3.4

	405238		Target Exon	3.4	
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.4
5	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.4
	406739	AI566709	Hs.182426	ribosomal protein S2	3.4
	442710	AI015631	Hs.23210	ESTs	3.4
	452526	W38537	Hs.280740	hypothetical protein MGC3040	3.4
	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	3.4
10	435005	U80743	Hs.306094	trinucleotide repeat containing 12	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
	425242	D13635	Hs.155287	KIAA0010 gene product	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	3.4
15	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	3.4
	428878	AA436884	Hs.48926	ESTs	3.3
	413774	AA131782	Hs.182314	ESTs	3.3
	400533			ENSP00000209376*:PRED65 protein (Fragmen	3.3
	422448	AW372922	Hs.116774	integrin, alpha 1	3.3
20	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.3
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.3
	427899	AA829286	Hs.332053	serum amyloid A1	3.3
	434206	AW136973	Hs.180479	ESTs, Weakly similar to S69890 mitogen i	3.3
	453387	AI990741	Hs.252809	ESTs	3.3
25	436265	AA731331	Hs.190668	ESTs	3.3
	412971	AA889628	Hs.35125	ESTs	3.3
	441701	AW339828	Hs.127497	ESTs	3.3
	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.3
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.3
30	418216	AA662240	Hs.283099	AF15q14 protein	3.3
	436137	AI056769	Hs.133512	ESTs	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.3
35	405046			C3000978:gi9280045 dbj BAB01579.1 (AB0	3.3
	437816	AI823445	Hs.280699	ESTs	3.3
	401272			C9000559*:gi12314195 emb CAB99338.1 (A	3.3
	408896	AI610447	Hs.48778	riban protein	3.3
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	3.3
40	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	3.3
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.3
	446134	AW161234	Hs.13993	TBP-like 1	3.3
45	412281	AI810054	Hs.14119	ESTs	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.3
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.3
	409463	AI458165	Hs.17296	hypothetical protein MGC2376	3.3
50	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.3
	450506	NM_004460		fibroblast activation protein, alpha	3.3
	451254	AI571016	Hs.172967	ESTs	3.3
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.3
55	433325	AW206986	Hs.143905	ESTs	3.3
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	3.3
	420552	AK000492	Hs.98806	hypothetical protein	3.3
	451778	AI826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	3.3
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.2
60	433507	AI817336	Hs.191791	ESTs	3.2
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.2
	440933	AI208217	Hs.142879	ESTs	3.2
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	3.2
	404120			C5000537*:gi3298595 gb AAC41376.1 (AF0	3.2
65	453920	AI133148	Hs.36602	I factor (complement)	3.2
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	3.2
	424479	AF064238	Hs.149098	smoothenin	3.2
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.2
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.2
70	407304	AA565832	Hs.271649	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.2
	411671	BE049094		ESTs	3.2
	420352	BE258835		gb:501117374F1 NIH_MGC_16 Homo sapiens c	3.2
	454765	AW819629		gb:RCS-ST0293-140200-014-H05 ST0293 Homo	3.2
	410407	X66839	Hs.63287	carbonic anhydrase IX	3.2
75	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.2
	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	3.2
	417124	BE122762	Hs.25338	ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.2
	439764	T26535	Hs.22744	hypothetical protein MGC13105	3.2
80	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	3.2
	446523	NM_003063	Hs.334629	sarcosin	3.2
	406060			Target Exon	3.2
	432250	AA452088	Hs.274170	Opa-interacting protein 2	3.2
	437269	AA334384	Hs.149420	ESTs	3.2

	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944.1 PRO06	3.2
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	3.2
	436210	AI825420	Hs.197824	ESTs	3.2
5	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 catci	3.2
	444371	BE540274	Hs.239	forkhead box M1	3.2
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.2
	445828	F05802	Hs.81907	ESTs	3.2
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.2
10	439533	W76021		gb:zd54c04.r1 Soares_fetal_heart_NbHH19W	3.2
	418079	R40058	Hs.6911	ESTs	3.2
	418781	T41160	Hs.8404	ESTs	3.2
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.2
	431319	AA873350	Hs.302232	ESTs	3.2
	445413	AA151342	Hs.12677	CGI-147 protein	3.2
15	424947	R77952		ESTs, Weakly similar to alternatively sp	3.2
	429490	A971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.2
	426765	AA743603	Hs.172108	nucleoporin 88kD	3.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.2
20	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.1
	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.1
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	3.1
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.1
25	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	443431	AI056847	Hs.20654	ESTs	3.1
	428289	M26301	Hs.2253	complement component 2	3.1
	415849	R20529	Hs.6806	ESTs	3.1
	419652	AL157485	Hs.91973	hypothetical protein	3.1
30	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	3.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.1
	420579	AA278449	Hs.137429	ESTs	3.1
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.1
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.1
35	405183			NM_016358:Homo sapiens iroquois homeobo	3.1
	420676	AA34780	Hs.4248	vav 2 oncogene	3.1
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	3.1
	431176	AI026984	Hs.293662	ESTs	3.1
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.1
40	437945	T78519		gb:yd68c08.r1 Soares fetal liver spleen	3.1
	404632			NM_022490:Homo sapiens hypothetical prot	3.1
	428917	AA437337	Hs.16689	ESTs	3.1
	429940	W25215		gb:zb87a09.r1 Soares_senescent_fibroblas	3.1
	444016	AA448154		gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
45	430701	AI760833	Hs.293971	ESTs	3.1
	402229	BE262804		mitochondrial ribosomal protein S2	3.1
	454177	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	3.1
	400090			Eos Control	3.1
	419326	W94915	Hs.42419	ESTs	3.1
50	435644	AA700867	Hs.269659	ESTs	3.1
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
	458810	BE407125	Hs.231510	ESTs	3.1
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.1
	449670	F07693	Hs.85603	Homo sapiens mRNA: cDNA DKFZp434K2172 (f	3.1
55	430288			C1001737:gi7511201 pir T27904 hypothe	3.1
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.1
	432044	AW972727		gb:EST384819 MAGE resequences, MAGL Homo	3.1
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.1
60	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	3.1
	439538	AA837323	Hs.56407	ESTs	3.1
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	443021	AA368546	Hs.8904	Ig superfamily protein	3.1
65	433894	AI907682	Hs.243293	ESTs	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.1
	449162	AI632740	Hs.10476	ESTs	3.1
	417893	AA290605	Hs.190002	ESTs	3.1
70	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.0
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.0
	450756	AI733488	Hs.144062	ESTs	3.0
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.0
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.0
75	431019	NM_005249	Hs.2714	forkhead box G1B	3.0
	434503	T96231	Hs.17762	ESTs	3.0
	455481	AW948317		gb:RCO-MT0015-280300-021-a09 MT0015 Homo	3.0
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	3.0
	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.0
80	458760	AI498631	Hs.111334	feritin, light polypeptide	3.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.0
	411543	AW851248		gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	435375	AI733610	Hs.187832	ESTs	3.0
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0

	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	3.0
	443338	R99575	Hs.302908	ESTs	3.0
	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.0
5	412135	AW895309		gb:QV4-NN0038-300300-155-e07 NN0038 Homo	3.0
	418669	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein	3.0
	449385	AJ650471	Hs.347290	ESTs	3.0
	426384	AJ472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW450938	Hs.180115	ESTs	3.0
10	440388	AJ693520	Hs.223000	ESTs	3.0
	427235	AJ126288	Hs.192232	ESTs	3.0
	420116	NM_013241	Hs.95231	FH1/FH2 domain-containing protein	3.0
	419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
15	445921	AW015211	Hs.146181	ESTs	3.0
	427695	R88483	Hs.172862	ESTs	3.0
	453324	W26592	Hs.232089	ESTs	3.0
	404272			Target Exon	3.0
	428538	AA46440	Hs.98643	ESTs	3.0
20	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	3.0
	444396	T65213	Hs.4257	ESTs	3.0
	440483	AJ200836	Hs.150386	ESTs	3.0
	429973	AJ423317	Hs.164680	ESTs	3.0
	450125	AA005418	Hs.158186	ESTs	3.0
25	417409	BE272506	Hs.82109	syndecan 1	3.0
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.0
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.0
	427954	J03060	Hs.247551	metaxin 1	3.0
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	3.0
30	427527	AJ809057	Hs.293441	immunoglobulin heavy constant mu	3.0
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.0
	451130	AJ762250	Hs.345554	ESTs	3.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	425248	AW957442	Hs.252766	ESTs	3.0
35	422757	AJ909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.0
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	3.0
	416355	H49875	Hs.268906	ESTs	3.0
	426406	AJ742501	Hs.169756	complement component 1, s subcomponent	3.0
	419829	AJ924228	Hs.115185	ESTs, Moderately similar to PC4259 feni	3.0
40	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm	3.0
	423869	BE409301	Hs.134012	C1q-related factor	2.9
	422710	AW936566	Hs.201876	ESTs	2.9
	445906	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.9
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	2.9
45	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.9
	443433	R44743	Hs.301667	ESTs	2.9
	444145	BE153823	Hs.282385	ESTs, Weakly similar to 2004399A chromos	2.9
	425262	D87119	Hs.155418	GS3955 protein	2.9
	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	2.9
50	443361	AJ792628	Hs.133273	ESTs	2.9
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.9
	415709	AA649850	Hs.278558	ESTs	2.9
	453385	AW296101	Hs.252806	ESTs	2.9
	442609	AL020996	Hs.8518	selenoprotein N	2.9
55	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2.9
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.9
	443502	AJ074528	Hs.133949	ESTs	2.9
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	2.9
	416308	AW291942	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxido	2.9
60	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.9
	408989	AW361666	Hs.49500	KIAA0746 protein	2.9
	427418	AA402587	Hs.325520	LAT1-3TM protein	2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.9
	426827	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	2.9
65	403290			C10001011::gij4758212[ref][NP_004411.1] d	2.9
	430890	X54232	Hs.2699	glypican 1	2.9
	441217	AJ922183	Hs.213246	ESTs	2.9
	418287	AJ872319	Hs.78935	methionine aminopeptidase; eIF-2-associa	2.9
	443836	BE221613	Hs.140553	ESTs	2.9
70	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	2.9
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	2.9
	420886	AA805453		ESTs, Weakly similar to T29012 hypotheti	2.9
	439379	AA835002	Hs.125611	ESTs	2.9
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.9
75	406679	AA070786		gb:zm66b07.r1 Stratagene neuroepithelium	2.9
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I38022 hypotheti	2.9
	432036	AF224266	Hs.272373	interleukin 20	2.9
	457364	AW971037		gb:EST383123 MAGE resequences, MAGK Homo	2.9
80	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.9
	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	2.9
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	2.9
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.9
	400850			Target Exon	2.9

	428896	AW291932	Hs.98936	ESTs	2.9
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	2.9
	408872	AJ476139	Hs.13291	ESTs	2.9
5	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	2.9
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.9
	416569	H64891		gb:yr68n03.r1 Soares fetal liver spleen	2.9
	439130	AA306090	Hs.124707	ESTs	2.9
	451433	AA021140	Hs.269265	ESTs, Weakly similar to A46010 X-linked	2.9
10	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.9
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.9
	420172	AA601122	Hs.95655	secreted and transmembrane 1	2.9
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.9
	416505	H66470	Hs.16004	ESTs	2.9
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.9
15	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.9
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	2.8
	447499	AW262580	Hs.147674	protocadherin beta 16	2.8
	411373	BE326276	Hs.8861	ESTs	2.8
20	456816	AK001509	Hs.144391	hypothetical protein FLJ10647	2.8
	414232	W86946	Hs.238246	hypothetical protein FLJ22479	2.8
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.8
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.8
	438624	AA889055	Hs.123468	ESTs	2.8
25	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	2.8
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	2.8
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	2.8
	421679	AI475110	Hs.203933	ESTs	2.8
	450651	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti	2.8
30	452785	AL359942	Hs.296434	erythroid differentiation and denudeati	2.8
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.8
	403291			Target Exon	2.8
	453096	AW294631	Hs.11325	ESTs	2.8
	422545	X02761	Hs.287820	fibronectin 1	2.8
35	440296	D30829	Hs.180610	splicing factor protine/glutamine rich (2.8
	427154	AL137262	Hs.325630	hypothetical protein MGC4289	2.8
	422282	AF019225	Hs.114309	apolipoprotein L	2.8
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.8
	414727	BE466804	Hs.190162	gb:hz28f03.x1 NCI_CGAP_G06 Homo sapiens	2.8
40	437437	AA226869		hypothetical protein DKFzP762L0311	2.8
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.8
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.8
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.8
	448432	AI783586	Hs.208575	ESTs	2.8
45	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	2.8
	447527	AI702896	Hs.42091	ESTs	2.8
	418557	BE140602	Hs.246645	ESTs	2.8
	409157	AA064631		gb:zf72c03.s1 Soares_pineal_gland_N3HPG	2.8
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.8
50	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	2.8
	439220	AW295340	Hs.130417	ESTs, Weakly similar to Z195_HUMAN ZINC	2.8
	418312	AW972468	Hs.170307	Rai guanine nucleotide exchange factor R	2.8
	454581	AW809189		gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	2.8
	400645			Target Exon	2.8
55	413951	AW051200	Hs.75640	natriuretic peptide precursor A	2.8
	441360	AI091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110	2.8
	404150			Target Exon	2.8
	402936			ENSP00000217246*:DJ803K15.1 (novel prote	2.8
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	2.8
	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	2.8
	403969			ENSP0000034663:Zinc finger protein 131	2.8
	447183	AI554733	Hs.173182	ESTs	2.8
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.8
65	426141	C05886	Hs.293972	ESTs	2.8
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	2.8
	430335	D80007	Hs.239499	KIAA0185 protein	2.8
	447071	AW236867	Hs.244376	ESTs	2.8
	428899	AA744610	Hs.194431	palladin	2.8
70	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	2.8
	403942			Target Exon	2.8
	420565	AI806770	Hs.30258	ESTs	2.8
	409734	BE161664	Hs.56155	hypothetical protein	2.8
	456645	AF227156	Hs.110103	RNA polymerase I transcription factor RR	2.8
75	401841			NM_015113:Homo sapiens KIAA0399 protein	2.8
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.8
	450150	AI754391	Hs.23510	Kruppel-like factor 12	2.8
	409154	U72882	Hs.50842	interferon-induced protein 35	2.8
	410267	AW978005	Hs.12600	N-ethylmaleimide-sensitive factor attach	2.8
80	448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ2356 fis, clone H	2.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.8
	447512	AW958148	Hs.129454	ESTs	2.8
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	2.8
	415293	R49462	Hs.106541	ESTs	2.8

	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC.2908, mRNA, comp	2.8
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	2.8
	425128	BE561929	Hs.154718	tumor protein D52-like 2	2.7
5	444491	AI151091	Hs.270714	ESTs	2.7
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	2.7
	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	2.7
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	2.7
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.7
10	438138	R98299	Hs.177502	ESTs	2.7
	425421	L11669	Hs.157145	tetracycline transporter-like protein	2.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.7
	451748	AK001612	Hs.26962	Homo sapiens cDNA FLJ10750 fis, clone NT	2.7
	452085	AW239140	Hs.25614	ESTs, Weakly similar to PC4396 mucin 3 T	2.7
15	405941			Target Exon	2.7
	417395	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	2.7
	449667	AB023227	Hs.23860	KIAA1010 protein	2.7
	428808	AA436007	Hs.188780	ESTs	2.7
	425843	BE313280	Hs.159627	death associated protein 3	2.7
20	438025	AW501360	Hs.258910	ESTs	2.7
	400924			Target Exon	2.7
	412898	AI129903	Hs.74669	vesicle-associated membrane protein 5 (m	2.7
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypothe	2.7
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.7
25	406736	AI254733	Hs.182426	ribosomal protein S2	2.7
	414280	BE410769	Hs.75873	zyrin	2.7
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	2.7
	442621	AI004333	Hs.130553	ESTs, Weakly similar to ALUA_HUMAN !!!	2.7
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.7
30	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.7
	416784	AA334592	Hs.79914	lumican	2.7
	413851	AW897510	Hs.137387	ESTs	2.7
	451767	AI625014	Hs.187328	ESTs	2.7
	441668	AI611973	Hs.136313	ESTs	2.7
35	435664	AI032087	Hs.269819	ESTs	2.7
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	439467	AW292275	Hs.158365	ESTs	2.7
	441329	AI203575	Hs.46821	hypothetical protein FLJ20086	2.7
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	2.7
40	427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	2.7
	449919	AI674685	Hs.200141	ESTs	2.7
	458070	AW503578	Hs.209406	ESTs, Weakly similar to I38600 zinc fing	2.7
	444794	AI419991	Hs.145225	ESTs	2.7
	410781	AI375672	Hs.165028	ESTs	2.7
45	449520	R34993	Hs.226666	ESTs, Moderately similar to I54374 gene	2.7
	439481	AF086294	Hs.125844	ESTs	2.7
	401702			NM_001171*:Homo sapiens ATP-binding cass	2.7
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	2.7
50	435545	AA687415	Hs.28107	ESTs	2.7
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	2.7
	420982	AW576160	Hs.100729	KIAA0692 protein	2.7
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	2.7
	444168	AW379879		gb:RC1-HT0256-081199-011-01 HT0256 Homo	2.7
55	419964	AA811657	Hs.220913	ESTs	2.7
	424480	AA341442	Hs.205299	ESTs	2.7
	436314	AI983409	Hs.189226	ESTs	2.7
	405516			ENSP00000200457*:Thyroid receptor intera	2.7
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	2.7
60	457876	AI821940		ESTs, Moderately similar to ALU8_HUMAN A	2.7
	423799	AW026300	Hs.132906	19A24 protein	2.7
	422551	AW967284		gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	2.7
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	2.7
65	428612	AA770001	Hs.188778	ESTs	2.7
	446139	H77395	Hs.39749	ESTs	2.7
	440478	AI733047	Hs.130005	ESTs	2.7
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.7
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.7
70	423713	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo	2.7
	402032			ENSP00000251056*:Plasma membrane calcium	2.7
	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE	2.7
	402799			Target Exon	2.7
	423352	AA324808	Hs.193576	ESTs	2.7
75	412021	AW885592		gb:RC4-OT0071-090300-011-g11 OT0071 Homo	2.7
	458617	Z25900	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	2.7
	404170			NM_000636*:Homo sapiens superoxide dismu	2.7
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	2.7
	414988	C17535		gb:C17535 Human placenta cDNA (TFujiwara	2.7
80	450325	AI935962	Hs.26289	ESTs	2.7
	458918	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypothesi	2.7
	405760			Target Exon	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	2.7

	400335	Y13187	Hs.248068	Homo sapiens dmd gene, intron 11	2.7
	435065	BE064391		gb:RC4-BT0310-110300-015-b08 BT0310 Homo	2.7
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.7
	406785	AA588061		gb:nk10d03.s1 NCL_CGAP_Co2 Homo sapiens	2.7
5	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29265 hypot	2.7
	428690	AI948490	Hs.98765	ESTs	2.7
	432692	AW974944	Hs.200577	ESTs	2.7
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	2.6
10	457035	AA398074	Hs.119143	ESTs, Moderately similar to KIAA1513 pro	2.6
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	2.6
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fs, clone NT	2.6
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	2.6
	422764	AI767727	Hs.47522	ESTs	2.6
15	403431			Target Exon	2.6
	439332	AW842747	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	2.6
	412749	AA378417	Hs.74564	signal sequence receptor, beta (transloc	2.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	2.6
	405717			CX000838:gil10092633[ref]NP_055314.1] pu	2.6
20	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	2.6
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	2.6
	452683	AI089575	Hs.9071	progesterone membrane binding protein	2.6
	447587	AW292139	Hs.115789	ESTs	2.6
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.6
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.6
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	419015	T79262	Hs.14463	ESTs	2.6
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.6
30	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.6
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.6
	404053			Target Exon	2.6
	415069	AA159831	Hs.29286	ESTs, Weakly similar to I49636 DNA-bindi	2.6
35	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	2.6
	438033	T26483	Hs.6059	EGF-containing fibulin-like extracellula	2.6
	451593	AF151879	Hs.26706	CGI-121 protein	2.6
	435828	AA700705	Hs.13852	ESTs	2.6
	443753	AW367578	Hs.134749	ESTs	2.6
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.6
40	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.6
	439755	AW748482	Hs.77873	B7 homolog 3	2.6
	408371	AF161545	Hs.44439	hypothetical protein	2.6
	445658	AI469062	Hs.172660	ESTs	2.6
	438166	N30158	Hs.122645	ESTs	2.6
45	449426	T92251	Hs.198882	ESTs	2.6
	422605	H16646	Hs.118666	hypothetical protein PP591	2.6
	415788	AW628686	Hs.78851	KIAA0217 protein	2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.6
	400295	W72838		AI905687:IL-BT095-190199-019 BT095 Homo	2.6
50	441128	AA570256		ESTs, Weakly similar to T23273 hypothi	2.6
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.6
	428977	AK001404	Hs.194698	cyclin B2	2.6
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	2.6
	445211	BE045601	Hs.118248	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
55	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.6
	417838	R24713	Hs.22514	ESTs	2.6
	420670	AW973577		ESTs	2.6
	403267			Target Exon	2.6
	454354	AW389896		gb:RC4-ST0173-191099-032-e12 ST0173 Homo	2.6
60	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothi	2.6
	427830	AA416598	Hs.98233	ESTs	2.6
	435953	AI767087	Hs.114142	ESTs	2.6
	430744	AA485229	Hs.105649	ESTs	2.6
	413335	AI613318	Hs.48442	ESTs	2.6
65	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothi	2.6
	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse t	2.6
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	447854	AW138454	Hs.11594	ESTs	2.6
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal S8 pool 1	2.6
70	455409	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.6
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	2.6
	434898	AW500458	Hs.29956	KIAA0460 protein	2.6
75	438118	AW753311	Hs.346690	ESTs	2.6
	431786	AW452784	Hs.220718	ESTs	2.6
	421689	N87820	Hs.106826	KIAA1696 protein	2.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.6
	424684	AW752714	Hs.5174	ribosomal protein S17	2.6
80	439823	AW665287	Hs.124514	ESTs	2.6
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	2.6
	445774	AI254165	Hs.339968	ESTs	2.6
	400492			C10001573:gil7302749[gb]AAF57827.1] (AE	2.6

	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	2.6
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.6
	440131	AI023425	Hs.222225	ESTs	2.6
5	438525	AW368528	Hs.100855	ESTs	2.6
	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.6
	406662	X62006	Hs.172550	polypyrimidine tract binding protein (he	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.6
10	429599	AA806106	Hs.123664	ESTs	2.6
	429562	AJ732767	Hs.158101	Homo sapiens cDNA FLJ14673 fis, clone NT	2.6
	432527	AW975028	Hs.102754	ESTs	2.6
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.6
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.6
15	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.6
	413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	416244	N39535	Hs.32748	ESTs	2.6
	403104			C8000064*:gil10432393[emb]CAC10283.1[(A	2.6
	400780			NM_007325*:Homo sapiens glutamate recept	2.6
20	433009	AA761668		gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	2.6
	424090	X99699	Hs.139262	XIAP associated factor-1	2.6
	403212			NM_019595:Homo sapiens intersectin 2 (IT	2.6
	407855	R54126	Hs.40500	similar to S. cerevisiae RER1	2.6
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	2.6
25	443462	AI064690	Hs.171176	ESTs	2.6
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.6
	450089	AI681883	Hs.209546	ESTs, Weakly similar to 2109260A B cell	2.6
	419571	AW674962	Hs.91146	protein kinase D2	2.6
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.6
30	444881	AI623288	Hs.192805	ESTs	2.6
	420658	AW965215	Hs.130707	ESTs	2.6
	437634	AW293046	Hs.255158	ESTs	2.6
	426894	AI204209	Hs.143911	ESTs	2.6
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.6
35	434171	BE247688	Hs.347349	KIAA0948 protein	2.6
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.6
	427245	AA421022	Hs.97739	ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.5
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	2.5
40	452221	C21322	Hs.288057	hypothetical protein FLJ22242	2.5
	439079	AF085937	Hs.38348	ESTs	2.5
	437287	AA748180	Hs.159346	hypothetical protein FLJ21369	2.5
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
	427624	AA406245	Hs.24895	ESTs	2.5
45	435177	AI018174	Hs.42936	ESTs	2.5
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	2.5
	447853	AI434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.5
	416704	H77795	Hs.39785	ESTs	2.5
	401696			Target Exon	2.5
50	445677	H96577	Hs.6838	ras homolog gene family, member E	2.5
	413840	AI301558	Hs.146381	RNA binding motif protein, X chromosome	2.5
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	2.5
	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.5
	421848	X15880	Hs.108885	collagen, type VI, alpha 1	2.5
55	421234	AA907153	Hs.190060	ESTs	2.5
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.5
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.5
	458199	AW136417		hypothetical protein FLJ14464	2.5
	433523	H29882		ESTs	2.5
60	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	2.5
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	2.5
	404748			ENSP00000238177*:Similar to kynurenine 3	2.5
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypotheti	2.5
	418886	AA993982	Hs.130858	ESTs	2.5
65	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	2.5
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	2.5
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	2.5
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	2.5
	450543	AI394037	Hs.170296	Homo sapiens cDNA: FLJ22090 fis, clone H	2.5
70	434818	AA650097	Hs.5996	ESTs	2.5
	444534	AW271626	Hs.42294	ESTs	2.5
	452113	AI859393		gb:wm11a02.x1 NCL_CGAP_U14 Homo sapiens	2.5
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	2.5
	434012	AA621425	Hs.186256	ESTs	2.5
75	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	2.5
	449505	AI653006	Hs.195374	ESTs	2.5
	419817	AA743434	Hs.193778	ESTs	2.5
	457986	AA781745	Hs.126920	Homo sapiens, clone IMAGE:4299555, mRNA,	2.5
	431454	AW975980	Hs.292918	ESTs	2.5
80	425018	BE245277	Hs.154196	E4F transcription factor 1	2.5
	427513	AI476318	Hs.192480	ESTs	2.5
	441318	AI078234	Hs.176130	ESTs	2.5
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	2.5
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.5

5	446089	AI860021	Hs.345028	ESTs, Moderately similar to A47582 B-cel	2.5
	415983	AI436798	Hs.117078	Homo sapiens cDNA: FLJ23028 fis, clone L	2.5
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	2.5
	446862	AV660697	Hs.282700	ESTs	2.5
	448970	AW138582		gb:U1-H-B11-acw-a-06-0-U1.s1 NCI_CGAP_Su	2.5
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	2.5
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.5
10	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	2.5
	441255	R06350	Hs.171635	ESTs	2.5
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	2.5
	438714	AA814859	Hs.294112	ESTs	2.5
	441020	W79283	Hs.35962	ESTs	2.5
15	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.5
	434267	AI206589	Hs.116243	ESTs	2.5
	446821	W03766		tropomodulin 3 (ubiquitous)	2.5
	402615			C1003844".gil6912550/reflNP_036483.1] ol	2.5
20	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares fetal liver spleen	2.5
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.5
	444884	AI201094	Hs.148540	ESTs	2.5
	440826	AW383618	Hs.346256	ESTs, Moderately similar to ALU2_HUMAN A	2.5
	431374	BE258532	Hs.251871	CTP synthase	2.5
	458093	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	2.5
25	422484	AA568770	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.5
	442804	AW300118	Hs.131257	ESTs	2.5
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.5
	451350	AI791447		gb:n113a05.y5 NCI_CGAP_Co4 Homo sapiens	2.5
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.5
30	430426	AA478807	Hs.125173	ESTs	2.5
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.5
	406290			Target Exon	2.5
	442085	AA975688	Hs.159955	ESTs	2.5
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	2.5
35	432888	T86823		gb:yd81a08.s1 Soares fetal liver spleen	2.5
	424126	AA335635	Hs.96917	ESTs	2.5
	459727	AI906494		gb:RC-BT113-060499-024 BT113 Homo sapien	2.5
	407989	AW135208	Hs.256092	ESTs	2.5
	404571			NM_015902".Homo sapiens progesterin induce	2.5
40	429139	F09092	Hs.66087	ESTs	2.5
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.5
	420608	BE548277	Hs.103104	ESTs	2.5
	432668	AA558601	Hs.43296	ESTs	2.5
	406871	AA993857	Hs.180842	ribosomal protein L13	2.5
45	443516	AA305821	Hs.9527	apoptosis related protein APR-3	2.5
	445985	BE621800	Hs.29444	putative small membrane protein NID67	2.5
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	458251	AL040927	Hs.210422	ESTs	2.5
50	431198	AL047634	Hs.231913	ESTs	2.5
	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	2.5
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-asso	2.5
	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.5
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.5
55	424662	NM_002870	Hs.151536	RAB13, member RAS oncogene family	2.5
	423779	AW071837	Hs.57971	ESTs	2.5
	405863			Target Exon	2.5
	458421	AI279978	Hs.22547	ESTs	2.5
	439019	AF085902	Hs.271737	ESTs	2.5
60	412577	Z22968	Hs.74076	CD163 antigen	2.5
	404891			Target Exon	2.5
	419043	T19167	Hs.89566	ets variant gene 1	2.5
	448482	AW294078	Hs.171092	ESTs	2.5
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	2.5
65	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.5
	450597	AI701635	Hs.207077	ESTs	2.5
	414386	X00442	Hs.75990	haptoglobin	2.5
	440473	BE562314	Hs.98711	Homo sapiens, clone IMAGE:3677165, mRNA,	2.5
	406851	AA609784		major histocompatibility complex, class	2.5
70	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.5
	417663	R07483	Hs.180461	ESTs	2.5
	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.5
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	2.5
	407198	H91679		gb:yv04g07.s1 Soares fetal liver spleen	2.5
75	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.5
	409449	H11341	Hs.13366	Homo sapiens cDNA: FLJ23567 fis, clone L	2.5

TABLE 14B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession
408292 1050507_1 AW178363 AW846011 AW845964 AW845988 AW845977 AW846002

	409157	110363_1	AA064631 AA722000 AA064793
	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119
			AA085208 AA085045
5	410886	1225822_1	AW809324 BE144977 BE144956
	411537	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
	411543	1249127_1	AW851248 AW851425 AW850805 AW851021 AW850905
	411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
	411671	125369_1	BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170
10	411688	1254076_1	AW953440 T08189 AW857085
	411962	126744_1	AA099050 AA099526 T47733
	412021	1272156_1	AW885592 AW885594 AW885579 AW885651
	412135	1279148_1	AW895309 AW895290 AW895307 AW895397 AW895378 AW895402 AW895403 AW895311 AW895298 AW895390 AW895488 AW895468 AW895481
			AW895288
15	412799	132817_1	AI267606 AA121045 AA126521
	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
			R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
	413986	140720_1	Z43567 H24159 AA134240
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
20	414988	1511316_1	C17535 D59244 D58878 D79090
	415131	1523680_1	D61119 D81508 D81734
	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	416569	1601567_1	H64891 R93444 R93458 R05590
	416871	1626761_1	H98716 N90792 N24283
25	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419896	1888662_1	Z99362 Z99363
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	420670	195442_1	AW973577 AA553621 AA279187
	420886	197344_1	AA805453 AA281379
30	422551	217767_1	AW967284 AA312192 AA312203
	423713	231290_1	AW754182 AW754198 AA329983
	424009	234177_1	F11690 AW965370 AA333586 D30830
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
35	424947	245247_1	R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
	425146	247244_1	AW954627 AW954629 AA351258 R25935
	425331	250199_1	AW962128 AA355353 AA427363
	426503	268283_1	AA380153 AA380233 AW963529
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
40	429940	310884_1	W25215 AA461079 AA461391
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
	432044	340773_1	AW972727 AA524829 AW972733
	432363	345469_1	AA534489 AW970240 AW970323
45	432888	355780_1	T86823 AI821425 AI732232 AA569589 AA570737
	433009	357371_1	AA761668 AA573621 R92814 R09670
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	433835	374758_1	AI806185 AA610063 AI693089 AI693075
	434589	38929_1	AF147363 T47219 T47218
50	435065	399329_1	BE064391 BE064395 AA663613 N99644
	435542	407744_1	AA687376 H74234 AW975503
	436608	42361_3	AA628980 AI126603 BE504035
	437034	431713_1	AA742643 AA808575 AW976668
	437437	43709_1	AA226869 AA296516 AW959753 AA186390 AL359619 AA356195 AA148427 R22748 AI033624 BE548853 H95327 AW579751 BE561649 AA397533
55			BE617136 AA236444 T89946 AA247450 N55777 W38725 AI743846 AI808406 AA922229 AI051464 W04713 R11251 W19656 AI042319 AA489276
			AI224533 H
	437945	44580_1	T78519 H59898 U72516
	438458	457837_1	AW975186 AA807807 D29548
60	439518	47334_1	W76326 AF086341 W72300
	439533	47349_1	W76021 AF088052 W72465
	439566	47387_1	AF086387 W77884 W72711
	439710	47550_1	AF086543 W96291 W96225
	441128	51021_2	AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359627
65	442476	543547_1	AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
	444016	58899_1	AF069475 AF069477 AF069476
	444168	593829_1	AA448154 AV647571
	446821	69435_1	AW379879 AI126285 H12014
	448970	791254_1	W03766 AI357775 AV660500 AV660731
70	449625	8113_1	AW138582 AI638298 AI631640 AI963868 AI611082
			NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
	450166	82677_1	N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450375	83327_1	AA429504 R41904 AA279467 H09648 AA007236
			AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
75	450506	836_1	AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
			NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
			AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296 AA436611 AW609728 W42634 AI682584 AA405569
			AI685653 AW0
	450625	84032_1	AW970107 AA513951 AA010406
80	451129	859870_1	BE072881 BE072946 AI762181
	451350	866945_1	AI791447 AI791327 AW886809
	452113	899664_1	AI859393 BE177742
	452203	903_2	X57522 AW295947 AI346197 AI304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R18264 T74452 AA346259
			AW602508 AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 AI819778 AA054458 AI346733
			AW361447 AI4

5	453331	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R7390
10	453682	977454_1	T79703 T96307 AL079725
15	454177	1049351_1	AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866
20	454354	1129859_1	AW389896 AW389898 AW389906 AW609203 AW389873
25	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
30	454581	1225710_1	AW809189 AW809219 AW813574
35	454765	1233905_1	AW819629 AW854320
40	454860	1237732_1	AW835767 AW835537 BE160187
45	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
50	455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665 BE064650 BE064691
55	455409	1288355_1	AW936832 AW936509 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW9
60	455481	1293182_1	AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324
65	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
70	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
75	455899	1381547_1	BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
80	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
85	457364	328154_1	AW971037 AA508019 AA492345
90	457876	42814_2	AI821940 N67106 AI744264 AA808846 AA643417 AA643416 Z70715
95	458199	504866_1	AW136417 AI141026 AI340960 AI091670 AI523802 AW572908 AI458860 AI924374 AI830572 AI400702 AI337539 AI968111 AI521308 AI492336 AI540779 AI672594 AW665077 AA971810 AA909139 AW082128 AI335251 AI807192 AW511744 AI023232 AI536899 AW207791 AI670910 AI002047 AW4

TABLE 14C:

30	Pkey:	Unique number corresponding to an Eos probeset
35	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
40	Strand:	Indicates DNA strand from which exons were predicted.
45	NI_position:	Indicates nucleotide positions of predicted exons.

40	Pkey	Ref	Strand	NI_position
45	400492	9213749	Minus	123881-124090
50	400533	6981826	Minus	277132-277595
55	400645	8117693	Minus	58471-58716
60	400658	8118459	Minus	73525-73644
65	400780	8131663	Minus	118372-118619
70	400850	1927150	Minus	4506-4691
75	400924	7107613	Minus	30309-30498
80	401272	9797373	Minus	98374-98509
85	401454	9186923	Minus	114659-114832
90	401696	3417290	Minus	46209-46401
95	401702	1871197	Minus	68182-68325
100	401841	7684597	Plus	89868-90006,91920-92085
105	402032	7656761	Plus	62293-62475
110	402082	8117478	Minus	190046-190183
115	402229	9965022	Minus	15739-15951,16166-16779
120	402239	7690131	Plus	38175-38304,42133-42266
125	402260	3399665	Minus	113765-113910,115653-115765,116808-116940
130	402274	2935596	Plus	5604-6527
135	402604	9909420	Plus	20393-20767
140	402615	9926801	Plus	131390-132157
145	402799	3355547	Plus	35718-35899
150	402855	9662953	Minus	59763-59909
155	402936	8894303	Plus	51655-51771
160	403011	6693597	Minus	3468-3623
165	403104	7331404	Minus	41800-41973
170	403108	8980955	Plus	93253-93667
175	403212	7630897	Minus	156037-156210
180	403267	7887182	Plus	116078-121885
185	403288	8081479	Plus	133763-133899,135813-135958
190	403290	8083176	Plus	19288-20076
195	403291	7230870	Plus	95177-95435
200	403349	8569773	Minus	167815-168374
205	403361	8570313	Minus	112496-112687
210	403431	7139839	Plus	56509-56860
215	403481	9965004	Plus	93496-93633
220	403696	3135242	Minus	143467-143634
225	403790	8084957	Minus	87826-87947,89835-90002
230	403849	7708855	Plus	95043-96519
235	403942	7711825	Minus	99606-99757
240	403961	7596976	Minus	110393-110603
245	403969	8569909	Plus	31237-31375,32405-32506
250	404053	3548785	Plus	61797-64205
255	404120	7342152	Plus	135775-136000
260	404150	7534008	Plus	165811-165943
265	404170	9930793	Plus	168836-169248
270	404209	5006246	Minus	11247-11514
275	404272	9885189	Plus	63207-63355,84358-84496,90519-90720,91371-91447

5	404407	7329316	Minus	48154-48499
	404571	7249169	Minus	112450-112648
	404584	9857511	Plus	138651-139153
	404592	9943965	Minus	39067-39225
	404632	9796668	Plus	45096-45229
	404748	7263437	Plus	11446-11591
	404891	7329392	Plus	84974-85125
	405046	7596829	Minus	4373-4528
10	405141	8980911	Plus	99861-100054
	405183	7209940	Plus	12335-12653
	405238	7249119	Minus	51728-51836
	405348	2914717	Minus	43310-43462
	405516	9454624	Plus	112707-112876, 113676-113854
	405558	1621110	Plus	4502-4644, 5983-6083
15	405605	5836195	Minus	117070-117270
	405717	9588573	Plus	11275-11973
	405760	6066938	Minus	37424-38045
	405863	7657810	Plus	49410-49620
20	405941	6758796	Plus	2798-3444
	406060	6899623	Minus	20339-20746
	406290	5686274	Plus	8711-9358
	406395	9256242	Minus	20805-20960
	406478	9857502	Plus	68314-68523, 68853-68950
25	406481	9864741	Minus	91439-91579

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 15A lists about 1033 genes up-regulated in glioblastoma compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" glioblastoma level was set to the 85th percentile amongst various brain tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of GLIOBLASTOMA to NORMAL ADULT TISSUES

40	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	60.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	54.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.1
	428321	AI699994	Hs.2868	peripheral myelin protein 2	49.6
45	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	45.4
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	43.9
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	42.7
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.3
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	39.1
50	430838	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
	417183	R52089	Hs.172717	ESTs	37.6
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	36.5
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	34.3
	429007	D80642		gb:HUM092E098 Human fetal brain (TFujw	33.9
55	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	33.9
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	32.7
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	32.3
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	29.0
	450133	AW969769	Hs.105201	ESTs	27.9
60	412733	AA984472	Hs.74554	KIAA0080 protein	27.6
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	27.3
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	27.1
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	25.2
	402604			Target Exon	24.3
65	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	24.3
	422656	AI870435	Hs.1569	LIM homeobox protein 2	23.6
	447359	NM_012093	Hs.18268	adenylate kinase 5	23.3
	436878	BE465204	Hs.47448	ESTs	22.9
	435708	AI362949	Hs.75169	ESTs	22.9
70	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	22.7
	439239	AI031540	Hs.235331	ESTs	22.4
	409395	U46745	Hs.336678	dystrobrevin, alpha	22.2
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	21.9
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	21.3
75	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	21.2
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	21.0
	419078	M93119	Hs.89584	insulinoma-associated 1	21.0
	425048	H05468	Hs.164502	ESTs	20.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.3
80	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	19.3
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	19.2
	447004	AW296968	Hs.157539	ESTs	18.6
	439415	F05538	Hs.4273	ESTs	18.6
	441497	R51064	Hs.23172	ESTs	18.5

	425523	AB007948	Hs.158244	KIAA0479 protein	18.3
	413597	AW302885	Hs.117183	ESTs	18.2
	433551	AI985544	Hs.12450	protocadherin 9	17.7
5	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	17.3
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	17.3
	418338	NM_002522	Hs.84154	neuronal pentraxin I	17.1
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	16.8
	408604	D51408	Hs.21925	ESTs	16.6
10	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	16.6
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	16.5
	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.4
	429466	M85835	Hs.12827	ESTs	16.3
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	15.9
15	448672	AI955511	Hs.225106	ESTs	15.8
	448743	AB032962	Hs.21896	KIAA1136 protein	15.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	441285	NM_002374	Hs.167	microtubule-associated protein 2	15.2
	431019	NM_005249	Hs.2714	forkhead box G1B	14.8
20	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	14.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	14.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	14.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	14.0
	444471	AB020684	Hs.11217	KIAA0877 protein	13.9
25	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	13.8
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	441440	AI807981	Hs.30495	ESTs	13.6
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.5
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	13.3
	459516	AI049662	Hs.246858	EST	13.2
30	421264	AL039123	Hs.103042	microtubule-associated protein 1B	13.2
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	13.1
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	12.9
	412959	D87458	Hs.75090	KIAA0282 protein	12.9
	439199	R40373	Hs.26299	ESTs	12.8
35	423419	R55336	Hs.23539	ESTs	12.5
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	12.4
	415849	R20529	Hs.6806	ESTs	12.4
	452372	AI885742	Hs.228474	ESTs	12.4
40	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	12.3
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	12.2
	415734	NM_014747	Hs.78748	KIAA0237 gene product	12.1
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	12.1
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26586 hypotheti	12.0
45	409049	AI423132	Hs.146343	ESTs	11.9
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.9
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	11.8
	453941	U39817	Hs.36820	Bloom syndrome	11.8
	424120	T80579	Hs.290270	ESTs	11.7
50	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	11.7
	411305	BE241596	Hs.69547	myelin basic protein	11.7
	424945	AI221919		hypothetical protein FLJ10582	11.6
	449539	W80363	Hs.58446	ESTs	11.5
	409638	AW450420	Hs.21335	ESTs	11.5
	441016	AW138653	Hs.25845	ESTs	11.4
55	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	11.3
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	11.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.2
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	11.2
60	424432	AB037821	Hs.146858	protocadherin 10	11.1
	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	11.1
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	11.1
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	11.1
	423678	AW963357	Hs.7847	ESTs	10.7
65	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	10.7
	430691	C14187	Hs.103538	ESTs	10.7
	428728	NM_016625	Hs.191381	hypothetical protein	10.6
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	10.6
	431988	AC002302	Hs.77202	protein kinase C, beta 1	10.5
70	433896	AW294729	Hs.274461	ESTs	10.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	10.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	10.3
	445041	T64183	Hs.282982	solute carrier	10.3
	446782	AI653048	Hs.144006	ESTs	10.2
75	451952	AL120173	Hs.301663	ESTs	10.2
	446711	AF169692	Hs.12450	protocadherin 9	10.1
	438054	AA776626	Hs.169309	ESTs	10.1
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	10.1
	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	10.0
80	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	10.0
	416857	AA188775	Hs.292453	ESTs	10.0
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.0
	419271	N34901	Hs.238532	ESTs	9.9
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	9.9

	415293	R49462	Hs.106541	ESTs	
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	9.9
	452526	W38537	Hs.280740	hypothetical protein MGC3040	9.8
5	427304	AA761526	Hs.163853	ESTs	9.8
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	9.7
	421659	NM_014459	Hs.106511	protocadherin 17	9.6
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	9.6
	429656	X05608	Hs.211584	neurofilament, light polypeptide (58kD)	9.6
10	447101	N72185	Hs.44189	ESTs	9.5
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	9.5
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	445102	AW204610	Hs.22270	ESTs	9.5
	435793	AB037734	Hs.4993	KIAA1313 protein	9.5
15	437948	AA772920	Hs.303527	ESTs	9.5
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	9.5
	415170	R44386	Hs.164578	ESTs	9.4
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	9.3
	435501	AW051819	Hs.129908	KIAA0591 protein	9.2
20	416072	AL110370	Hs.79000	growth associated protein 43	9.2
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	9.2
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN !!!	9.1
	425187	AW014486	Hs.22509	ESTs	9.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	9.1
25	430091	AB032958	Hs.233023	KIAA1132 protein	9.0
	427540	R12014	Hs.20976	ESTs	9.0
	447198	D61523	Hs.283435	ESTs	9.0
	449611	AI970394	Hs.197075	ESTs	9.0
	444124	R43097	Hs.6818	ESTs	8.9
30	451996	AW514021	Hs.245510	ESTs	8.9
	454048	H05626	Hs.6921	ESTs	8.8
	412266	N59006	Hs.26133	ESTs	8.8
	433597	AA708205	Hs.100343	ESTs	8.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.7
35	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	8.6
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	8.6
	423135	N67655	Hs.26411	ESTs	8.5
	418097	R45137	Hs.21868	ESTs	8.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
40	419721	NM_001650	Hs.288650	aquaporin 4	8.4
	449300	AI656959	Hs.346514	ESTs	8.4
	436954	AA740151	Hs.130425	ESTs	8.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	8.3
	424997	AL138167	Hs.96920	ESTs	8.3
45	442710	AI015631	Hs.23210	ESTs	8.3
	449625	NM_014253		odt (odd Ozten-m, Drosophila) homolog 1	8.2
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-l	8.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.2
	449605	AW138581	Hs.198416	ESTs	8.0
50	407886	AW969688	Hs.100826	ESTs	8.0
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	8.0
	429946	R49390	Hs.254129	KIAA1678	7.9
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	7.9
55	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	7.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.9
	415279	F04237	Hs.1447	glial fibrillary acidic protein	7.8
	429918	AW873986	Hs.119383	ESTs	7.8
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	7.8
	422411	AW749443	Hs.22511	ESTs	7.8
60	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	7.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.7
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.7
	407168	R45175	Hs.117183	ESTs	7.7
	448555	AI536697	Hs.159863	ESTs	7.6
65	428536	AI143139	Hs.2288	visinin-like 1	7.6
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	7.6
	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.6
	435624	AF218942	Hs.24889	formin 2	7.6
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	7.6
70	412058	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	7.6
	445568	H00918	Hs.268744	KIAA1796 protein	7.6
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	7.5
75	458332	AI000341	Hs.220491	ESTs	7.5
	409902	AI337658	Hs.156351	ESTs	7.4
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.3
	420345	AW295230	Hs.25231	ESTs	7.3
	402855			NM_001839: Homo sapiens calponin 3, acid	7.3
80	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.2
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	7.2
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	7.2
	415651	AI207162	Hs.3815	stathmin-like-protein RB3	7.2
	412709	AL022327	Hs.74518	KIAA0027 protein	7.1

	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	7.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	7.1
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	7.1
5	418030	BE207573	Hs.83321	neuromedin B	7.1
	400292	AA250737	Hs.72472	BMP-R1B	7.1
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	7.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0
10	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	7.0
	440152	AB002376	Hs.7006	KIAA0378 protein	7.0
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.0
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.0
15	426814	AF036943	Hs.172619	myelin transcription factor 1-like	6.9
	416836	D54745	Hs.80247	cholecystokinin	6.9
	447350	AI375572	Hs.172634	ESTs	6.9
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	6.9
	436039	AW023323	Hs.121070	ESTs	6.9
20	444396	T65213	Hs.4257	ESTs	6.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	6.9
	438330	AW450572	Hs.257316	ESTs	6.8
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	6.8
	421141	AW117261	Hs.125914	ESTs	6.7
25	412788	AA120960	Hs.198416	ESTs	6.7
	411078	AI222020	Hs.182364	CocoaCrisp	6.7
	443455	AB001025	Hs.9349	ryanodine receptor 3	6.7
	448769	N66037	Hs.38173	ESTs	6.7
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	6.7
30	414214	D49958	Hs.75819	glycoprotein M6A	6.6
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	6.6
	437036	AI571514	Hs.133022	ESTs	6.6
	429239	AA448419	Hs.45209	ESTs	6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6
35	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.5
	452834	AI638627	Hs.105685	KIAA1688 protein	6.5
	441916	AA993571	Hs.129075	ESTs	6.5
	451516	AI800515	Hs.12024	ESTs	6.5
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.5
40	452461	N78223	Hs.108106	transcription factor	6.5
	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
	434811	AW971205	Hs.114280	ESTs	6.4
	424624	AB032947	Hs.151301	Ca2-dependent activator protein for secr	6.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.3
45	414245	BE148072	Hs.75850	WAS protein family, member 1	6.3
	433447	U29195	Hs.3281	neuronal pentraxin II	6.3
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	6.3
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.3
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.3
50	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	6.2
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.2
	433929	AI375499	Hs.27379	ESTs	6.2
	423346	AI267677	Hs.127416	synaptojanin 1	6.2
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.2
55	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	6.2
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
	420608	BE548277	Hs.103104	ESTs	6.2
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.2
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	6.1
60	428845	AL157579	Hs.153610	KIAA0751 gene product	6.1
	439274	AF086092	Hs.48372	ESTs	6.1
	447499	AW262580	Hs.147674	protocadherin beta 16	6.1
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1
	453924	R49295	Hs.24886	ESTs	6.1
65	449340	AW235786	Hs.195359	hypothetical protein MGC10954	6.1
	420077	AW512260	Hs.87767	ESTs	6.1
	431721	AB032996	Hs.268044	KIAA1170 protein	6.1
	433701	AW445023	Hs.15155	ESTs	6.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.1
70	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	6.0
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	6.0
75	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
	448243	AW369771	Hs.52620	integrin, beta 8	6.0
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.0
	419704	AA429104	Hs.45057	ESTs	6.0
	436936	AL134451	Hs.197478	ESTs	6.0
80	428409	AW117207	Hs.98523	ESTs	6.0
	433244	AB040943	Hs.271285	KIAA1510 protein	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	6.0
	408096	BE250162	Hs.83765	dihydrofolate reductase	6.0
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	6.0

	422544	AB018259	Hs.118140	KIAA0716 gene product	6.0
	413627	BE182082	Hs.246973	ESTs	6.0
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	6.0
5	410366	AI267589	Hs.302689	hypothetical protein	6.0
	429183	AB014604	Hs.197955	KIAA0704 protein	5.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.9
	441102	AA973905		intermediate filament protein syncoilin	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
10	407182	AA312551	Hs.230157	ESTs	5.9
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.9
	433523	H29882		ESTs	5.9
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.9
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.9
15	420156	AW449258	Hs.6187	ESTs	5.9
	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo sapiens cDNA	5.8
	446727	AB011095	Hs.16032	KIAA0523 protein	5.8
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	5.8
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	5.8
20	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	5.8
	419629	AB020695	Hs.91662	KIAA0888 protein	5.8
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.8
	407808	AA663559	Hs.279789	histone deacetylase 3	5.8
	414737	AI160386	Hs.125087	ESTs	5.8
25	432154	AI701523	Hs.112577	ESTs	5.8
	410099	AA081630		KIAA0036 gene product	5.8
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	5.8
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.8
	424560	AA158727	Hs.150555	protein predicted by clone 23733	5.7
30	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	5.7
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.7
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
	419088	AI538323	Hs.52620	integrin, beta 8	5.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
35	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.7
	451752	AB032997	Hs.26966	KIAA1171 protein	5.7
	413492	D87470	Hs.75400	KIAA0280 protein	5.7
	414683	S78296	Hs.76888	hypothetical protein MGC12702	5.7
	418079	R40058	Hs.6911	ESTs	5.6
40	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	5.6
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	419544	AI909154		gb:CV-BT200-010499-007 BT200 Homo sapien	5.6
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	5.6
	408081	AW451597	Hs.167409	ESTs	5.6
45	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	5.6
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	5.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	5.6
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	5.5
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.5
50	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.5
	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	5.5
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	5.5
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	5.5
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	5.5
55	440866	AI703103	Hs.271360	hypothetical protein MGC16275	5.4
	428976	AL037824	Hs.194695	ras homolog gene family, member I	5.4
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.4
	452799	AI948829	Hs.213786	ESTs	5.4
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	5.4
60	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	5.4
	424332	AA338919	Hs.101615	ESTs	5.4
	440210	AW674562	Hs.125296	ESTs	5.4
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.4
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
65	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	5.4
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	5.4
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	5.4
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	5.4
	419683	AA248897	Hs.48784	ESTs	5.4
70	407728	AW071502	Hs.175931	ESTs	5.4
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	5.4
	422094	AF129535	Hs.272027	F-box only protein 5	5.4
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	5.4
	434792	AA649253	Hs.132458	ESTs	5.4
75	412190	R16180	Hs.274461	ESTs	5.4
	425588	F07396	Hs.46627	ESTs	5.3
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	5.3
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	5.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	5.3
80	446997	AA383439	Hs.16758	Spir-1 protein	5.3
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	5.3
	439607	BE540565	Hs.159460	ESTs	5.3
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.3
	410037	AB020725	Hs.58009	KIAA0918 protein	5.3

	451407	AA131376	Hs.343809	fibroblast growth factor 12B	5.3
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.3
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated to	5.3
5	418512	AW498974		diacylglycerol kinase, zeta (104kD)	5.3
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.3
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZNS1_HUMAN Z	5.2
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	5.2
	404819			NM_002688*:Homo sapiens peanut (Drosophi	5.2
10	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.2
	405348			C7001664:gil12698061 dbj BAB21849.1 (AB	5.2
	431552	A1815863	Hs.259873	axonal transport of synaptic vesicles	5.2
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.2
	427250	R35941	Hs.25418	ESTs	5.2
15	428037	N47474	Hs.89230	potassium intermediate/small conductance	5.2
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	5.2
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	423869	BE409301	Hs.134012	C1q-related factor	5.2
	416220	N49776	Hs.170994	hypothetical protein MGC10946	5.2
20	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	5.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.1
	410631	AA086469	Hs.47171	ESTs	5.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	5.1
25	420133	AA426117	Hs.155543	ESTs	5.1
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	5.1
	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCL_CGAP_GC6 Homo sapiens	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	5.1
30	437387	A198874	Hs.28847	AD026 protein	5.0
	400533			ENSP00000209376*:PRE065 protein (Fragmen	5.0
	430979	A1479755	Hs.129010	ESTs	5.0
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.0
	444600	R41398	Hs.6996	ESTs	5.0
35	453785	A1368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	428878	AA436884	Hs.48926	ESTs	5.0
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.0
	440471	AA886146	Hs.307944	ESTs	5.0
	410434	AF051152	Hs.63668	tol1-like receptor 2	5.0
40	441390	AU692560	Hs.131175	ESTs	4.9
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (tr	4.9
	422263	AA307639	Hs.129908	KIAA0591 protein	4.9
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.9
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
45	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.9
	420092	AA814043	Hs.88045	ESTs	4.9
	449571	AW016812	Hs.200266	ESTs	4.9
	412811	H06382		ESTs	4.9
50	409100	H98216	Hs.42245	ESTs, Moderately similar to I38022 hypot	4.9
	403142			NM_002706*:Homo sapiens protein phosphat	4.9
	414300	A1304870	Hs.188680	ESTs	4.9
	436607	AW661783	Hs.211061	ESTs	4.9
	431553	X78075	Hs.2799	cartilage linking protein 1	4.9
55	449328	A1962493	Hs.345303	ESTs	4.9
	420805	L10333	Hs.99947	reticulin 1	4.9
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	4.9
	452898	AA814497	Hs.78792	ESTs	4.9
60	427958	AA418000	Hs.98280	potassium intermediate/small conductance	4.9
	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.9
	408453	A1369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	4.8
	428841	A418430	Hs.104935	ESTs	4.8
	416439	AA180363	Hs.118769	ESTs	4.8
	447458	A1741082	Hs.158961	ESTs	4.8
65	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	4.8
	436511	AA721252	Hs.291502	ESTs	4.8
	443392	A1055821	Hs.293420	ESTs	4.8
	423600	A1633559	Hs.310359	ESTs	4.8
70	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothesi	4.8
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.7
	427624	AA406245	Hs.24895	ESTs	4.7
75	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.7
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	4.7
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	4.7
	411555	AF113537	Hs.70669	HMP19 protein	4.7
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.7
80	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	4.7
	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	4.7
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	4.7
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.7
	453096	AW294631	Hs.11325	ESTs	4.7

	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	4.7
	410276	AI554545	Hs.68301	angiopoietin-2	4.7
5	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
	421633	AF121860	Hs.106260	sorting nexin 10	4.7
	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheri	4.7
	439566	AF086387		gb:Homo sapiens full length insert cDNA	4.7
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	4.6
	402145			Target Exon	4.6
10	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	4.6
	458760	AI498631	Hs.111334	ferritin, light polypeptide	4.6
	453362	H14988	Hs.107375	ESTs	4.6
	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	4.6
15	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fs, clone H	4.6
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.6
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	4.6
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fs, clone HE	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fs, clone PL	4.6
20	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheri	4.6
	437762	T78028	Hs.154679	synaptotagmin I	4.6
	439249	AF086060	Hs.170053	G-protein coupled receptor 88	4.6
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fs, clone PL	4.6
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.6
25	415257	F03016	Hs.27513	ESTs	4.6
	426186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.6
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	4.6
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	4.5
	424998	U58515	Hs.154138	chitinase 3-like 2	4.5
30	422709	AA315331	Hs.153485	ESTs	4.5
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.5
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.5
	457465	AW301344	Hs.122908	DNA replication factor	4.5
	427712	AI368024	Hs.283696	ESTs	4.5
35	444656	AI277924	Hs.145199	ESTs	4.5
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.5
	429399	AA452244	Hs.16727	ESTs	4.5
	450639	AI703186	Hs.277174	ESTs	4.5
	452106	AI141031	Hs.21342	ESTs	4.5
40	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.5
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	4.5
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.5
	428189	AA424030	Hs.46627	ESTs	4.5
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5
45	445133	AW157646	Hs.198689	ESTs	4.5
	418771	AA807881	Hs.25329	ESTs	4.4
	438456	AA913381	Hs.20594	ESTs	4.4
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fs, clone H	4.4
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypotheri	4.4
50	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	4.4
	420560	AW207748	Hs.59115	ESTs	4.4
	439662	H97552	Hs.269060	ESTs	4.4
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	445034	AW293376	Hs.143659	ESTs	4.4
55	402605			Target Exon	4.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	4.4
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.4
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (4.4
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.4
60	452752	AW044058	Hs.33578	KIAA0820 protein	4.4
	439108	AW163034	Hs.6467	synaptogyrin 3	4.4
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	4.4
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.4
65	420871	AA702972	Hs.65300	ESTs	4.4
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	4.4
	429269	AA449013	Hs.99203	ESTs	4.4
	427463	AA442224	Hs.97900	ESTs	4.3
	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	4.3
70	412046	Y07847	Hs.73088	RAS-related on chromosome 22	4.3
	427194	AA399018	Hs.250835	ESTs	4.3
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.3
	409172	Z99399	Hs.122593	ESTs	4.3
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.3
75	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	4.3
	446936	H10207	Hs.47314	ESTs	4.3
	433932	AW954599	Hs.169330	neuronal protein	4.3
80	424800	AL035588	Hs.153203	MyoD family inhibitor	4.3
	421988	AW450481	Hs.161333	ESTs	4.3
	442632	AW206560	Hs.253569	ESTs	4.3
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.2
	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	4.2

	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.2
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.2
	438624	AA889055	Hs.123468	ESTs	4.2
	421027	AA761198	Hs.55254	ESTs	4.2
5	417632	R20855	Hs.5422	glycoprotein M6B	4.2
	419412	AW161058	Hs.90297	synuclein, beta	4.2
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.2
	450813	AI739625	Hs.203376	ESTs	4.2
	412505	AA974491	Hs.21734	ESTs	4.2
10	440168	AA868507	Hs.126141	ESTs	4.2
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	438703	AI803373	Hs.31599	ESTs	4.2
	444127	N63620	Hs.13281	ESTs	4.2
	447397	BE247676	Hs.18442	E-1 enzyme	4.2
15	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.2
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	4.2
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	408838	AI669535	Hs.40369	ESTs	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	4.2
20	404584			Target Exon	4.2
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	4.2
	409091	AW970386	Hs.269423	ESTs	4.2
	437117	AL049256	Hs.122593	ESTs	4.2
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.2
25	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.2
	408177	AI241733	Hs.43871	ESTs	4.2
	438875	AA827640	Hs.189059	ESTs	4.2
	447877	AI435184	Hs.164252	ESTs	4.2
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	4.2
30	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.2
	449714	AB033015	Hs.23941	KIAA1189 protein	4.2
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.2
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.1
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	4.1
35	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.1
	440483	AI200836	Hs.150386	ESTs	4.1
	429421	AL031658		Human DNA sequence from clone RP1-310013	4.1
40	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.1
	424001	W67883	Hs.137476	paternally expressed 10	4.1
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.1
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	4.1
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4.1
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	4.1
45	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	4.1
	415796	R87548	Hs.78854	ATPase, Na ⁺ transporting, beta 2 polypep	4.1
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
50	412777	AI335773	Hs.270123	ESTs	4.1
	445225	AI216555	Hs.202398	ESTs	4.1
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	4.1
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.1
55	443301	AI733614	Hs.220587	ESTs, Moderately similar to ALU5_HUMAN A	4.1
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	4.1
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.1
	417355	D13168	Hs.82002	endothelin receptor type B	4.1
60	410359	R38624	Hs.106313	ESTs	4.1
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	4.1
	433323	AA805132	Hs.159142	ESTs	4.1
	434933	R91095	Hs.4276	KIAA1701 protein	4.1
	453331	AI240665		ESTs	4.1
65	422661	NM_014700	Hs.119004	KIAA0665 gene product	4.1
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	4.0
	441797	AI936933	Hs.214635	ESTs	4.0
	424282	R76421	Hs.135694	ESTs	4.0
70	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.0
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	4.0
	453312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.0
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	4.0
75	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.0
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.0
	450581	AF081513	Hs.25195	TGF-beta 4	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
80	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	4.0
	445666	R59960	Hs.282386	ESTs	4.0
	450582	AI339732		G-rich RNA sequence binding factor 1	4.0

	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
	449277	AA001064	Hs.43670	ESTs	4.0
5	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	4.0
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GC81 Homo sapiens	4.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.0
	422564	AI148006	Hs.222120	ESTs	4.0
10	443992	AW022228	Hs.322922	ESTs	4.0
	435542	AA687376		ESTs	4.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.0
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.0
	439285	AL133916		hypothetical protein FLJ20093	4.0
15	449655	AI021987	Hs.59970	ESTs	4.0
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.0
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	4.0
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.0
	432683	AW995441	Hs.10475	ESTs	4.0
20	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.0
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	4.0
	450927	AI807804	Hs.134342	TASP for testis-specific adriamycin sens	4.0
	448985	AA324885	Hs.22777	carbonic anhydrase XI	4.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.0
25	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.9
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	3.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	3.9
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9
30	453438	AI469935	Hs.22792	ESTs	3.9
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.9
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	3.9
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.9
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.9
35	439935	S75105	Hs.8358	glutamate receptor, ionotropic, kainate	3.9
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.9
	432809	AA565509	Hs.131703	ESTs	3.9
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	3.9
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	3.9
40	435743	T66861	Hs.12962	ESTs	3.9
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.9
	448526	AB028946	Hs.21361	KIAA1023 protein	3.9
	445890	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.9
45	425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	3.8
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.8
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	3.8
	410592	R94088	Hs.43569	ESTs	3.8
	443361	AI792628	Hs.133273	ESTs	3.8
50	403696			C4001100*:gil5852342[gb]AAD54015.1[AF0	3.8
	437756	AA767537	Hs.197096	ESTs	3.8
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.8
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.8
55	437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKFZp762G113 (fr	3.8
	421040	AA715026	Hs.135280	ESTs	3.8
	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	3.8
	443740	R56434	Hs.21062	ESTs	3.8
	441668	AI811973	Hs.136313	ESTs	3.8
60	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.8
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.8
	438142	T90309	Hs.269651	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
	436899	AA764852	Hs.291567	ESTs	3.8
65	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.8
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.8
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.8
	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.8
70	438944	AA302517	Hs.92732	KIAA1444 protein	3.8
	445078	AI869975	Hs.4775	junctional protein 3	3.8
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	3.8
	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	3.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.8
75	411252	AB018549	Hs.69328	MD-2 protein	3.7
	448275	BE514434	Hs.20830	kinesin-like 2	3.7
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.7
	400777			NM_007325*:Homo sapiens glutamate recept	3.7
	419586	AI088485	Hs.144759	ESTs, Weakly similar to I38022 hypotheti	3.7
80	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.7
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.7
	448451	AW015994	Hs.345433	gb:UH-B10p-abh-g-09-0-ULs1 NCI_CGAP_S	3.7
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.7
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	3.7

	458912	AJ911066		ESTs	3.7
	428110	AI312485	Hs.138294	ESTs, Moderately similar to Z195_HUMAN Z	3.7
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.7
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.7
5	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	428873	AI701609	Hs.98908	ESTs	3.7
	438208	AL041224	Hs.65379	ESTs	3.7
	414040	N58513	Hs.32171	ESTs	3.7
10	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.7
	425010	T16837	Hs.4241	ESTs	3.7
	427209	H06509	Hs.92423	KIAA1566 protein	3.7
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.6
	410126	BE169274		KIAA0036 gene product	3.6
15	426646	AA382787	Hs.122713	ESTs	3.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.6
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	3.6
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	3.6
	448425	AI500359	Hs.346112	ESTs	3.6
	423611	AB011163	Hs.129908	KIAA0591 protein	3.6
	438831	BE263273	Hs.6439	synapsin II	3.6
	419235	AW470411	Hs.288433	neurotrimin	3.6
25	451027	AW519204	Hs.40808	ESTs	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	424947	R77952		ESTs, Weakly similar to alternatively sp	3.6
	404150			Target Exon	3.6
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6
30	443715	AI583187	Hs.9700	cyclin E1	3.6
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	432488	AA551010	Hs.216640	ESTs	3.6
	431342	AW971018	Hs.21659	ESTs	3.6
35	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	3.6
	448448	NM_014954	Hs.21239	KIAA0985 protein	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	445105	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
40	409557	BE182896	Hs.211193	ESTs	3.6
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	3.6
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.6
	412799	AI267606		gb:aa91h03.x1 Stanley Frontal S8 pool 1	3.6
45	435040	AI932350	Hs.152825	ESTs	3.6
	434149	Z43829	Hs.244624	hypothetical protein MGC5469	3.6
	415709	AA649850	Hs.278558	ESTs	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypotheti	3.6
50	445953	AI612775	Hs.145710	ESTs	3.6
	449256	AA059050	Hs.59847	ESTs	3.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.6
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	3.6
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.6
55	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	3.6
	443912	R37257	Hs.184780	ESTs	3.6
	424572	M19650		2',3'-cyclic nucleotide 3' phosphodiester	3.5
	424899	AL119387	Hs.119062	ESTs	3.5
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.5
60	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	3.5
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.5
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.5
	407624	AW157431	Hs.248941	ESTs	3.5
	419038	AW134924	Hs.190325	ESTs	3.5
65	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.5
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.5
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.5
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.5
	424340	AA339036	Hs.7033	ESTs	3.5
70	425790	AW136286	Hs.288446	ESTs	3.5
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.5
	453896	AW293483	Hs.255205	KIAA1853 protein	3.5
	434784	AA649051	Hs.164007	ESTs	3.5
	452449	AW068658	Hs.20943	ESTs	3.5
75	425212	AW962253	Hs.171618	ESTs	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.5
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	3.5
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.5
80	439450	R51613	Hs.125304	ESTs	3.5
	435545	AA687415	Hs.28107	ESTs	3.5
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.5
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	3.5
	412590	AL134388	Hs.135033	ESTs, Weakly similar to I38022 hypotheti	3.5

	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	441111	AI806867	Hs.126594	ESTs	3.5
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-J	3.5
	439920	H05430	Hs.288433	neurotrophin	3.5
5	421268	AI126821	Hs.30514	ESTs	3.5
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	3.5
	412719	AW016610	Hs.816	ESTs	3.5
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.5
10	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.4
	421183	AL135740	Hs.102447	TSC-22-like	3.4
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.4
	413812	AW188687	Hs.44748	ESTs	3.4
15	449932	AI675444	Hs.263024	ESTs	3.4
	447067	R42098	Hs.21964	ESTs	3.4
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.4
	447028	AI973128	Hs.167257	brain link protein-1	3.4
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.4
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	3.4
	417084	H08370	Hs.33067	ESTs	3.4
	444534	AW271626	Hs.42294	ESTs	3.4
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4
25	436637	AI783629	Hs.26766	ESTs	3.4
	412820	BE001236		gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3.4
	428138	AA773842	Hs.293799	ESTs	3.4
	453033	AA325869	Hs.31463	KIAA0281 gene product	3.4
	453305	R39224	Hs.267997	EHM2 gene	3.4
30	459660	M79082		ESTs	3.4
	418821	AA436002	Hs.183161	ESTs	3.4
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	437085	AA743935	Hs.202329	ESTs	3.4
35	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	3.4
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4
	441287	AW293132	Hs.131373	ESTs	3.4
	425870	R13406	Hs.56782	ESTs	3.4
	443672	AA323362	Hs.9667	butyrolactone (gamma), 2-oxoglutarate di	3.4
40	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
	405238			Target Exon	3.4
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	3.4
	453590	AF150278	Hs.33578	KIAA0820 protein	3.4
	450756	AI733488	Hs.144062	ESTs	3.4
45	404283			ENSP00000244751*:Copine-like protein KIA	3.4
	423257	AW161039	Hs.125878	synapsin III	3.4
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.4
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.4
50	420050	AL118615	Hs.94653	neurochondrin	3.4
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	3.4
	408601	U47928	Hs.86122	protein A	3.4
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	3.4
	449919	AI674685	Hs.200141	ESTs	3.4
55	426380	AI291267	Hs.149990	ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.3
	443257	AI334040	Hs.11614	HSPC065 protein	3.3
	432731	R31178	Hs.287820	fibronectin 1	3.3
	421679	AI475110	Hs.203933	ESTs	3.3
60	453169	AB037815	Hs.32156	KIAA1394 protein	3.3
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	3.3
	443310	BE552018	Hs.133152	ESTs	3.3
	423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.3
65	408449	NM_004408	Hs.166161	dynamitin 1	3.3
	417402	BE503227	Hs.134759	ESTs	3.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.3
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.3
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.3
70	450337	AI693256	Hs.202427	ESTs	3.3
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp761I1224 (f	3.3
	433236	NM_004296	Hs.3221	regulator of G-protein signalling 6	3.3
	417868	AI078534	Hs.122592	ESTs	3.3
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
75	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	418216	AA662240	Hs.283099	AF15q14 protein	3.3
	458060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 f1s, clone MA	3.3
	449145	AI632122	Hs.198408	ESTs	3.3
80	415101	R45531	Hs.144534	ESTs	3.3
	401272			C9000559:gij12314195jembjCAB99338.1j[A	3.3
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	419991	AI000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.3
	443761	AI525743	Hs.345187	ESTs	3.3

	427317	AB028955	Hs.175780	KIAA1032 protein	3.3
	426920	AA393351	Hs.132121	ESTs	3.3
	433894	AI907682	Hs.243293	ESTs	3.3
5	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.3
	419647	AA348947	Hs.91816	hypothetical protein	3.3
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	3.3
	428670	AA431682	Hs.134832	ESTs	3.3
10	435375	AI733610	Hs.187832	ESTs	3.3
	419043	T19167	Hs.89566	ets variant gene 1	3.3
	403341			Target Exon	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.3
15	456209	W60633	Hs.297792	ESTs	3.3
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.3
	451254	AI571016	Hs.172967	ESTs	3.3
20	435056	AW023337	Hs.5422	glycoprotein M6B	3.3
	433842	AI652156	Hs.26346	ESTs	3.3
	433325	AW206986	Hs.143905	ESTs	3.3
	451066	AI758660	Hs.206132	ESTs	3.3
	436114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.3
25	421686	AB011156	Hs.106794	KIAA0584 protein	3.3
	429228	AI553633	Hs.326447	ESTs	3.3
	450325	AI935962	Hs.26289	ESTs	3.3
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.3
	451778	AI826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	3.3
30	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.2
	450475	AW805634	Hs.205015	ESTs	3.2
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.2
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.2
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.2
35	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.2
	409248	AB033035	Hs.51965	KIAA1209 protein	3.2
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	3.2
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	3.2
40	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	3.2
	407304	AA565832	Hs.271649	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.2
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.2
	435071	D60683	Hs.35495	ESTs	3.2
45	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
	412193	AI684467	Hs.144057	ESTs	3.2
	442320	AI287817	Hs.129636	ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.2
	414528	AA148950	Hs.188836	ESTs	3.2
50	439764	T26535	Hs.22744	hypothetical protein MGC13105	3.2
	410425	BE278367	Hs.63510	KIAA0141 gene product	3.2
	429876	AB028977	Hs.225974	KIAA1054 protein	3.2
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.2
	439039	AI656707	Hs.48713	ESTs	3.2
55	447925	AW292271	Hs.250718	ESTs	3.2
	447714	AW296313	Hs.255537	ESTs	3.2
	434574	AI424458	Hs.33470	ESTs	3.2
	437269	AA334384	Hs.149420	ESTs	3.2
	416845	H95279	Hs.293788	gb:yu20h02.s1 Soares fetal liver spleen	3.2
60	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothei	3.2
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.2
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	3.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.2
	445828	F05802	Hs.81907	ESTs	3.2
65	423779	AW071837	Hs.57971	ESTs	3.2
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.2
	453792	AL134539	Hs.254129	KIAA1678	3.2
	428167	AA770021	Hs.16332	ESTs	3.2
	445413	AA151342	Hs.12677	CGI-147 protein	3.2
70	415314	N88802	Hs.5422	glycoprotein M6B	3.2
	425115	R44664	Hs.123956	ESTs	3.2
	432625	AJ243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.1
	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	3.1
75	427951	AW293165	Hs.143134	ESTs	3.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.1
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	3.1
	443431	AI056847	Hs.20654	ESTs	3.1
80	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	419617	AL008583	Hs.91622	neuronal pentraxin receptor	3.1
	444326	AI939357	Hs.270710	ESTs	3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1

	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.1
5	432682	AI376400	Hs.159588	ESTs	3.1
	450661	AW952160	Hs.83849	ESTs	3.1
	417636	R08916	Hs.191212	ESTs	3.1
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.1
	454032	W31790	Hs.194293	ESTs, Weakly similar to t54374 gene NF2	3.1
10	443150	AI034487	Hs.34650	ESTs	3.1
	404632			NM_022490:Homo sapiens hypothetical prot	3.1
	425537	AB007913	Hs.158291	KIAA0444 protein	3.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.1
	400090			Eos Control	3.1
15	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.1
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	3.1
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.1
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	3.1
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
20	449722	BE280074	Hs.23960	cyclin B1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.1
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.1
25	405605			C2001342.gij127814 sp P26434 NAH4_RAT SO	3.1
	417565	AI203405	Hs.47831	ESTs	3.1
	439538	AA837323	Hs.56407	ESTs	3.1
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.1
	430818	AI311928	Hs.348156	gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	3.1
30	408508	AI806109	Hs.135736	KIAA1580 protein	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.1
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
	417169	R13550	Hs.246773	ESTs	3.1
35	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	3.1
	428060	AA420616	Hs.249483	ESTs	3.1
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	3.1
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.0
	429163	AA884768		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	3.0
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.0
	433290	R20077	Hs.302185	Homo sapiens clone Z3618 mRNA sequence	3.0
	412507	L36645	Hs.73964	EphA4	3.0
	415827	H17462	Hs.23079	ESTs	3.0
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	3.0
	457358	AI479755	Hs.129010	ESTs	3.0
	441732	AW298818	Hs.127341	ESTs	3.0
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.0
	426384	AI472078	Hs.203662	hypothetical protein FLJ13189 (FLJ13189)	3.0
50	436267	AW450938	Hs.180115	ESTs	3.0
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.0
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	3.0
	459080	AW192083	Hs.290855	ESTs	3.0
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.0
55	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.0
	443753	AW367578	Hs.134749	ESTs	3.0
	445921	AW015211	Hs.146181	ESTs	3.0
	427695	R88483	Hs.172862	ESTs	3.0
	438283	AI458931	Hs.37282	ESTs	3.0
60	453324	W26592	Hs.232089	ESTs	3.0
	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.0
	433434	AA588429		gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens	3.0
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-link	3.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	3.0
65	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.0
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.0
	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.0
	433229	AB040925	Hs.91625	KIAA1492 protein	3.0
	429046	X57436	Hs.194772	oligodendrocyte myelin glycoprotein	3.0
70	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.0
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	3.0
	440261	M81886	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0
	441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	3.0
75	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.0
	429168	AA984682	Hs.146589	ESTs, Weakly similar to JC5238 galactosy	3.0
	453739	AL120266		ESTs	3.0

TABLE 158:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

5	410099	117647_1	AA081630 T08671 A1174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 AI439658 AA283724 AI805992 AI457096 AA084618 BE467736 AI092635 AI887863 AI697593 AA436618 AI167419 AI418634 T31586 AA436630 AA706191 AI041169 AI422304 T03534 AA211402 AI204899 AI366472 AW827081 AA788593 T32736 AI767935 AA167791 AA747914 AA663870 AI865504 BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880
10	410126	117761_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
15	411565	1249756_1	AI267606 AA121045 AA126521
20	412799	132817_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
25	412820	1330039_1	BE001236 BE001177 BE001180 BE001234
30	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
35	415131	1523680_1	D61119 D81508 D81734
40	416871	1626761_1	H98716 N90792 N24283
45	418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649
50	419544	185760_2	AI909154 AA526337 AA244193 AI909153
55	420111	190755_1	AA255652 AA280911 AW967920 AA262684
60	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
65	422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
70	423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 AI299437 AL133995 AA057405 N78357 AA917450 AI002692 T09262 T65008 H29290 AI200874 AA894415 AI732887 AI791768 AI733447 AA988785 N62128 T09261 AW956936
75	424572	24097_1	MI9650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303
80			AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 AI858240 R73218 H30477 H17776 AA659570 BE276750 AL118657 AA375861 AA352427 AW581695 AI141188 N63474 AA654162 H17659 AI120696 T28867 AW498868 AI355918 AA902349 AA569098 AI088231 AI042604 AA555133 AI183611 AI608822 AI275941 AW316805 AA349486 AI355233 R85117 AW613626 R49234 AA458846 N20669 H18693 AA977567 T15423 AW002084 AI824721 N36242 AI417281 AI018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916639 AI872560 F00482 H45184 AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 AI807085 AA808009 AA915914 F00007 AA019749 AL121560
			AW675544 AW090233 AW072071 AI810932 AI089733 AW026222 AA770155 AI089647 AI085733 AW516061 AL037636 AL037635 AI863947 H50420 R11203 AA019133 N49772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13146 AA349487 AU077160 BE255671 BE276795 BE250823 AL120301 BE311390 BE252483
	424945	245223_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665
	424947	245247_1	R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
	425331	250199_1	AW962128 AA355353 AA427363
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426919	273507_1	AL041228 D82004 D61361 AI1203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429007	298301_1	D80642 AA443145 AL119015 AW904500
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	429421	30431_1	AL031658 AI693758 AL040619 AW977914 AA811957 AI352198 AW104364 AA648367 AA897604 AW341668 AI201382 AL040620
	430183	31412_2	BE010038 AA676833 AI311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909
	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 AI352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
	433009	357371_1	AA761668 AA573621 R92814 R09670
	433434	366095_1	AA588429 AI972567 AW504832 AI299694
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	435542	407744_1	AA687376 H74234 AW975503
	437034	431713_1	AA742643 AA808575 AW976668
	437056	432262_1	AI147061 AA743380 AA765223 AW976398 AI803927
	438458	457837_1	AW975186 AA807807 D29548
	439285	47065_1	AI133916 H79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
	439518	47334_1	W76326 AF086341 W72300
	439566	47387_1	AF086387 W77884 W72711
	441102	509504_1	AA973905 AI299888 AA917019 H63235 T90771
	446692	689623_1	Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983
	447197	711623_1	R36075 AI366546 R36167
	448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
	453331	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
	453739	979419_1	AL120266 AW269469 AW890114
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	458912	823104_1	AI911066 AI933734 AI680888 AIJ003599

TABLE 15C:

Pkey:

Unique number corresponding to an Eos probelet

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400533	6981826	Minus	277132-277595
400777	8131663	Plus	70745-71121
401272	9797373	Minus	98374-98509
402145	8018280	Plus	113086-114800
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973
402855	9662953	Minus	59763-59909
403142	9444521	Plus	89286-90131
403341	8569175	Plus	30699-30910
403696	3135242	Minus	143467-143634
403790	8084957	Minus	87826-87947,89835-90002
404150	7534008	Plus	165811-165943
404283	2276311	Minus	99460-99564
404541	8318559	Plus	103456-103664
404584	9857511	Plus	138651-139153
404632	9796668	Plus	45096-45229
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
405238	7249119	Minus	51728-51836
405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
405348	2914717	Minus	43310-43462
405605	5836195	Minus	117070-117270
405819	4007557	Plus	2830-2967

TABLE 16A: ABOUT 859 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 16A lists about 859 genes up-regulated in glioblastoma multiforma (GBM) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 3.0. The "average" GBM level was set to the 85th percentile amongst various GBM tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of GLIOBLASTOMA MULTIFORMA to CNS

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	47.2
422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	44.9
423961	D13666	Hs.136348	periostin (OSF-2os)	33.3
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	25.9
449539	W80363	Hs.58446	ESTs	25.8
417308	H60720	Hs.81892	KIAA0101 gene product	23.3
424800	AL035588	Hs.153203	MyoD family inhibitor	23.0
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	19.6
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	18.7
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	17.8
444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	17.8
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	17.7
417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	17.5
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	17.0
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	15.9
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	15.6
424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fs, clone PL	15.2
408243	Y00787	Hs.624	interleukin 8	14.7
422672	X12784	Hs.119129	collagen, type IV, alpha 1	14.7
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	14.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	14.2
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	14.2
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	14.1
446584	U53445	Hs.15432	downregulated in ovarian cancer 1	14.0
444969	AI203334	Hs.160628	ESTs	13.5
430691	C14187	Hs.103538	ESTs	12.9
426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	12.4
445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	12.1
441269	AW015206	Hs.178784	ESTs	11.9
417426	NM_002291	Hs.82124	laminin, beta 1	11.9
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	11.8
422163	AF027208	Hs.112360	prominin (mouse)-like 1	11.3
411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	11.3
449722	BE280074	Hs.23960	cyclin B1	11.2
436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	11.0
435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	10.9
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.9
419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fs, clone C	10.6
417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	10.6
413929	BE501689	Hs.75617	collagen, type IV, alpha 2	10.6

	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	10.6
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	10.4
	406972	M32053		gb:Human H19 RNA gene, complete cds.	10.4
5	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	10.3
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	10.3
	449611	AI970394	Hs.197075	ESTs	10.1
	427581	NM_014788	Hs.179703	KIAA0129 gene product	10.1
	431512	BE270734	Hs.2795	lactate dehydrogenase A	9.9
10	429183	AB014604	Hs.197955	KIAA0704 protein	9.8
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	9.7
	424840	D79987	Hs.153479	extra spindle poles, <i>S. cerevisiae</i> , homo	9.7
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	9.7
	433647	AA603367	Hs.222294	ESTs	9.7
	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	9.5
15	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.3
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	9.3
	409902	AI337658	Hs.156351	ESTs	9.3
	450375	AA009647		a disintegrin and metalloproteinase doma	9.2
20	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	9.1
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	9.1
	452461	N78223	Hs.108106	transcription factor	9.1
	434846	AW295389	Hs.119768	ESTs	9.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	9.0
25	425187	AW014486	Hs.22509	ESTs	9.0
	443247	BE614387	Hs.333893	c-Myc target JPO1	8.7
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	8.7
	410276	AI554545	Hs.68301	angiotensin-2	8.6
	402855			NM_001839: Homo sapiens calponin 3, acid	8.6
30	439710	AF086543		gb:Homo sapiens full length insert cDNA	8.6
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	8.6
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	8.6
	436895	AF037335	Hs.5338	carbonic anhydrase XII	8.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	8.6
35	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	8.5
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	8.5
	449961	AW265634	Hs.133100	ESTs	8.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	8.4
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.3
40	453884	AA355925	Hs.36232	KIAA0186 gene product	8.3
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.2
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	8.1
	411078	AI222020	Hs.182364	CocoaCrisp	8.1
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.0
45	447726	AL137638	Hs.19368	matrilin 2	8.0
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.9
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	7.9
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	7.9
50	447004	AW296968	Hs.157539	ESTs	7.9
	436140	W87355	Hs.269587	ESTs	7.9
	436607	AW661783	Hs.211061	ESTs	7.8
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	7.7
	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	7.7
55	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	7.7
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.7
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	7.7
	424587	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.6
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.6
60	421988	AW450481	Hs.161333	ESTs	7.6
	452620	AA436504	Hs.119286	ESTs	7.6
	453941	U39817	Hs.36820	Bloom syndrome	7.5
	416737	AF154335	Hs.79691	LIM domain protein	7.5
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	7.5
65	418400	BE243026	Hs.301989	KIAA0246 protein	7.5
	437036	AI571514	Hs.133022	ESTs	7.5
	421899	AJ011895	Hs.109281	Nef-associated factor 1	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	7.4
70	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.3
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	7.3
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	7.3
	449571	AW016812	Hs.200266	ESTs	7.3
	427899	AA829286	Hs.332053	serum amyloid A1	7.3
75	447458	AI741082	Hs.158961	ESTs	7.3
	430630	AW269920	Hs.2621	cystatin A (stefin A)	7.2
	411252	AB018549	Hs.69328	MD-2 protein	7.2
	432731	R31178	Hs.287820	fibronectin 1	7.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	7.2
80	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	7.2
	428728	NM_016625	Hs.191381	hypothetical protein	7.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	7.1
	410434	AF051152	Hs.63668	toll-like receptor 2	7.1

	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	7.1
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	7.1
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	7.0
5	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	7.0
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	7.0
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	7.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.9
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	6.9
10	424381	AA285249	Hs.145329	protein kinase Chk2	6.9
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	6.9
	415682	AI347128	Hs.191870	ESTs	6.9
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.8
	429447	AW812452	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	6.8
15	423198	M81933	Hs.1634	cell division cycle 25A	6.8
	413627	BE182082	Hs.246973	ESTs	6.8
	412777	AI335773	Hs.270123	ESTs	6.8
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	6.8
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	6.8
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.7
	446131	NM_000929	Hs.290	phospholipase A2, group V	6.7
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	6.7
	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.7
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	6.7
25	408161	AW952912	Hs.300383	hypothetical protein MGC3032	6.7
	440704	M69241	Hs.162	insulin-like growth factor binding prote	6.7
	407182	AA312551	Hs.230157	ESTs	6.7
	445837	AI261700	Hs.145544	ESTs	6.7
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	6.6
30	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.6
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	6.6
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.5
	450506	NM_004460		fibroblast activation protein, alpha	6.5
35	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	6.5
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	6.5
	452799	AI948829	Hs.213786	ESTs	6.5
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	6.4
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	6.4
	443884	N20617	Hs.194397	leptin receptor	6.4
40	420560	AW207748	Hs.59115	ESTs	6.4
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	6.3
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
	457465	AW301344	Hs.122908	DNA replication factor	6.3
	440332	AI218517	Hs.188051	ESTs	6.3
45	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	6.3
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.2
	448275	BE514434	Hs.20830	kinesin-like 2	6.2
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	6.2
50	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbH19W	6.1
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	6.1
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	6.1
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	6.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	6.0
55	413786	AW613780	Hs.13500	ESTs	6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
	400419	AF084545		Target	5.9
	408380	AF123050	Hs.44532	diubiquitin	5.9
60	426108	AA622037	Hs.166468	programmed cell death 5	5.9
	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.9
	437695	AA769202	Hs.192142	ESTs	5.8
	409463	AI458165	Hs.17296	hypothetical protein MGC2376	5.8
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	5.8
	443731	AI083928	Hs.145418	ESTs	5.8
65	405558			Target Exon	5.8
	422094	AF129535	Hs.272027	F-box only protein 5	5.8
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	5.8
	425882	U83115	Hs.161002	absent in melanoma 1	5.8
	412471	M83193	Hs.73946	endothelial cell growth factor 1 (platelet	5.8
70	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	5.8
	436827	H72187	Hs.5322	guanine nucleotide binding protein (G pr	5.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	5.7
	414053	BE391635	Hs.75725	transgelin 2	5.7
	436805	AA731533	Hs.270751	ESTs	5.7
75	442201	AW516704	Hs.208726	ESTs	5.7
	453361	AA035197	Hs.107375	ESTs	5.7
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.6
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	5.6
	423081	AF262992	Hs.123159	sperm associated antigen 4	5.6
80	407013	U35637		gb:Human nebulin mRNA, partial cds	5.5
	406478			Target Exon	5.5
	435937	AA830893	Hs.119769	ESTs	5.5
	453362	H14988	Hs.107375	ESTs	5.5
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	5.5

	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.5
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	5.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	5.5
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	5.4
5	407624	AW157431	Hs.248941	ESTs	5.4
	448769	N66037	Hs.38173	ESTs	5.4
	417124	BE122762	Hs.25338	ESTs	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	5.3
10	418596	AW976721	Hs.293327	ESTs	5.3
	410295	AA741357	Hs.5174	nidogen (enactin)	5.3
	433323	AA805132	Hs.159142	ESTs	5.3
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.3
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	5.3
15	420075	AF142482	Hs.203846	TEA domain family member 3	5.2
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	5.2
	407729	T40707	Hs.270862	ESTs	5.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	5.2
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.2
20	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	5.2
	424998	U58515	Hs.154138	chitinase 3-like 2	5.2
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	5.2
	445118	AI208762	Hs.345572	ESTs	5.2
	408523	AW833259	Hs.314287	ESTs	5.2
25	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	5.2
	449300	AI656959	Hs.346514	ESTs	5.2
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.2
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	5.1
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
30	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.1
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	5.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	5.1
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.1
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	5.0
35	424009	F11690		gb:HSC3D041 normalized infant brain cDN	5.0
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	5.0
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.0
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
40	418097	R45137	Hs.21868	ESTs	5.0
	453331	AI240665		ESTs	4.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.9
	426044	AA502490	Hs.170290	ESTs	4.9
	444161	NS2543	Hs.142940	ESTs	4.9
45	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.9
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.9
	447752	M73700	Hs.105938	lactotransferrin	4.9
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.9
50	402274			C19000498*gi4567179 gb AAD23607.1 AC00	4.9
	444656	AI277924	Hs.145199	ESTs	4.9
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	4.9
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	4.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.9
55	409112	BE243971	Hs.50649	quinone oxidoreductase homolog	4.8
	403481			Target Exon	4.8
	443740	R56434	Hs.21062	ESTs	4.8
	435005	U80743	Hs.306094	trinucleotide repeat containing 12	4.8
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	4.8
60	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	4.8
	428403	AI393048	Hs.326159	leucine rich repeat (in FLJ) interactin	4.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.8
	425212	AW962253	Hs.171618	ESTs	4.8
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	4.8
65	431176	AI026984	Hs.293662	ESTs	4.8
	420092	AA814043	Hs.88045	ESTs	4.8
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	403011			ENSP00000215330*Probable serine/threoni	4.7
70	405348			C7001664:gi12698061 dbj BAB21849.1 (AB	4.7
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.7
	443318	AI051603	Hs.133141	ESTs	4.7
	421027	AA761198	Hs.55254	ESTs	4.7
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.7
75	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.7
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	4.7
	450166	AA429504		ESTs	4.7
	438456	AA913381	Hs.20594	ESTs	4.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	4.7
80	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	4.7
	458946	AA009716	Hs.42311	ESTs	4.7
	454860	AW835767		gb:OV4-LT0016-240200-110-b08 LT0016 Homo	4.7
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.7
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.6

	422648	D86983	Hs.118893	Melanoma associated gene	4.6
	431319	AA873350	Hs.302232	ESTs	4.6
	445666	R59960	Hs.282386	ESTs	4.6
5	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.6
	422887	AJ751848	Hs.49215	ESTs	4.6
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.6
	405141	Y14443		zinc finger protein 200	4.6
	440210	AW674562	Hs.125296	ESTs	4.6
10	432527	AW975028	Hs.102754	ESTs	4.6
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	4.6
	435143	R12375	Hs.194600	ESTs	4.6
	422170	AJ791949	Hs.112432	an6-Mullerian hormone	4.6
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	4.6
15	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) nmb	4.6
	412568	A878826	Hs.74034	caveolin 1, caveolae protein, ZkD	4.5
	426215	AW963419	Hs.155223	stanniocalcin 2	4.5
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	4.5
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	4.5
20	419735	AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	4.5
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.5
	441217	AJ922183	Hs.213246	ESTs	4.5
	435542	AA687376		ESTs	4.5
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	4.5
25	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	4.5
	416114	AJ695549	Hs.183868	glucuronidase, beta	4.5
	437323	AA371145	Hs.194397	leptin receptor	4.5
	425139	AW630488	Hs.25338	protease, serine, 23	4.5
	423678	AW963357	Hs.7847	ESTs	4.5
30	403961			Target Exon	4.5
	443462	AJ064690	Hs.171176	ESTs	4.5
	418483	W26076	Hs.221847	ESTs	4.5
	428873	AJ701609	Hs.98908	ESTs	4.5
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.5
35	408298	AJ745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	4.5
	449145	AJ632122	Hs.198408	ESTs	4.4
	439574	AJ69788	Hs.165190	ESTs	4.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.4
	453387	AJ990741	Hs.252809	ESTs	4.4
40	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	4.4
	433507	AJ817336	Hs.191791	ESTs	4.4
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	4.4
	421064	AJ245432	Hs.101382	tumor necrosis factor, alpha-induced pro	4.4
	402604			Target Exon	4.4
45	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.4
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	4.4
	423600	AJ633559	Hs.310359	ESTs	4.4
	403361			NM_002210*:Homo sapiens integrin, alpha	4.4
	408432	AW195262		gb:xn67b05.x1 NCL CGAP_CML1 Homo sapiens	4.4
50	424489	T48851	Hs.274470	D-siglec precursor,	4.3
	442264	AJ278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.3
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	4.3
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.3
55	439566	AF086387		gb:Homo sapiens full length insert cDNA	4.3
	425242	D13635	Hs.155287	KIAA0010 gene product	4.3
	423529	T87318	Hs.120411	ESTs	4.3
	439538	AA837323	Hs.56407	ESTs	4.3
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	4.3
60	425259	AL049280	Hs.155397	Homo sapiens mRNA: cDNA DKFZp564K143 (fr	4.3
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	4.3
	426649	AJ914936	Hs.97152	ESTs	4.3
	438875	AA827640	Hs.189059	ESTs	4.3
	445868	BE169357	Hs.207428	ESTs	4.3
65	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	4.3
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4.3
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	4.3
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	4.2
70	443950	NM_001425	Hs.9999	epithelial membrane protein 3	4.2
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	4.2
	452994	AW962597	Hs.31305	KIAA1547 protein	4.2
	420841	AJ625251	Hs.94037	hypothetical protein FLJ23053	4.2
	441255	R06350	Hs.171635	ESTs	4.2
75	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	4.2
	411789	AF245505	Hs.72157	Adican	4.2
	409638	AW450420	Hs.21335	ESTs	4.2
	439192	AW970536	Hs.105413	ESTs	4.2
	440684	AJ253123	Hs.127356	ESTs, Highly similar to S21424 nestin (H	4.2
80	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	4.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	4.2
	401454			NM_014226*:Homo sapiens renal tumor anti	4.2
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	4.2
	442326	H92962	Hs.124813	hypothetical protein MGC14817	4.2

	419402	Z68155	Hs.90291	laminin, beta 2 (laminin S)	4.2
	435703	AW630133	Hs.83313	GK003 protein	4.2
	444609	AW571659	Hs.278081	ESTs	4.2
5	404407			Target Exon	4.2
	450581	AF081513	Hs.25195	TGF-beta 4	4.2
	407838	BE146411	Hs.40342	putative nuclear protein	4.1
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.1
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.1
10	438898	AI819863	Hs.106243	ESTs	4.1
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	4.1
	445921	AW015211	Hs.146181	ESTs	4.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	4.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.1
15	427463	AA442224	Hs.97900	ESTs	4.1
	450639	AI703186	Hs.277174	ESTs	4.1
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.1
	437269	AA334384	Hs.149420	ESTs	4.1
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	4.1
20	414300	AI304870	Hs.188680	ESTs	4.1
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.1
	415024	AI983981	Hs.189114	ESTs	4.1
	408102	U46351	Hs.621	lectin, galactoside-binding, soluble, 3	4.1
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.1
25	451433	AA021140	Hs.269265	ESTs, Weakly similar to A46010 X-linked	4.1
	446523	NM_003063	Hs.334629	sarcophilin	4.1
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	4.1
	402239			Target Exon	4.1
	423713	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.1
30	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.1
	414948	C15240	Hs.182155	ESTs	4.0
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp43B0425 (f	4.0
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
35	449655	AI021987	Hs.59970	ESTs	4.0
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.0
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.0
	422282	AF019225	Hs.114309	apolipoprotein L	4.0
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	4.0
40	449256	AA059050	Hs.59847	ESTs	4.0
	453385	AW296101	Hs.252806	ESTs	4.0
	443715	AI583187	Hs.9700	cyclin E1	4.0
	451778	AI826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	4.0
	441287	AW293132	Hs.131373	ESTs	4.0
45	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.0
	420894	AA744597	Hs.88854	ESTs	4.0
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	4.0
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	4.0
	453948	AI970797	Hs.64859	ESTs	4.0
50	444170	AW613879	Hs.102408	ESTs	4.0
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	418216	AA662240	Hs.283099	AF15q14 protein	4.0
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	4.0
55	430890	X54232	Hs.2699	glypican 1	3.9
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.9
	436265	AA731331	Hs.190668	ESTs	3.9
	407304	AA565832	Hs.271649	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.9
60	433244	AB040943	Hs.271285	KIAA1510 protein	3.9
	446960	AW294936	Hs.156762	ESTs	3.9
	406627	T64904	Hs.163780	ESTs	3.9
	420552	AK000492	Hs.98806	hypothetical protein	3.9
	402082			C18000743:gil6678363[ref]NP_033416.1[(3.9
65	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.9
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.9
	422564	AI148006	Hs.222120	ESTs	3.9
	418781	T41160	Hs.8404	ESTs	3.9
70	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	3.9
	413095	AA494359	Hs.30715	potassium voltage-gated channel, tsx-rel	3.9
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.9
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	3.9
	422173	BE385828	Hs.250619	phorbol-like protein MDS019	3.9
75	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	3.8
	403849			Target Exon	3.8
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.8
	445075	AI651827	Hs.344767	ESTs	3.8
	420004	AW975532	Hs.164039	ESTs, Moderately similar to I38022 hypot	3.8
80	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.8
	424479	AF064238	Hs.149098	smoothelin	3.8
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	3.8
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	3.8
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.8

5	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.8
	453920	AI133148	Hs.36602	I factor (complement)	3.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.8
	406872	AI760903		gbwi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	3.8
	403696			C4001100:gi 5852342 gb AAD54015.1 (AF0	3.8
10	417791	AW965339	Hs.111471	ESTs	3.8
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	3.8
	404209			Target Exon	3.8
	431454	AW975980	Hs.292918	ESTs	3.8
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.8
15	406739	AI566709	Hs.182426	ribosomal protein S2	3.8
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.8
	457876	AI821940		ESTs, Moderately similar to ALU8_HUMAN A	3.8
	435718	R06569	Hs.269534	ESTs	3.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.8
20	442710	AI015631	Hs.23210	ESTs	3.8
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.8
	419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	3.8
	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	3.8
	408896	AI610447	Hs.48778	niban protein	3.8
25	425300	AW601773	Hs.270259	ESTs	3.8
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.8
	424090	X99699	Hs.139262	XIAP associated factor-1	3.7
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	3.7
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.7
30	420579	AA278449	Hs.137429	ESTs	3.7
	406038	Y14443		zinc finger protein 200	3.7
	412590	AL134388	Hs.135033	ESTs, Weakly similar to I38022 hypotheri	3.7
	406714	AI219304	Hs.266959	hemoglobin, gamma G	3.7
	412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	3.7
35	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.7
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.7
	408955	BE315170	Hs.8087	Target CAT	3.7
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.7
	413774	AA131782	Hs.182314	ESTs	3.7
40	440225	BE295782	Hs.159	tumor necrosis factor receptor superfam	3.7
	414528	AA148950	Hs.188836	ESTs	3.7
	436137	AI056769	Hs.133512	ESTs	3.7
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.7
	406785	AA588061		gbnk10d03.s1 NCI_CGAP_Co2 Homo sapiens	3.7
45	443361	AI792628	Hs.133273	ESTs	3.7
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.7
	409557	BE182896	Hs.211193	ESTs	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427695	R88483	Hs.127862	ESTs	3.7
50	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	3.6
	444371	BE540274	Hs.239	forkhead box M1	3.6
	437816	AI823445	Hs.280699	ESTs	3.6
55	405605			C2001342:gi 127814 sp P26434 NAH4_RAT SO	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	430540	AW245422	Hs.106357	Homo sapiens cDNA: FLJ22105 fis, clone H	3.6
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	3.6
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.6
60	403267			Target Exon	3.6
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.6
	447497	AW167254	Hs.205722	ESTs	3.6
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.6
	428715	AW293716	Hs.53126	ESTs	3.6
65	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	3.6
	453438	AI469935	Hs.22792	ESTs	3.6
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.6
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.6
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	3.6
70	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	3.6
	435523	T62849	Hs.11080	membrane-spanning 4-domains, subfamily A	3.6
	418287	AI872319	Hs.78935	methionine aminopeptidase; eIF-2 associa	3.6
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.6
	441224	AU076964	Hs.7753	calumenin	3.6
75	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.6
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.6
	433325	AW206986	Hs.143905	ESTs	3.6
	420683	AA830168	Hs.271305	ESTs	3.6
	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.6
80	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.6
	404584			Target Exon	3.5
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.5
	425822	AL157466	Hs.162751	Homo sapiens mRNA: cDNA DKFZp761E2423 (f	3.5
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.5
	412971	AA889628	Hs.35125	ESTs	3.5
	451593	AF151879	Hs.26706	CGI-121 protein	3.5
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	3.5

	427809	M26380	Hs.180878	lipoprotein lipase	3.5
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	3.5
	42765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.5
	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	3.5
5	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.5
	432250	AA452088	Hs.274170	Opa-interacting protein 2	3.5
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
	410507	AA355288	Hs.76064	transitional epithelia response protein	3.5
10	412436	AA665089		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	3.5
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.5
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.5
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.5
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.5
15	422448	AW372922	Hs.116774	integrin, alpha 1	3.5
	420676	AA434780	Hs.4248	vav 2 oncogene	3.5
	417663	R07483	Hs.180461	ESTs	3.5
	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fs, clone C	3.5
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	3.5
20	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	3.5
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	3.5
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	3.5
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	3.5
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Prl1 Homo sapiens	3.5
25	449162	AI632740	Hs.10476	ESTs	3.5
	437774	AW978199	Hs.291648	ESTs, Weakly similar to i38022 hypotheti	3.5
	426827	AW067805	Hs.172665	methyleneetetrahydrofolate dehydrogenase	3.4
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.4
	450325	AI935962	Hs.26289	ESTs	3.4
30	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.4
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.4
	417409	BE272506	Hs.82109	syndecan 1	3.4
	412811	H06382		ESTs	3.4
	430758	T91568	Hs.270616	ESTs, Moderately similar to A34087 hypot	3.4
35	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.4
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.4
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	3.4
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.4
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.4
40	446134	AW161234	Hs.13993	TBP-like 1	3.4
	418669	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein	3.4
	425006	R38685	Hs.222746	ESTs	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	453379	AA035261	Hs.61753	ESTs	3.4
45	448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ22356 fs, clone H	3.4
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.4
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.4
	417395	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	3.4
	405046			C3000978:gi9280045:dbj BAB01579.1 (AB0	3.4
50	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	455142	AW861840		gb:CM0-CT0337-250200-243-g01 CT0337 Homo	3.4
	418819	AA228776	Hs.191721	ESTs	3.4
	428289	M26301	Hs.2253	complement component 2	3.4
55	412799	AI267606		gb:aq91h03.x1 Stanley Frontal S8 pool 1	3.4
	403108			ENSP00000241415*:Hypothetical 67.7 kDa p	3.4
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.4
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	3.4
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	3.4
60	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4
	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.4
	439867	AA847510	Hs.161292	ESTs	3.4
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.4
	420982	AW576160	Hs.100729	KIAA0692 protein	3.4
	440826	AW383618	Hs.346256	ESTs, Moderately similar to ALU2_HUMAN A	3.4
65	427687	AW003867	Hs.1570	histamine receptor H1	3.4
	400533			ENSP00000209376*:PRED65 protein (Fragmen	3.3
	436314	AI983409	Hs.189226	ESTs	3.3
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	3.3
70	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.3
	402229	BE262804		mitochondrial ribosomal protein S2	3.3
	410687	U24389	Hs.65436	lysyl oxidase-like 1	3.3
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	3.3
	443338	R99575	Hs.302908	ESTs	3.3
75	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.3
	405303			Target Exon	3.3
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.3
	431721	AB032996	Hs.268044	KIAA1170 protein	3.3
80	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	3.3
	425262	D87119	Hs.155418	GS3955 protein	3.3
	424947	R77952		ESTs, Weakly similar to alternatively sp	3.3
	437634	AW293046	Hs.255158	ESTs	3.3
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	3.3

	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	3.3
	447499	AW262580	Hs.147674	protocadherin beta 16	3.3
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.3
5	435644	AA700867	Hs.269659	ESTs	3.3
	406060			Target Exon	3.3
	425018	BE245277	Hs.154196	E4F transcription factor 1	3.3
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	3.3
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.3
10	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.3
	435375	AI733610	Hs.187832	ESTs	3.3
	432693	AW449630	Hs.293790	ESTs	3.3
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.3
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.3
15	448002	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.3
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.3
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheri	3.3
	452526	W38537	Hs.280740	hypothetical protein MGC3040	3.3
	416664	H77780	Hs.20289	ESTs	3.3
20	444911	U06117	Hs.250	xanthene dehydrogenase	3.3
	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	3.3
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.3
	444046	AI360834	Hs.135094	ESTs	3.3
	411373	BE326276	Hs.8861	ESTs	3.3
25	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse t	3.3
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.3
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.3
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	3.3
	416379	N38857	Hs.203933	ESTs	3.3
30	416308	AW291942	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxido	3.3
	427954	J03060	Hs.247551	metaxin 1	3.3
	459660	M79082		ESTs	3.3
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.3
	437945	T78519		gb:yd68c08.r1 Soares fetal liver spleen	3.3
35	400850			Target Exon	3.3
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I38022 hypotheri	3.3
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	3.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.3
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	3.2
40	440933	AI208217	Hs.142879	ESTs	3.2
	418079	R40058	Hs.6911	ESTs	3.2
	414280	BE410769	Hs.75873	zyxin	3.2
	425295	AA431366	Hs.37251	ESTs	3.2
	408872	AI476139	Hs.13291	ESTs	3.2
45	416857	AA188775	Hs.292453	ESTs	3.2
	429599	AA806106	Hs.123664	ESTs	3.2
	437437	AA226869		hypothetical protein DKFZp762L0311	3.2
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.2
	403349	NM_001406		ephrin-B3	3.2
50	449385	AI650471	Hs.347290	ESTs	3.2
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.2
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	3.2
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.2
	432044	AW972727		gb:EST384819 MAGE resequences, MAGL Homo	3.2
55	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.2
	408431	AI338631	Hs.43266	Homo sapiens cDNA: FLJ22536 fis, clone H	3.2
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.2
	439332	AW842747	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	3.2
60	418030	BE207573	Hs.83321	neuromedin B	3.2
	428878	AA436884	Hs.48926	ESTs	3.2
	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	3.2
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	3.2
	448432	AI783586	Hs.208575	ESTs	3.2
65	433894	AI907682	Hs.243293	ESTs	3.2
	436210	AI825420	Hs.197824	ESTs	3.2
	433791	AA719352	Hs.112718	ESTs	3.2
	450150	AI754391	Hs.23510	Kruppel-like factor 12	3.2
	427513	AI476318	Hs.192480	ESTs	3.2
70	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	3.2
	451350	AI791447		gb:ni13a05.y5 NCL_CGAP_Co4 Homo sapiens	3.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.2
	416784	AA334592	Hs.79914	lumican	3.2
	406851	AA609784		major histocompatibility complex, class	3.2
75	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	3.2
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	3.2
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	3.2
	415709	AA649850	Hs.278558	ESTs	3.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2
80	437807	AI017875	Hs.136829	ESTs	3.2
	425171	AW732240	Hs.16365	ESTs	3.2
	448108	AW300021	Hs.170685	ESTs	3.2
	402523			C1001173:gil9743439[gb]AAF79932.2[AF2	3.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	3.2

	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.2
	422081	AW136820	Hs.196011	ESTs	3.2
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	3.2
5	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.2
	442609	AL020996	Hs.8518	selenoprotein N	3.2
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	3.2
	441544	AW300043	Hs.127137	ESTs	3.2
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.2
10	419652	AL157485	Hs.91973	hypothetical protein	3.2
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	3.2
	441701	AW339828	Hs.127497	ESTs	3.2
	426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.2
	420886	AA805453		ESTs, Weakly similar to T29012 hypotheti	3.2
15	428896	AW291932	Hs.98936	ESTs	3.2
	458253	AW296952	Hs.196802	ESTs	3.2
	456895	AA354771	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	3.2
	434818	AA650097	Hs.5996	ESTs	3.2
20	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3.2
	434131	AI858275	Hs.143659	ESTs	3.2
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.1
	443021	AA368546	Hs.8904	Ig superfamily protein	3.1
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.1
25	429973	AI423317	Hs.164580	ESTs	3.1
	422545	X02761	Hs.287820	fibronectin 1	3.1
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.1
	420116	NM_013241	Hs.95231	FH1/FH2 domain-containing protein	3.1
	401841			NM_015113:Homo sapiens KIAA0399 protein	3.1
30	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.1
	431019	NM_005249	Hs.2714	forkhead box G1B	3.1
	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	3.1
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.1
35	430701	AI760833	Hs.293971	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	458918	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.1
	439764	T26535	Hs.22744	hypothetical protein MGC13105	3.1
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	3.1
40	403969			ENSP0000034663:Zinc finger protein 131	3.1
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.1
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.1
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.1
45	444168	AW379879		gb:RC1-HT0256-081199-011-01 HT0256 Homo	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	444881	AI623288	Hs.192805	ESTs	3.1
	440381	AA917808	Hs.190495	ESTs	3.1
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	3.1
50	439130	AA306090	Hs.124707	ESTs	3.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.1
	406736	AI254733	Hs.182426	ribosomal protein S2	3.1
	420172	AA601122	Hs.95655	secreted and transmembrane 1	3.1
	428060	AA420616	Hs.249483	ESTs	3.1
55	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.1
	409154	U72882	Hs.50842	interferon-induced protein 35	3.1
	449426	T92251	Hs.198882	ESTs	3.1
	458760	AI498631	Hs.111334	ferritin, light polypeptide	3.1
	450811	AI739486	Hs.245497	ESTs	3.1
60	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	3.1
	445211	BE045601	Hs.118248	ESTs, Weakly similar to YC18_HUMAN HYPOT	3.1
	441318	AI078234	Hs.176130	ESTs	3.1
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	3.1
	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypotheti	3.1
65	444672	Z95636	Hs.11669	laminin, alpha 5	3.1
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.1
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypotheti	3.1
	439755	AW748482	Hs.77873	B7 homolog 3	3.1
	435520	AA297990	Hs.9315	HNOEL-iso protein	3.1
70	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.1
	440948	AW188311	Hs.128619	ESTs	3.1
	412851	AI826502	Hs.106149	ESTs	3.1
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	3.1
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.1
75	411671	BE049094		ESTs	3.1
	430444	AW296421	Hs.121035	ESTs	3.1
	425843	BE313280	Hs.159627	death associated protein 3	3.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3.1
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	3.1
80	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	435664	AI032087	Hs.269819	ESTs	3.1
	453085	AW954243		KIAA0251 protein	3.1
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.0
	447527	AI702896	Hs.42091	ESTs	3.0

5	432682	AI376400	Hs.159588	ESTs	3.0
	416941	BE000150	Hs.48778	niban protein	3.0
	455481	AW948317		gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	445906	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	3.0
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	3.0
10	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.0
	436443	AW138211	Hs.128746	ESTs	3.0
	425421	L11669	Hs.157145	tetracycline transporter-like protein	3.0
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.0
	456816	AK001509	Hs.144391	hypothetical protein FLJ10647	3.0
15	404632			NM_022490:Homo sapiens hypothetical prot	3.0
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.0
	428917	AA437337	Hs.16689	ESTs	3.0
	424584	H10692	Hs.13310	ESTs	3.0
	452483	AI903731	Hs.106357	valosin-containing protein	3.0
20	404453			C8000963*:gq6329915jdbjBAA86452.1 (AB	3.0
	426931	NM_003416	Hs.2076	zinc finger protein 7 (K0X 4, clone HF.1	3.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.0
	452188	AI864208	Hs.176275	ESTs	3.0
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	3.0
25	413922	AI535895	Hs.221024	ESTs	3.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.0
	434070	AF116652	Hs.270087	hypothetical protein PRO0813	3.0
	406679	AA070786		gb:zm66b07.r1 Stratagene neuroepithelium	3.0
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.0
30	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	3.0
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	3.0
	408989	AW361666	Hs.49500	KIAA0746 protein	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.0
35	426765	AA743603	Hs.172108	nucleoporin 88kD	3.0
	400295	W72838		AI905687:IL-BT095-190199-019 BT095 Homo	3.0
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	3.0
	429940	W25215		gb:zb87a09.r1 Soares_senescent_fibroblas	3.0
	412281	AI810054	Hs.14119	ESTs	3.0
40	434898	AW500458	Hs.29956	KIAA0460 protein	3.0
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.0
	459727	AI906494		gb:RC-BT113-060499-024 BT113 Homo sapien	3.0
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.0
	458729	AI364504	Hs.93967	ESTs, Weakly similar to NBHUC8 decorin p	3.0
45	402105			C18000230*:gq12585552spjQ9Y2Q1J2257_HU	3.0
	425248	AW957442	Hs.252766	ESTs	3.0
	440995	T57773	Hs.10263	ESTs	3.0
	441360	AI091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110	3.0
	432692	AW974944	Hs.200577	ESTs	3.0
50	428899	AA744610	Hs.194431	palladin	3.0
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	3.0
	447183	AI554733	Hs.173182	ESTs	3.0
	429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro	3.0
	416505	H66470	Hs.16004	ESTs	3.0
55	420144	AA811813	Hs.119421	ESTs	3.0
	439184	AW021842	Hs.16533	myosin phosphatase, target subunit 1	3.0
	438033	T26483	Hs.6059	EGF-containing fibulin-like extracellular	3.0
	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	3.0
	441035	AI694309	Hs.126458	ESTs	3.0
60	458810	BE407125	Hs.231510	ESTs	3.0
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.0
	450879	AI742685	Hs.210347	ESTs	3.0
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	3.0
65	403780			C4001759:gq1133250spjP19474jRO52_HUMAN	3.0
	411543	AW851248		gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.0
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	3.0
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	3.0
70	413945	NM_000591	Hs.75627	CD14 antigen	3.0
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	3.0
	422605	H16646	Hs.118666	hypothetical protein PP591	3.0
	443502	AI074528	Hs.133949	ESTs	3.0
	410781	AI375672	Hs.165028	ESTs	3.0
75	449428	AI651280	Hs.195685	ESTs	3.0
	436671	AW137159	Hs.146151	ESTs	3.0
TABLE 16B:					
80	Pkey:	Unique Eas probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
80	Pkey	CAT Number	Accession		
	408432	1058667_1	AW195262 R27868 AW811262		
	410886	1225822_1	AW809324 BE144977 BE144956		
	411537	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529		
	411543	1249127_1	AW851248 AW851425 AW850805 AW851021 AW850905		

5	411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
	411671	125369_1	BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170
	411688	1254076_1	AW953440 T08189 AW857085
	412436	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	412799	132817_1	AI267606 AA121045 AA126521
	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
	414372	143909_1	R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
10	415131	1523680_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	415688	154643_1	D61119 D81508 D81734
	416871	1626761_1	AA166963 AW971218 AA493942
	416913	163001_1	H98716 N90792 N24283
	419896	1888662_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	420886	197344_1	Z99362 Z99363
15	422156	212379_1	AA805453 AA281379
	423713	231290_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
	424009	234177_1	AI334966 W32951 H62656 H53902 R88904 AW835732
	424947	245247_1	AW754182 AW754198 AA329983
20	425331	250199_1	F11690 AW965370 AA333586 D30830
	429163	300543_1	R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
	429940	310884_1	AW962128 AA355353 AA427363
	430968	326269_1	AA884766 AW974271 AA592975 AA447312
25	432044	340773_1	W25215 AA461079 AA461391
	432363	345469_1	AW972830 AA527647 AA489820 AA570362
	435542	407744_1	AW972727 AA524829 AW972733
	437437	43709_1	AA534489 AW970240 AW970323
			AA687376 H74234 AW975503
30			AA226869 AA296516 AW959753 AA186390 AI359619 AA356195 AA148427 R22748 AI033624 BE548853 H95327 AW579751 BE561649 AA397533
			BE617136 AA236444 T89946 AA247450 N55777 W38725 AI743846 AI808406 AA922229 AI051464 W04713 R11251 W19656 AI042319 AA489276
			AI224533 H
	437945	44580_1	T78519 H59898 U72516
	439518	47334_1	W76326 AF086341 W72300
	439566	47387_1	AF086387 W77884 W72711
	439710	47550_1	AF086543 W96291 W96225
35	442476	543547_1	AF069475 AF069477 AF069476
	444168	593829_1	AW379879 AI126285 H12014
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
			N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450166	82677_1	AA429504 R41904 AA279467 H09648 AA007236
40	450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
			AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
	450506	836_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
			AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296 AA436611 AW609728 W42634 AI682584 AA405569
			AI685653 AW0
45	450625	84032_1	AW970107 AA513951 AA010406
	451129	859870_1	BE072881 BE072946 AI762181
	451350	856945_1	AI791447 AI791327 AW886809
	452203	903_2	X57522 AW295947 AI346197 AI304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R18264 T74462 AA346259
			AW062508 AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 AI819778 AA054458 AI346733
			AW361447 AI4
50	453085	94851_1	AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306 AA918481 AI183314 D83907
			AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767267 W56507 AA847787 AA568692 T10502
			AI247870
	453331	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292
55			R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870
			R7390
	453682	977454_1	T79703 T96307 AL079725
	454860	1237732_1	AW835767 AW835537 BE160187
	455142	1254887_1	AW861840 AW858329 AW858192 AW858189 AW858224 AW858351
60	455481	1293182_1	AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455899	1381547_1	BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457876	42814_2	AI821940 N67106 AI744264 AA808846 AA643417 AA643416 Z70715
65	TABLE 16C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
70	Nt_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand Nt_position
	400533	6981826	Minus 277132-277595
	400850	1927150	Minus 4506-4691
75	401454	9186923	Minus 114659-114832
	401841	7684597	Plus 89868-90006,91920-92085
	402082	8117478	Minus 190046-190183
	402105	8131588	Minus 22856-24055
	402229	9965022	Minus 15739-15951,16166-16779
80	402239	7690131	Plus 38175-38304,42133-42266
	402274	2935596	Plus 5604-6527
	402523	9798518	Minus 18729-19283
	402604	9909420	Plus 20393-20767

5	402855	9662953	Minus	59763-59909
	403011	6693597	Minus	3468-3623
	403108	8980955	Plus	93253-93667
	403267	7887182	Plus	116078-121885
	403349	8569773	Minus	167815-168374
	403361	8570313	Minus	112496-112687
	403481	9965004	Plus	93496-93633
	403696	3135242	Minus	143467-143634
10	403780	8076989	Plus	93160-93409
	403849	7708855	Plus	95043-96519
	403961	7596976	Minus	110393-110803
	403969	8569909	Plus	31237-31375,32405-32506
	404209	5006246	Minus	11247-11514
15	404407	7329316	Minus	48154-48499
	404453	7657714	Plus	27768-29179
	404584	9857511	Plus	138651-139153
	404632	9796668	Plus	45096-45229
	405046	7596829	Minus	4373-4528
20	405141	8980911	Plus	99861-100054
	405303	2078453	Minus	130607-130802
	405348	2914717	Minus	43310-43462
	405558	1621110	Plus	4502-4644,5983-6083
	405605	5836195	Minus	117070-117270
25	406038	8389537	Plus	37764-37877
	406060	6899623	Minus	20339-20746
	406478	9857502	Plus	68314-68523,68853-68950

TABLE 17A: ABOUT 1040 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT TISSUES

Table 17A lists about 1040 genes up-regulated in glioblastoma multiforma (GBM) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" GBM level was set to the 85th percentile amongst various GBM tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 RT: Ratio of GLIOBLASTOMA MULTIFORMA compared to NORMAL ADULT TISSUES

40	Pkey	ExAccn	UnigenelD	Unigene Title	RT
	431917	D16181	Hs.2868	peripheral myelin protein 2	57.9
	428321	A1699994	Hs.2868	peripheral myelin protein 2	50.1
	427343	A1880044	Hs.176977	protein kinase C binding protein 2	49.6
45	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	43.9
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.9
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	42.5
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	37.1
50	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	37.0
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	32.7
	425842	A1587490	Hs.159623	NK-2 (Drosophila) homolog B	32.4
	419078	M93119	Hs.89584	insulinoma-associated 1	32.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	29.9
55	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	28.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	28.5
	417183	R52089	Hs.172717	ESTs	27.6
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	27.6
	412733	AA984472	Hs.74554	KIAA0080 protein	25.9
60	422656	A1870435	Hs.1569	LIM homeobox protein 2	25.6
	436878	BE465204	Hs.47448	ESTs	24.9
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	24.3
	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	23.1
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	23.1
65	409395	U46745	Hs.336678	dystrobrein, alpha	23.0
	435708	A1362949	Hs.75169	ESTs	22.5
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	22.2
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	22.1
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	22.0
70	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	21.7
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	20.9
	433551	A1985544	Hs.12450	protocadherin 9	19.8
	452744	A1267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	19.1
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	19.0
75	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	19.0
	447004	AW296968	Hs.157539	ESTs	18.6
	425048	H05468	Hs.164502	ESTs	18.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	18.0
80	421264	AL039123	Hs.103042	microtubule-associated protein 1B	18.0
	453642	AJ370936	Hs.34074	dipeptidylpeptidase VI	17.8
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	17.7
	444471	AB020684	Hs.11217	KIAA0877 protein	17.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	17.2
	430691	C14187	Hs.103538	ESTs	16.7

	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	16.6
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	16.6
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	16.5
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	16.4
5	431019	NM_005249	Hs.2714	forkhead box G1B	16.4
	449539	W80363	Hs.58446	ESTs	16.4
	450133	AW969769	Hs.105201	ESTs	16.1
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.0
10	447359	NM_012093	Hs.18268	adenylate kinase 5	15.4
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	459516	AI049662	Hs.246858	EST	14.9
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	14.7
	429466	M85835	Hs.12827	ESTs	14.7
15	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	14.7
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	14.6
	439415	F05538	Hs.4273	ESTs	14.5
	408604	D51408	Hs.21925	ESTs	14.5
	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	14.3
20	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	14.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	14.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	13.9
	439239	AI031540	Hs.235331	ESTs	13.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	13.7
25	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	13.5
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.4
	441440	AI807981	Hs.30495	ESTs	13.0
	412959	D87458	Hs.75090	KIAA0282 protein	12.8
30	413597	AW302885	Hs.117183	ESTs	12.8
	441016	AW138653	Hs.25845	ESTs	12.7
	418338	NM_002522	Hs.84154	neuronal pentraxin I	12.6
	423419	R55336	Hs.23539	ESTs	12.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	12.6
35	441497	R51064	Hs.23172	ESTs	12.4
	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	12.2
	453941	U39817	Hs.36820	Bloom syndrome	12.2
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	12.2
	446782	AI653048	Hs.144006	ESTs	12.1
40	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	12.1
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	11.9
	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	11.9
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	11.9
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	11.7
45	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	11.7
	424432	AB037821	Hs.146858	protocadherin 10	11.6
	451996	AW514021	Hs.245510	ESTs	11.4
	423678	AW963357	Hs.7847	ESTs	11.4
	445041	T64183	Hs.282982	solute carrier	11.3
50	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	11.2
	419721	NM_001650	Hs.288650	aquaporin 4	11.2
	446711	AF169692	Hs.12450	protocadherin 9	11.1
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	11.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.7
55	428728	NM_016625	Hs.191381	hypothetical protein	10.6
	415849	R20529	Hs.6806	ESTs	10.6
	447198	D61523	Hs.283435	ESTs	10.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	10.3
	435793	AB037734	Hs.4993	KIAA1313 protein	10.3
60	409049	AI423132	Hs.146343	ESTs	10.2
	449511	AI970394	Hs.197075	ESTs	10.2
	402604			Target Exon	10.1
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	10.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	10.0
65	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN !!!!	10.0
	419271	N34901	Hs.238532	ESTs	9.9
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.8
	449605	AW138581	Hs.198416	ESTs	9.8
	408081	AW451597	Hs.167409	ESTs	9.8
70	452526	W38537	Hs.280740	hypothetical protein MGC3040	9.8
	411305	BE241596	Hs.69547	myelin basic protein	9.8
	443455	AB001025	Hs.9349	ryanodine receptor 3	9.8
	427540	R12014	Hs.20976	ESTs	9.7
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	9.7
75	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	9.6
	452461	N78223	Hs.108106	transcription factor	9.6
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	9.6
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	439199	R40373	Hs.26299	ESTs	9.5
80	433896	AW294729	Hs.274461	ESTs	9.3
	416072	AL110370	Hs.79000	growth associated protein 43	9.3
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	9.2
	435624	AF218942	Hs.24889	formin 2	9.2
	412788	AA120960	Hs.198416	ESTs	9.2

	409902	AI337658	Hs.156351	ESTs	9.2
	427304	AA761526	Hs.163853	ESTs	9.2
	429918	AW873986	Hs.119383	ESTs	9.1
5	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypothe	9.1
	425187	AW014486	Hs.22509	ESTs	9.1
	436954	AA740151	Hs.130425	ESTs	9.1
	442710	AI015631	Hs.23210	ESTs	9.1
	411078	AI222020	Hs.182364	CocoaCrisp	9.1
10	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.0
	437036	AI571514	Hs.133022	ESTs	9.0
	448672	AI955511	Hs.225106	ESTs	9.0
	451952	AL120173	Hs.301663	ESTs	9.0
	448743	AB032962	Hs.21896	KIAA1136 protein	8.9
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	8.9
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.9
	419088	AI538323	Hs.52620	integrin, beta 8	8.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	8.8
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	8.8
20	449571	AW016812	Hs.200266	ESTs	8.8
	425354	U62027	Hs.155935	complement component 3a receptor 1	8.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	8.7
	410276	AI554545	Hs.68301	angiopoietin-2	8.7
	435501	AW051819	Hs.129908	KIAA0591 protein	8.7
25	407728	AW071502	Hs.175931	ESTs	8.6
	415293	R49462	Hs.106541	ESTs	8.6
	416857	AA188775	Hs.292453	ESTs	8.6
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	8.6
	450375	AA009647		a disintegrin and metalloproteinase doma	8.5
30	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.5
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	8.4
	421659	NM_014459	Hs.106511	protocadherin 17	8.4
	418097	R45137	Hs.21868	ESTs	8.4
	429183	AB014604	Hs.197955	KIAA0704 protein	8.3
35	424945	AI221919		hypothetical protein FLJ110582	8.2
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	8.2
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	8.2
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	8.1
40	431721	AB032996	Hs.268044	KIAA1170 protein	8.1
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	8.1
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	8.1
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.1
	436039	AW023323	Hs.121070	ESTs	8.1
45	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	8.0
	427463	AA442224	Hs.97900	ESTs	8.0
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	8.0
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.9
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	7.8
50	419929	U90268	Hs.93810	cerebral cavernous malformations 1	7.7
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	7.7
	448555	AI536697	Hs.159863	ESTs	7.7
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	7.7
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.7
55	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	7.7
	420362	U79734	Hs.97206	huntinglin interacting protein 1	7.6
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	7.5
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	7.5
	436140	W87355	Hs.269587	ESTs	7.4
60	449340	AW235786	Hs.195359	hypothetical protein MGC10954	7.4
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	7.4
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	7.4
	410434	AF051152	Hs.63668	tol-like receptor 2	7.4
	454048	H05626	Hs.6921	ESTs	7.4
65	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	7.4
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypothe	7.4
	438330	AW450572	Hs.257316	ESTs	7.4
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	7.3
70	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	7.3
	402855			NM_001839: Homo sapiens calponin 3, acid	7.2
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.2
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	7.2
	433447	U29195	Hs.3281	neuronal pentraxin II	7.2
75	412709	AL022327	Hs.74518	KIAA0027 protein	7.2
	445745	AB007924	Hs.13245	KIAA0455 gene product	7.2
	447101	N72185	Hs.44189	ESTs	7.2
	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	7.1
	409248	AB033035	Hs.51965	KIAA1209 protein	7.1
80	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	7.1
	424998	U58515	Hs.154138	chitinase 3-like 2	7.1
	436607	AW661783	Hs.211061	ESTs	7.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.1
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.1

	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.1
	421633	AF121860	Hs.106260	sorting nexin 10	7.0
	428976	AL037824	Hs.194695	ras homolog gene family, member I	7.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	7.0
5	408096	BE250162	Hs.83765	dihydrofolate reductase	7.0
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	6.9
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	6.9
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.9
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	6.9
10	415279	F04237	Hs.1447	glial fibrillary acidic protein	6.9
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	6.9
	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 (H	6.9
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	6.9
	447499	AW262580	Hs.147674	protocadherin beta 16	6.8
15	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	6.8
	441255	R06350	Hs.171635	ESTs	6.8
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	6.8
	439566	AF086387		gb:Homo sapiens full length insert cDNA	6.8
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	6.8
20	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	6.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.8
	458332	AI000341	Hs.220491	ESTs	6.8
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.7
25	413627	BE182082	Hs.246973	ESTs	6.7
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	6.7
	418677	S83308	Hs.87224	SRV (sex determining region Y)-box 5	6.7
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.7
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	6.7
	421141	AW117261	Hs.125914	ESTs	6.6
30	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	6.6
	432154	AI701523	Hs.112577	ESTs	6.6
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypothei	6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6
35	407182	AA312551	Hs.230157	ESTs	6.6
	445034	AW293376	Hs.143659	ESTs	6.6
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	6.6
	441102	AA973905		intermediate filament protein syncollin	6.6
	452834	AI638627	Hs.105685	KIAA1688 protein	6.6
40	429239	AA448419	Hs.45209	ESTs	6.6
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.5
	449300	AI656959	Hs.346514	ESTs	6.5
	446727	AB011095	Hs.16032	KIAA0523 protein	6.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.5
45	420560	AW207748	Hs.59115	ESTs	6.5
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	6.5
	441390	AI692560	Hs.131175	ESTs	6.5
	407168	R45175	Hs.117183	ESTs	6.4
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	6.4
50	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.4
	433597	AA708205	Hs.100343	ESTs	6.4
	414528	AA148950	Hs.188836	ESTs	6.4
	414214	D49958	Hs.75819	glycoprotein M6A	6.4
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	6.4
55	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	6.4
	440152	AB002376	Hs.7006	KIAA0378 protein	6.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.3
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	6.3
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp7111912 (f	6.3
60	452799	AI948829	Hs.213786	ESTs	6.3
	425523	AB007948	Hs.158244	KIAA0479 protein	6.3
	444395	T65213	Hs.4257	ESTs	6.3
	422094	AF129535	Hs.272027	F-box only protein 5	6.3
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
65	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	6.3
	447350	AI375572	Hs.172634	ESTs	6.2
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.2
	436936	AL134451	Hs.197478	ESTs	6.2
	448243	AW369771	Hs.52620	integrin, beta 8	6.2
70	414727	BE466904	Hs.190162	gb:h228f03.x1 NC1_CGAP_GC6 Homo sapiens	6.2
	420608	BE548277	Hs.103104	ESTs	6.2
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	6.1
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	6.1
75	423361	AW170055	Hs.47628	ESTs	6.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	6.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	6.1
	415651	AI207162	Hs.3815	slathmin-like-protein RB3	6.0
	418030	BE207573	Hs.83321	neuromedin B	6.0
80	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.0
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	416439	AA180363	Hs.118769	ESTs	6.0
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	6.0

	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	6.0
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	6.0
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.0
5	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	432328	AJ572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	5.9
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	5.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	5.9
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	5.9
10	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	5.9
	457465	AW301344	Hs.122908	DNA replication factor	5.9
	453362	H14988	Hs.107375	ESTs	5.9
	453924	R49295	Hs.24886	ESTs	5.9
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.9
15	433701	AW445023	Hs.15155	ESTs	5.8
	412777	AI335773	Hs.270123	ESTs	5.8
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.8
	438054	AA776626	Hs.169309	ESTs	5.8
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	5.8
20	400292	AA250737	Hs.72472	BMP-R1B	5.8
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	5.8
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	5.8
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.8
	411252	AB018549	Hs.69328	MD-2 protein	5.8
25	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.8
	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypothe	5.7
	419704	AA429104	Hs.45057	ESTs	5.7
	420077	AW512260	Hs.87767	ESTs	5.7
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.7
30	436511	AA721252	Hs.291502	ESTs	5.7
	424560	AA158727	Hs.150555	protein predicted by clone 23733	5.7
	423346	AI267677	Hs.127416	synaptotagmin 1	5.7
	439249	AF086060	Hs.170053	G-protein coupled receptor 88	5.7
	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.7
35	450927	AI807804	Hs.134342	TASP for testis-specific adriamycin sens	5.7
	451752	AB032997	Hs.26966	KIAA1171 protein	5.7
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.6
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	5.6
	448275	BE514434	Hs.20830	kinesin-like 2	5.6
40	413492	D87470	Hs.75400	KIAA0280 protein	5.6
	444600	R41398	Hs.6996	ESTs	5.6
	421988	AW450481	Hs.161333	ESTs	5.6
	443297	AI049864	Hs.133029	ESTs	5.6
	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
45	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.5
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.5
	447458	AI741082	Hs.158961	ESTs	5.5
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.5
	407886	AW969688	Hs.100826	ESTs	5.5
50	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.5
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.5
	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.5
	410099	AA081630		KIAA0036 gene product	5.5
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	5.5
55	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.5
	420345	AW295230	Hs.25231	ESTs	5.5
	420092	AA814043	Hs.88045	ESTs	5.5
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	5.5
	429876	AB028977	Hs.225974	KIAA1054 protein	5.4
60	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	5.4
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypothe	5.4
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	5.4
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	5.4
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	5.4
65	439662	H97552	Hs.269060	ESTs	5.4
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.4
	439192	AW970536	Hs.105413	ESTs	5.4
	448769	N66037	Hs.38173	ESTs	5.3
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.3
70	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.3
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	5.3
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	5.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 lis, clone L	5.3
	422544	AB018259	Hs.118140	KIAA0716 gene product	5.3
75	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.2
	441797	AI936933	Hs.214635	ESTs	5.2
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	5.2
	418079	R40058	Hs.6911	ESTs	5.2
80	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	5.2
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 lis, clone PL	5.2
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.2
	433647	AA603367	Hs.222294	ESTs	5.2
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothe	5.1

	436443	AW138211	Hs.128746	ESTs	5.1
	408243	Y00787	Hs.624	interleukin 8	5.1
	404819			NM_002688:Homo sapiens peanut (Drosophi	5.1
5	424914	AA348410	Hs.119065	ESTs	5.1
	453331	AI240665		ESTs	5.1
	444656	AI277924	Hs.145199	ESTs	5.1
	437387	AI198874	Hs.28847	ADO26 protein	5.1
	421027	AA761198	Hs.55254	ESTs	5.1
10	410631	AA086469	Hs.47171	ESTs	5.1
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	5.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	5.1
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	5.1
	421040	AA715026	Hs.135280	ESTs	5.1
15	415170	R44386	Hs.164578	ESTs	5.1
	412590	AL134388	Hs.135033	ESTs, Weakly similar to I38022 hypotheti	5.1
	448985	AA324885	Hs.22777	carbonic anhydrase XI	5.0
	433929	AI375499	Hs.27379	ESTs	5.0
	409638	AW450420	Hs.21335	ESTs	5.0
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	5.0
	400533			ENSP00000209376:PRED65 protein (Fragmen	5.0
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.0
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.0
	414737	AI160386	Hs.125087	ESTs	5.0
25	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo sapiens cDNA	5.0
	428878	AA436884	Hs.48926	ESTs	5.0
	428841	AI418430	Hs.104935	ESTs	5.0
	428110	AI312485	Hs.138294	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	444170	AW613879	Hs.102408	ESTs	4.9
30	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.9
	452106	AI141031	Hs.21342	ESTs	4.9
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
	414300	AI304870	Hs.188680	ESTs	4.9
	429399	AA452244	Hs.16727	ESTs	4.9
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	4.9
	428873	AI701609	Hs.98908	ESTs	4.9
	451516	AI800515	Hs.12024	ESTs	4.9
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.9
	416836	D54745	Hs.80247	cholecystokinin	4.9
40	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.9
	436805	AA731533	Hs.270751	ESTs	4.9
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.9
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	4.9
	422263	AA307639	Hs.129908	KIAA0591 protein	4.8
45	443715	AI583187	Hs.9700	cyclin E1	4.8
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.8
	434811	AW971205	Hs.114280	ESTs	4.8
	441287	AW293132	Hs.131373	ESTs	4.8
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	4.8
50	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypothesi	4.8
	443740	R56434	Hs.21062	ESTs	4.8
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.8
	441916	AA993571	Hs.129075	ESTs	4.8
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	4.8
55	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.8
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.8
	448425	AI500359	Hs.346112	ESTs	4.8
	423600	AI633559	Hs.310359	ESTs	4.8
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.8
60	423869	BE409301	Hs.134012	C1q-related factor	4.8
	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	4.7
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.7
	407808	AA663559	Hs.279789	histone deacetylase 3	4.7
	428748	AW593206	Hs.98785	Ksp37 protein	4.7
65	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.7
	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	4.7
	409100	H98216	Hs.42245	ESTs, Moderately similar to I38022 hypot	4.7
	420133	AA426117	Hs.155543	ESTs	4.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.7
70	443462	AI064690	Hs.171176	ESTs	4.7
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	4.7
	431454	AW975980	Hs.292918	ESTs	4.7
	432682	AI376400	Hs.159588	ESTs	4.7
	434933	R91095	Hs.4276	KIAA1701 protein	4.7
75	421247	BE391727	Hs.102910	general transcription factor IIH, polype	4.7
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	4.7
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	4.7
	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.7
80	412256	N59006	Hs.26133	ESTs	4.7
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	4.6
	422564	AI148006	Hs.222120	ESTs	4.6
	427250	R35941	Hs.25418	ESTs	4.6
	427695	R88483	Hs.172862	ESTs	4.6
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	4.6

	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	4.6
	427687	AW003867	Hs.1570	histamine receptor H1	4.6
	427194	AA399018	Hs.250835	ESTs	4.6
5	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	4.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.6
	458760	AI498631	Hs.111334	ferritin, light polypeptide	4.6
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.6
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.6
10	427712	AI368024	Hs.283696	ESTs	4.6
	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.6
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (I	4.6
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.6
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.6
15	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	4.6
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	4.6
	428409	AW117207	Hs.98523	ESTs	4.5
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	4.5
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.5
20	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.5
	422411	AW749443	Hs.22511	ESTs	4.5
	443361	AI792628	Hs.133273	ESTs	4.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.5
	408432	AW195262		gb:zn67b05.x1 NCI_CGAP_CML1 Homo sapiens	4.5
25	444127	N63620	Hs.13281	ESTs	4.5
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	4.5
	422661	NM_014700	Hs.119004	KIAA0665 gene product	4.5
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	4.5
	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypothe	4.5
30	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.5
	441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	4.5
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.5
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	4.5
	426503	AA380153		gb:EST93093 Skin tumor i Homo sapiens cD	4.5
35	418771	AA807881	Hs.25329	ESTs	4.4
	414706	AW340125	Hs.76989	KIAA0097 gene product	4.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	4.4
	441217	AI922183	Hs.213246	ESTs	4.4
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	4.4
40	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.4
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.4
	435342	AA687376		ESTs	4.4
	443912	R37257	Hs.184780	ESTs	4.4
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	4.4
45	432527	AW975028	Hs.102754	ESTs	4.4
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	4.4
	446936	H10207	Hs.47314	ESTs	4.4
	425212	AW962253	Hs.171618	ESTs	4.4
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.4
50	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.4
	439274	AF086092	Hs.48372	ESTs	4.4
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	4.4
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (4.4
	405348			C7001664:g 12698061 dbj BAB21849.1 (AB	4.4
55	419412	AW161058	Hs.90297	synuclein, beta	4.3
	447397	BE247676	Hs.18442	E-1 enzyme	4.3
	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.3
	433323	AA805132	Hs.159142	ESTs	4.3
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.3
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.3
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.3
	433610	AA806822	Hs.112547	ESTs	4.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	4.3
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	4.3
65	430979	AI479755	Hs.129010	ESTs	4.3
	452092	BE245374	Hs.27842	hypothetical-protein FLJ11210	4.3
	438456	AA913381	Hs.20594	ESTs	4.3
	433236	NM_004296	Hs.3221	regulator of G-protein signalling 6	4.3
	445133	AW157646	Hs.198689	ESTs	4.3
70	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.2
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.2
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.2
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	4.2
	424489	T48851	Hs.274470	D-siglec precursor,	4.2
75	453682	T79703		ghyd71e08.r1 Soares fetal liver spleen	4.2
	445568	H00918	Hs.268744	KIAA1796 protein	4.2
	448526	AB028946	Hs.21361	KIAA1023 protein	4.2
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	4.2
	415796	R87548	Hs.78854	ATPase, Na ⁺ transporting, beta 2 polypep	4.2
80	438875	AA827640	Hs.189059	ESTs	4.2
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	4.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.2
	445921	AW015211	Hs.146181	ESTs	4.2
	412190	R16180	Hs.274461	ESTs	4.2

	445666	R59960	Hs.282386	ESTs	4.2
	439538	AA837323	Hs.56407	ESTs	4.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.2
5	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	4.2
	409091	AW970386	Hs.269423	ESTs	4.2
	459527	AW977556	Hs.291735	ESTs, Weakly similar to 178885 serine/th	4.2
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	4.2
	432731	R31178	Hs.287820	fibronectin 1	4.2
	423135	N67655	Hs.26411	ESTs	4.2
10	446131	NM_000929	Hs.290	phospholipase A2, group V	4.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.2
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	4.2
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.2
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.2
15	429421	AL031658		Human DNA sequence from clone RP1-310013	4.2
	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	402145			Target Exon	4.1
	440483	AI200836	Hs.150386	ESTs	4.1
	425018	BE245277	Hs.154196	E4F transcription factor 1	4.1
20	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	4.1
	445868	BE169357	Hs.207428	ESTs	4.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.1
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	4.1
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.1
25	450325	AI935962	Hs.26289	ESTs	4.1
	450639	AI703186	Hs.277174	ESTs	4.1
	445102	AW204610	Hs.22270	ESTs	4.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
30	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.1
	439519	AA837118	Hs.118366	ESTs	4.1
	442326	H92962	Hs.124813	hypothetical protein MGC14817	4.1
	404150			Target Exon	4.1
35	420805	L10333	Hs.99947	reticulin 1	4.1
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	4.1
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.1
	444534	AW271626	Hs.42294	ESTs	4.1
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	4.1
40	418512	AW498974		diacylglycerol kinase, zeta (104kD)	4.1
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.1
	449328	AI962493	Hs.345303	ESTs	4.1
	432683	AW995441	Hs.10475	ESTs	4.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.1
45	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	4.1
	453096	AW294631	Hs.11325	ESTs	4.1
	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.0
	433523	H29882		ESTs	4.0
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.0
50	424120	T80579	Hs.290270	ESTs	4.0
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.0
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	4.0
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	4.0
	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	4.0
55	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	4.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.0
	450581	AF081513	Hs.25195	TGF-beta 4	4.0
60	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	424001	W67883	Hs.137476	paternally expressed 10	4.0
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	423713	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.0
65	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	439108	AW163034	Hs.6467	synaptogyrin 3	4.0
	440866	AI703103	Hs.271360	hypothetical protein MGC16275	4.0
	422887	AI751848	Hs.49215	ESTs	4.0
	405331			NM_024560:Homo sapiens hypothetical prot	4.0
70	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	4.0
	437948	AA772920	Hs.303527	ESTs	4.0
	440471	AA886146	Hs.307944	ESTs	4.0
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	4.0
	449655	AI021987	Hs.59970	ESTs	4.0
75	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	4.0
	435743	T66861	Hs.12962	ESTs	4.0
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	4.0
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN H8STO	3.9
	437807	AI017875	Hs.136829	ESTs	3.9
80	440085	BE270761	Hs.23158	ESTs	3.9
	449722	BE280074	Hs.23960	cyclin B1	3.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	3.9
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	3.9
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.9

	447519	U46258	Hs.339665	ESTs	
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	3.9
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.9
5	404584			Target Exon	3.9
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.9
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.9
	433290	R20977	Hs.302185	Homo sapiens clone 23618 mRNA sequence	3.9
	441707	R42637	Hs.21963	hypothetical protein DKFZp76180514	3.9
10	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	3.9
	434149	Z43829	Hs.244624	hypothetical protein MGC5469	3.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.9
	411555	AF113537	Hs.70669	HMP19 protein	3.9
	426646	AA382787	Hs.122713	ESTs	3.9
15	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.9
	429228	AI553633	Hs.326447	ESTs	3.9
	451433	AA021140	Hs.269265	ESTs, Weakly similar to A46010 X-linked	3.9
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	3.9
20	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.9
	417632	R20855	Hs.5422	glycoprotein M6B	3.9
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.9
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.9
	453438	AI469935	Hs.22792	ESTs	3.9
25	408449	NM_004408	Hs.166161	dynamitin 1	3.9
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.8
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.8
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.8
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.8
30	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	3.8
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.8
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	3.8
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	3.8
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.8
35	417791	AW965339	Hs.111471	ESTs	3.8
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	3.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	3.8
	449145	AI632122	Hs.198408	ESTs	3.8
40	446997	AA383439	Hs.16758	Spir-1 protein	3.8
	407304	AA565832	Hs.271649	gbln[32b03.s1 NCL_CGAP_AA1 Homo sapiens	3.8
	437269	AA334384	Hs.149420	ESTs	3.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	3.8
	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
45	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypothesi	3.8
	432488	AA551010	Hs.216640	ESTs	3.8
	450582	AI339732		G-rich RNA sequence binding factor 1	3.8
50	426380	AI291267	Hs.149990	ESTs	3.8
	451407	AA131376	Hs.343809	fibroblast growth factor 12B	3.8
	451778	AI826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	3.8
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.8
	412820	BE001236		gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3.8
	412193	AI684467	Hs.144057	ESTs	3.8
55	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	3.8
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.8
	437756	AA767537	Hs.197096	ESTs	3.8
	451367	AA923729	Hs.26322	cell cycle related kinase	3.8
60	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	3.8
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	3.8
	425843	BE313280	Hs.159627	death associated protein 3	3.8
	443301	AI733614	Hs.220587	ESTs, Moderately similar to ALU5_HUMAN A	3.8
	440210	AW674562	Hs.125296	ESTs	3.7
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.7
65	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	3.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
70	403696			C4001100*:gij5852342[gb]AADS4015.1)(AF0	3.7
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	3.7
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	3.7
	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	3.7
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	3.7
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.7
75	440553	AA689416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	3.7
	428536	AI143139	Hs.2288	visinin-like 1	3.7
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.7
	409172	Z99399	Hs.122593	ESTs	3.7
80	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	3.7
	418216	AA662240	Hs.283099	AF15q14 protein	3.7
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.7
	437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKFZp762G113 (fr	3.7
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	3.7
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.7

	436961	AW375974	Hs.156704	ESTs	3.7
	409953	AA332277	Hs.57691	cadherin 18, type 2	3.7
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	3.7
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	3.6
5	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.6
	440168	AA868507	Hs.126141	ESTs	3.6
	427624	AA406245	Hs.24895	ESTs	3.6
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.6
10	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.6
	458912	AI911066		ESTs	3.6
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	3.6
	449256	AA059050	Hs.59847	ESTs	3.6
	425010	T16837	Hs.4241	ESTs	3.6
15	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.6
	400777			NM_007325: Homo sapiens glutamate recept	3.6
	438831	BE263273	Hs.6439	synapsin II	3.6
	419235	AW470411	Hs.288433	neurotrimin	3.6
	424947	R77952		ESTs, Weakly similar to alternatively sp	3.6
20	407624	AW157431	Hs.248941	ESTs	3.6
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.6
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	3.6
	439267	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	3.6
	424340	AA339036	Hs.7033	ESTs	3.6
25	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	453875	AW001783	Hs.232711	ESTs	3.6
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.6
30	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	3.6
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3.6
	434131	AI858275	Hs.143659	ESTs	3.6
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	3.6
	415709	AA649850	Hs.278558	ESTs	3.6
35	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypothe	3.6
	419586	AI088485	Hs.144759	ESTs, Weakly similar to I38022 hypothe	3.6
	414040	N58513	Hs.32171	ESTs	3.6
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.6
	410711	AB002316	Hs.65746	KIAA0318 protein	3.6
40	445953	AI612775	Hs.145710	ESTs	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	3.6
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	3.6
	415283	R40504	Hs.21245	ESTs	3.6
45	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.5
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.5
	430818	AI311928	Hs.348156	gb:q089h04.x1 NCI_CGAP_Kd5 Homo sapiens	3.5
	433932	AW954599	Hs.169330	neuronal protein	3.5
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	3.5
50	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	3.5
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	3.5
	451455	AI937227	Hs.8821	hepcidin antimicrobial peptide	3.5
	412719	AW016610	Hs.816	ESTs	3.5
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.5
55	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	3.5
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.5
	439710	AF086543		gb:Homo sapiens full length insert cDNA	3.5
	453896	AW293483	Hs.255205	KIAA1853 protein	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
60	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	3.5
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.5
	424332	AA338919	Hs.101615	ESTs	3.5
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
65	404295			Target Exon	3.5
	427209	H06509	Hs.92423	KIAA1566 protein	3.5
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.5
	427513	AI476318	Hs.192480	ESTs	3.5
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypothe	3.5
70	435545	AA687415	Hs.28107	ESTs	3.5
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.5
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	3.5
	452449	AW068658	Hs.20943	ESTs	3.5
	443257	AI334040	Hs.11614	HSPC065 protein	3.5
75	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	3.5
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.5
	424090	X99699	Hs.139262	XIAP associated factor-1	3.5
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	3.5
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	3.5
80	439920	H05430	Hs.288433	neurotrimin	3.5
	436899	AA764852	Hs.291567	ESTs	3.5
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.5
	418365	AW014345	Hs.161690	ESTs	3.4
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.4

	452571	W31518	Hs.34665	ESTs	
	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.4
	408955	BE315170	Hs.8087	Target CAT	3.4
5	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.4
	419617	AL008583	Hs.91622	neuronal pentraxin receptor	3.4
	454171	AW854832		gb:OV2-CT0261-201099-011-005 CT0261 Homo	3.4
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	3.4
	440652	AI216751	Hs.143977	ESTs	3.4
10	450813	AI739625	Hs.203376	ESTs	3.4
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.4
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	3.4
	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	3.4
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.4
15	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.4
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	453305	R39224	Hs.267997	EHM2 gene	3.4
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	3.4
20	417663	R07483	Hs.180461	ESTs	3.4
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.4
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.4
	457876	AI821940		ESTs, Moderately similar to ALU8_HUMAN A	3.4
	407842	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.4
25	422676	D28481	Hs.1570	histamine receptor H1	3.4
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.4
	430762	AI343652	Hs.105667	ESTs	3.4
	430890	X54232	Hs.2699	glypican 1	3.4
	445078	AI869975	Hs.4775	junctophilin 3	3.4
30	423257	AW161039	Hs.125878	synapsin III	3.4
	417402	BE503227	Hs.134759	ESTs	3.4
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	3.4
	404541			NM_030795:Homo sapiens slathmin-like 4 (3.4
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	3.4
35	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.4
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.4
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.4
	420692	AW976345		gb:EST388454 MAGE resequences, MAGN Homo	3.4
40	410507	AA355288	Hs.76064	transitional epithelia response protein	3.4
	412436	AA665089		gb:nu76d01.s1 NCL_CGAP_Alh1 Homo sapiens	3.4
	448112	AW245919	Hs.34969	hypothetical protein DKFZp566N034	3.4
	429269	AA449013	Hs.99203	ESTs	3.4
	408037	AW271720	Hs.42233	hypothetical protein FLJ10300	3.4
45	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	420050	AL118615	Hs.94653	neurochondrin	3.3
	436277	R88520	Hs.120917	ESTs	3.3
	430412	AW341754	Hs.189305	ESTs	3.3
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.3
50	432663	AI984317	Hs.122589	ESTs	3.3
	449919	AI674685	Hs.200141	ESTs	3.3
	438509	R45367	Hs.101191	ESTs	3.3
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.3
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	3.3
55	425537	AB007913	Hs.158291	KIAA0444 protein	3.3
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	3.3
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	3.3
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.3
	410592	R94088	Hs.43569	ESTs	3.3
60	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothesi	3.3
	435375	AI733610	Hs.187832	ESTs	3.3
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	3.3
	425588	F07396	Hs.46627	ESTs	3.3
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	3.3
65	425242	D13635	Hs.155287	KIAA0010 gene product	3.3
	417280	AW173116	Hs.250103	ESTs	3.3
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.3
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor I	3.3
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	3.3
70	435718	R06569	Hs.269534	ESTs	3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fls, clone HE	3.3
	409557	BE182896	Hs.211193	ESTs	3.3
	439285	AL133916		hypothetical protein FLJ20093	3.3
75	421183	AL135740	Hs.102447	TSC-22-like	3.3
	433894	AI907682	Hs.243293	ESTs	3.3
	445225	AI216555	Hs.202398	ESTs	3.3
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	3.3
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
80	436870	AW204219	Hs.155560	catenin	3.3
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.3
	408547	AA574291	Hs.57837	ESTs	3.3
	420982	AW576160	Hs.100729	KIAA0692 protein	3.3
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.3

	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.3
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.3
	423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.3
5	441243	AI767056	Hs.193002	ESTs	3.3
	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.3
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.3
	446416	AV658299	Hs.163959	ESTs	3.3
	437762	T78028	Hs.154679	synaptotagmin I	3.3
10	450336	AA046814	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone H	3.3
	433842	AI652156	Hs.26346	ESTs	3.3
	444124	R43097	Hs.6818	ESTs	3.3
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.3
	454792	AW820794	Hs.252406	hypothetical protein FLJ12296 similar to	3.3
15	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.3
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	3.2
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	3.2
	433325	AW206986	Hs.143905	ESTs	3.2
	449092	U91641	Hs.22985	alpha2,8-sialyltransferase	3.2
20	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	3.2
	424899	AL119387	Hs.119062	ESTs	3.2
	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.2
	410126	BE169274		KIAA0036 gene product	3.2
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.2
25	405303			Target Exon	3.2
	420871	AA702972	Hs.65300	ESTs	3.2
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.2
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.2
	442320	AI287817	Hs.129636	ESTs	3.2
30	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.2
	439764	T26535	Hs.22744	hypothetical protein MGC13105	3.2
	410425	BE278367	Hs.63510	KIAA0141 gene product	3.2
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.2
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.2
35	457358	AI479755	Hs.129010	ESTs	3.2
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3.2
	452372	AI885742	Hs.228474	ESTs	3.2
	459660	M79082		ESTs	3.2
	437085	AA743935	Hs.202329	ESTs	3.2
40	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.2
	440080	AW051597	Hs.143707	ESTs	3.2
	449714	AB033015	Hs.23941	KIAA1189 protein	3.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	3.2
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	3.2
45	449961	AW265634	Hs.133100	ESTs	3.2
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	3.2
	419855	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	3.2
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	3.2
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
50	424641	AB001106	Hs.151413	glia maturation factor, beta	3.2
	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	3.2
	447877	AI435184	Hs.164252	ESTs	3.2
	419683	AA248897	Hs.48784	ESTs	3.2
	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	3.2
55	422709	AA315331	Hs.153485	ESTs	3.2
	432809	AA565509	Hs.131703	ESTs	3.2
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.2
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	3.2
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.2
60	445413	AA151342	Hs.12677	CGI-147 protein	3.2
	438703	AI803373	Hs.31599	ESTs	3.1
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.1
	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
65	433434	AA588429		gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens	3.1
	427961	AW293165	Hs.143134	ESTs	3.1
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	420552	AK000492	Hs.98806	hypothetical protein	3.1
	456209	W60633	Hs.297792	ESTs	3.1
	418819	AA228776	Hs.191721	ESTs	3.1
70	438944	AA302517	Hs.92732	KIAA1444 protein	3.1
	439086	AF085947		gb:Homo sapiens full length insert cDNA	3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.1
	415257	F03016	Hs.27513	ESTs	3.1
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.1
75	432675	AI791855	Hs.105884	ESTs	3.1
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	3.1
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.1
	439039	AI656707	Hs.48713	ESTs	3.1
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	3.1
80	400850			Target Exon	3.1
	417636	R08916	Hs.191212	ESTs	3.1
	425790	AW136286	Hs.288446	ESTs	3.1
	415314	N88802	Hs.5422	glycoprotein M6B	3.1

	436456	AW292677	Hs.248122	G protein-coupled receptor 24	
	408601	U47928	Hs.86122	protein A	3.1
	420886	AA805453		ESTs, Weakly similar to T29012 hypothei	3.1
5	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.1
	445704	AA493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.1
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.1
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	3.1
	431553	X78075	Hs.2799	cartilage linking protein 1	3.1
10	405605			C2001342:gil127814[sp]P26434/NAH4_RAT SO	3.1
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	3.1
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	3.1
	412507	L36645	Hs.73964	EphA4	3.1
	413448	AL134467	Hs.25307	Homo sapiens clone 24812 mRNA sequence	3.1
15	444168	AW379879		gb:RC1-HT0256-081199-011-401 HT0256 Homo	3.1
	400090			Eos Control	3.1
	433642	BE466341	Hs.189746	ESTs, Weakly similar to I38022 hypothei	3.1
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.1
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	3.1
20	428896	AW291932	Hs.98936	ESTs	3.1
	449277	AA001064	Hs.43670	ESTs	3.1
	426509	M31166	Hs.2050	pentactin-related gene, rapidly induced b	3.1
	412216	AW901517		gb:RC5-NN1013-310300-021-C03 NN1013 Homo	3.1
	428845	AL157579	Hs.153610	KIAA0751 gene product	3.1
25	431512	BE270734	Hs.2795	lactate dehydrogenase A	3.1
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.1
	450661	AW952160	Hs.83849	ESTs	3.0
	448448	NM_014954	Hs.21239	KIAA0985 protein	3.0
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.0
30	419687	AI638859	Hs.227699	ESTs, Weakly similar to T203_HUMAN TRANS	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
	435060	AI422719	Hs.120873	ESTs, Weakly similar to fork head like p	3.0
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.0
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	3.0
35	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.0
	416737	AF154335	Hs.79691	UIM domain protein	3.0
	445314	AI689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.0
	425870	R13406	Hs.56782	ESTs	3.0
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.0
40	416404	AA180138	Hs.107924	ESTs	3.0
	413995	BE048146	Hs.75671	syntactin 1A (brain)	3.0
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	3.0
45	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.0
	406917	X65964		gb:H.sapiens nestin gene.	3.0
	425262	D87119	Hs.155418	GS3955 protein	3.0
	401558			ENSP00000220478*:SECRETGRANIN III.	3.0
50	439345	AW444759	Hs.146171	ESTs	3.0
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	3.0
	453976	BE463830	Hs.163714	ESTs	3.0
	404283			ENSP00000244751*:Copine-like protein KIA	3.0
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	3.0
55	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	3.0
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
	443753	AW367578	Hs.134749	ESTs	3.0
	417868	AI078534	Hs.122592	ESTs	3.0
60	443898	AW804296	Hs.9950	Sec61 gamma	3.0
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.0
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.0
	447714	AW296313	Hs.255537	ESTs	3.0
	426581	AB040956	Hs.135890	KIAA1523 protein	3.0
65	421126	M74587	Hs.102122	insulin-like growth factor binding prote	3.0
	410762	AF226053	Hs.66170	HSKM-B protein	3.0
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	3.0
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.0
70	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	3.0
	426501	AW043782	Hs.293616	ESTs	3.0
	405558			Target Exon	3.0
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	3.0
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	3.0
75	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.0
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.0
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	3.0
	429371	NM_001703	Hs.200586	brain-specific angiogenesis inhibitor 2	3.0
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	3.0
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.0
80	404632			NM_022490:Homo sapiens hypothetical prot	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.0
	419038	AW134924	Hs.190325	ESTs	3.0
	453563	AW508906	Hs.181163	hypothetical protein MGC5629	3.0

405239 U89281 oxidative 3 alpha hydroxysteroid dehydro

3.0

TABLE 17B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408432	1058667_1	AW195262 R27868 AW811262
410099	117647_1	AA081630 T08671 A1174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 A1439658 AA283724 A1805992 A1457096 AA084618 BE467736 A1092635 A1887863 A1697593 AA436618 A1167419 A1418634 T31586 AA436630 AA706191 A1041169 A1422304 T03534 AA211402 A1204899 A1366472 AW827081 AA788593 T32736 A1767935 AA167791 AA747914 AA663870 A1865504
410126	117761_1	BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880
412216	1283670_1	AW901517 AW901523 AW901521 AW901547
412436	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
412799	132817_1	A1267606 AA121045 AA126521
412820	1330039_1	BE001236 BE001177 BE001180 BE001234
414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
416871	1626761_1	H98716 N90792 N24283
418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649
419544	185760_2	A1909154 AA526337 AA244193 A1909153
420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
420692	195649_1	AW976345 AA279423 AA761070
420886	197344_1	AA805453 AA281379
422156	212379_1	N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 A1334966 W32951 H62656 H53902 R88904 AW835732
422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H23379 R19493 AW134660 A1299437 AL133995 AA057405 N78357 AA917450 A1002692 T09262 T65008 H29290 A1200874 AA894415 A1732887 A1791768 A1733447 AA988785 N62128 T09261 AW956936
423713	231290_1	AW754182 AW754198 AA329983
424945	245223_1	A1221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A1341345 AW298800 AA724961 AA931158 A1741227 A1806660 A1982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 A1492961 A1361526 F04002 AA452141 T23551 A1472655 A193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665
424947	245247_1	R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973
426413	266650_1	AA377823 AW954494 A1022688
426503	268283_1	AA380153 AA380233 AW963529
426919	273507_1	AL041228 D82004 D61361 A1203314 A1990307 AW900295 A1018308 AW087473 AW183530 AA393346 H50055 AA935601
428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340
429007	298301_1	D80642 AA443145 AL119015 AW904500
429163	300543_1	AA884766 AW974271 AA592975 AA447312
429421	30431_1	AL031658 A1693758 AL040619 AW977914 AA811957 A1352198 AW104364 AA648367 AA897604 AW341668 A1201382 AL040620
430183	31412_2	BE010038 AA676833 A1311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039909
430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029
430968	326269_1	AW972830 AA527647 AA489820 AA570362
433009	357371_1	AA761668 AA573621 R92814 R09670
433434	366095_1	AA588429 A1972567 AW504832 A1299694
433523	368873_1	H29882 AW665533 A1149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
435542	407744_1	AA687376 H74234 AW975503
438869	46651_1	AF075009 R63109 R63068
439086	46852_1	AF085947 H70981 H78989
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 A1346341 A1867454 N54784 A1655270 A1421279 AW014882 AA775552 N62351 N59253 AA626243 A1341407 BE175639 AA456968 A1358918 AA457077
439518	47334_1	W76326 AF086341 W72300
439566	47387_1	AF086387 W77884 W72711
439710	47550_1	AF086543 W96291 W96225
441102	509604_1	AA973905 A129888 AA917019 H63235 T90771
444168	593829_1	AW379879 A1126285 H12014
446692	689623_1	Z44514 A1352097 A1803984 AW235923 A196558 A1954637 A1336983
447197	711623_1	R36075 A1366546 R36167
449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45526 T61415 AA331486
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067
450582	83933_1	A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
451320	86576_1	AW118072 A1631982 T15734 AA224195 A1701458 W20198 F26326 AA890570 N90552 AW071907 A1671352 A1375892 T03517 R88265 A1124088 AA224388 A1084316 A1354686 T33652 A1140719 A1720211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 A1222556 T33511 T33785 A1419606 D55612
453331	96214_1	A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 A1360919 H03502 BE208298 R68588 A1350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
453682	977454_1	T79703 T96307 AL079725
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
457728	393853_1	AW974811 AA651634 AA650072
457876	42814_2	A1821940 N67106 A1744264 AA808846 AA643417 AA643416 Z70715
458912	823104_1	A1911066 A1933734 A1680888 A1003599

TABLE 17C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400533	6981826	Minus	277132-277595
400777	8131663	Plus	70745-71121
400850	1927150	Minus	4506-4691
401558	7139678	Plus	103510-104090
402145	8018280	Plus	113086-114800
402604	9909420	Plus	20393-20767
402855	9662953	Minus	59763-59909
403696	3135242	Minus	143467-143634
403790	8084957	Minus	87826-87947,89835-90002
404150	7534008	Plus	165811-165943
404283	2276311	Minus	99460-99564
404295	9856663	Minus	75747-75947
404541	8318559	Plus	103456-103664
404584	9857511	Plus	138651-139153
404632	9796668	Plus	45096-45229
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
405303	2078453	Minus	130607-130802
405331	3236226	Minus	32502-32690
405348	2914717	Minus	43310-43462
405558	1621110	Plus	4502-4644,5983-6083
405605	5836195	Minus	117070-117270
405819	4007557	Plus	2830-2967

TABLE 18A: ABOUT 446 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS

Table 18A lists about 446 CNS-enriched genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
R1:	Ratio of CNS to GLIOBLASTOMA MULTIFORMA				
R2:	Ratio of CNS to NON-CNS NORMAL ADULT TISSUES				
Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
425489	M58594	Hs.1905	prolactin	38.8	10.5
410330	AW023630	Hs.159425	ESTs	23.4	23.4
430538	AB032435	Hs.242821	differentiation-associated Na-dependent	22.6	22.6
417275	X63578	Hs.295449	parvalbumin	22.4	6.0
453590	AF150278	Hs.33578	KIAA0820 protein	22.3	22.3
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8	21.8
453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	19.9	19.9
411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	19.4	19.4
408040	A1266496	Hs.22905	ESTs, Weakly similar to RHG6_HUMAN RHO-G	19.4	19.4
435145	A1277259	Hs.116631	ESTs	18.5	3.8
407039	X00368		gb:Human prolactin gene 5' region.	18.1	18.1
409263	AA069573	Hs.50319	ESTs	16.8	16.8
449078	AK001256	Hs.22975	KIAA1576 protein	16.1	16.1
426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	15.3	15.3
432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	15.1	15.1
424645	NM_014682	Hs.151449	KIAA0535 gene product	15.1	15.1
450590	A1701507	Hs.273740	ESTs	14.9	3.8
417175	R44558	Hs.94002	ESTs	14.6	8.9
423449	A1497900	Hs.33067	ESTs	14.5	14.5
441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	14.4	14.9
405560	AW887701		hypothetical protein FLJ20628	14.0	8.0
440209	H05049	Hs.247837	neurexin 3	13.9	18.7
439238	N47305	Hs.302161	ESTs	13.9	5.3
452022	AW072330	Hs.293875	ESTs	13.8	13.8
459080	AW192083	Hs.290855	ESTs	13.5	13.5
425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	13.4	38.6
413324	V00571	Hs.75294	corticotropin releasing hormone	13.2	13.2
443992	AW022228	Hs.322922	ESTs	13.1	13.1
410635	D58863	Hs.334372	chorionic somatomammotropin hormone 1 (p	12.9	6.6
420156	AW449258	Hs.6187	ESTs	12.5	12.5
416490	AF090116	Hs.79348	regulator of G-protein signalling 7	12.5	12.5
450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	12.2	3.2
410037	AB020725	Hs.58009	KIAA0918 protein	12.2	12.2
433940	H05129		cyclic AMP-regulated phosphoprotein, 21	12.0	12.0
434367	AB020700	Hs.3830	KIAA0893 protein	11.6	5.6
410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	11.5	11.5

	431988	AC002302	Hs.77202	protein kinase C, beta 1	11.2	10.5
	451783	R42554	Hs.210862	T-box, brain, 1	11.2	11.2
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	10.7	10.7
	452238	F01811	Hs.345757	ESTs	10.6	3.8
5	417167	AW206437	Hs.4290	ESTs	10.4	10.4
	420033	D59502	Hs.292590	ESTs	10.4	10.4
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	10.4	3.9
	424153	AA451737	Hs.141496	MAGE-like 2	10.3	5.1
10	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	10.0	10.0
	400438	AF185611	Hs.115352	Target	9.9	5.1
	447750	AI422234	Hs.143434	contactin 1	9.8	9.8
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	9.8	22.2
	418207	C14685	Hs.34772	ESTs	9.8	9.8
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	9.4	9.4
15	447746	AW015920	Hs.161359	ESTs	9.2	9.9
	406311			NM_021979: Homo sapiens heat shock 70kD	9.1	11.5
	444330	AI597655	Hs.49265	ESTs	9.1	9.1
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	9.0	4.1
20	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	8.9	8.9
	439450	R51613	Hs.125304	ESTs	8.7	8.3
	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	8.6	8.6
25	410309	BE043077	Hs.278153	ESTs	8.5	8.5
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	8.5	8.5
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	8.5	14.2
	416851	AW963951	Hs.85618	ESTs	8.5	8.5
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	8.4	15.7
30	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	8.4	27.9
	427061	AB032971	Hs.173392	KIAA1145 protein	8.4	8.4
	412049	N53437	Hs.18268	adenylate kinase 5	8.3	10.7
	452752	AW044058	Hs.33578	KIAA0820 protein	8.2	13.4
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	8.2	4.5
35	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.1	5.8
	435648	H24347	Hs.27524	ESTs	8.1	8.1
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	8.0	8.0
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
	438208	AL041224	Hs.65379	ESTs	7.9	5.8
	436427	AI344378	Hs.143399	ESTs	7.8	7.8
40	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7	7.7
	442023	AI187878	Hs.144549	ESTs	7.7	5.6
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	7.7	7.7
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
45	450642	R39773	Hs.7130	copine IV	7.6	5.6
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapie	7.5	12.4
	438283	AI458931	Hs.37282	ESTs	7.5	7.5
	437073	AI885608	Hs.94122	ESTs	7.5	7.5
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	7.4	7.4
50	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.3	7.3
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
	450474	AW872844	Hs.117494	ESTs	7.2	7.2
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	7.2	6.1
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.2	7.2
55	450181	H05254	Hs.201198	ESTs	7.2	7.2
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	419318	AW969742	Hs.291005	ESTs	7.1	3.1
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	7.0	7.0
	434460	AA478486	Hs.3852	KIAA0368 protein	7.0	4.8
60	433921	AA618174		gb:nq14f01.s1 NCL_CGAP_Thy1 Homo sapiens	7.0	7.0
	418940	H17739	Hs.288513	Human DNA sequence from clone RPS-899C14	7.0	7.0
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	7.0	8.0
	457012	R41480	Hs.302754	ESTs	6.9	6.9
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.9	14.0
65	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	6.9	10.2
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
	409031	AA376836	Hs.288856	ESTs	6.8	6.8
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	6.8	3.6
70	436568	H12049	Hs.91564	ESTs	6.8	6.8
	442593	R39804	Hs.31961	ESTs	6.7	6.7
	437948	AA772920	Hs.303527	ESTs	6.7	24.8
	412266	N59006	Hs.26133	ESTs	6.6	30.9
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	6.6	45.2
75	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	6.5	6.5
	429946	R49390	Hs.254129	KIAA1678	6.4	4.5
	445279	R41900	Hs.22245	ESTs	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
	407868	NM_000950	Hs.40637	proline-rich Glu (G-carboxyglutamic acid	6.4	3.3
80	434104	AF116691	Hs.116459	hypothetical protein PRO2198	6.4	4.0
	443244	AI457235	Hs.166479	ESTs	6.3	3.0
	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	6.2	6.2
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.2	43.2
	428536	AI143139	Hs.2288	visinin-like 1	6.0	22.1

	415114	D60468	Hs.94181	ESTs	6.0	6.0
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.9	6.0
5	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
	414545	AA149287	Hs.76605	ESTs	5.8	5.8
	418202	N48521	Hs.26549	KIAA1708 protein	5.8	5.8
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.7	9.6
	444124	R43097	Hs.6818	ESTs	5.7	9.3
10	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	5.6	5.6
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.6	9.6
	425523	AB007948	Hs.158244	KIAA0479 protein	5.6	35.0
	459697	AA408062	Hs.98002	ESTs	5.6	5.4
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	5.6
15	420111	AA255652		gbzs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.5	3.2
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	5.3	5.3
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
20	425580	L11144	Hs.1907	gatanin	5.3	3.5
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.3	3.8
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3	4.9
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.2	5.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	5.2	3.0
25	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
	410240	AL157424	Hs.61289	synaptotagmin 2	5.2	4.6
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	5.2	7.7
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	5.2	33.0
	428508	BE252383	Hs.184668	SBB131 protein	5.2	4.1
30	446353	AJ290919	Hs.153661	ESTs	5.1	5.1
	423135	N67655	Hs.26411	ESTs	5.1	8.2
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	5.1	5.1
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	5.1	5.1
35	411379	A816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	5.0	11.2
	408068	AW148652	Hs.167398	ESTs	5.0	5.0
	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.0	27.4
	439607	BE540565	Hs.159460	ESTs	5.0	5.6
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	4.9	29.3
40	414631	AW970130	Hs.65405	ESTs	4.9	4.9
	437117	AL049256	Hs.122593	ESTs	4.9	3.8
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	4.9	4.9
45	443150	AI034467	Hs.34650	ESTs	4.9	7.6
	422411	AW749443	Hs.22511	ESTs	4.9	12.0
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	4.9	3.4
	430456	AA314998	Hs.241503	hypothetical protein	4.8	4.7
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.8	3.9
50	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
	427287	NM_014903	Hs.174188	KIAA0938 protein	4.8	4.8
	416101	R24854	Hs.268806	ESTs	4.8	3.3
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
55	458268	AA428403	Hs.106131	ESTs	4.7	3.9
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.7	8.2
	445102	AW204610	Hs.22270	ESTs	4.7	19.2
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7
	414949	C15314	Hs.323349	ESTs	4.7	3.8
	453534	NM_014796	Hs.33187	KIAA0748 gene product	4.7	4.7
60	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	4.7	4.0
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	4.7	4.9
	434792	AA649253	Hs.132458	ESTs	4.7	3.8
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.7	3.0
65	430537	X62692	Hs.2593	phosphodiesterase 6B, cGMP-specific, rod	4.6	4.6
	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	429876	AB028977	Hs.225974	KIAA1054 protein	4.6	16.8
	451516	AI800515	Hs.12024	ESTs	4.6	6.3
	433670	AA604405		gb:nc087h09.s1 NCI_CGAP_AA1 Homo sapiens	4.6	3.9
70	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.5	3.8
	410366	AJ267589	Hs.302689	hypothetical protein	4.5	10.4
	419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	4.5	3.3
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	4.5	10.2
75	432736	AA788898	Hs.179902	transporter-like protein	4.4	4.0
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	4.4	3.2
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	4.3	3.3
	435040	AI932350	Hs.152825	ESTs	4.3	4.7
	451301	AI769514	Hs.209890	EST	4.3	4.3
80	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	4.3	7.8
	433109	N58907	Hs.162430	EST	4.3	3.9
	431342	AW971018	Hs.21659	ESTs	4.3	8.0
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	4.3	3.4

	422414	AW875237	Hs.13701	ESTs	4.2	5.3
	439274	AF086092	Hs.48372	ESTs	4.2	18.3
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
	429956	A1374651	Hs.22542	ESTs	4.2	3.2
5	427317	AB028955	Hs.175780	KIAA1032 protein	4.2	5.3
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	4.1	7.9
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
	433803	A1823593	Hs.27688	ESTs	4.1	4.1
10	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	4.1	4.0
	448117	H49129	Hs.172982	ESTs	4.1	4.1
	450600	BE079478	Hs.24880	ESTs	4.1	3.9
	429550	AW293055	Hs.119357	ESTs	4.1	6.4
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	4.0	7.2
	458694	F12832	Hs.3610	ESTs	4.0	4.0
15	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.0	7.9
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	4.0	13.1
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
20	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	3.9	21.4
	442412	R77677	Hs.346644	ESTs	3.9	3.9
	424001	W67883	Hs.137476	paternally expressed 10	3.9	5.4
	440293	AJ004193	Hs.22123	ESTs	3.9	3.9
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.9	3.6
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
25	412949	AJ471639	Hs.71913	ESTs	3.8	3.7
	427457	AW779105	Hs.164682	ESTs	3.8	11.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.8	4.4
	442676	AJ733585	Hs.130897	ESTs	3.8	3.8
	434998	AW975157	Hs.26037	ESTs	3.7	3.7
30	424945	AJ221919		hypothetical protein FLJ10582	3.7	30.5
	415257	F03016	Hs.27513	ESTs	3.7	8.6
	407886	AW969688	Hs.100826	ESTs	3.7	20.2
	400844			NM_003105*:Homo sapiens sortilin-related	3.7	3.1
	456765	AJ497900	Hs.33067	ESTs	3.7	3.7
35	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.6	7.6
	452667	T87219	Hs.13219	ESTs	3.6	3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	424120	T80579	Hs.290270	ESTs	3.6	14.7
	446574	AJ310135	Hs.335933	ESTs	3.6	3.5
40	432453	AJ885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	3.6	3.9
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	3.6
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
	439239	AJ031540	Hs.235331	ESTs	3.6	49.5
45	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.6	4.1
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	3.6	4.8
	423346	AJ267677	Hs.127416	synaptotagmin 1	3.6	20.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	442106	AW205881	Hs.326728	ESTs	3.5	3.2
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
50	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.5	13.5
	452311	AW304029	Hs.252744	ESTs	3.5	3.5
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	3.5	21.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4	3.4
	400098			Eos Control	3.4	3.4
55	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.4	5.9
	437268	AJ754847	Hs.227571	regulator of G-protein signaling 4	3.4	14.0
	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.4	3.3
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	3.3	17.1
60	419629	AB020695	Hs.91662	KIAA0888 protein	3.3	13.4
	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	3.3	4.1
	417063	N50515	Hs.45061	ESTs	3.3	3.3
	435071	D60683	Hs.35495	ESTs	3.3	3.3
	446377	AW014022	Hs.170953	ESTs	3.3	3.3
	412453	R20205	Hs.75236	ESTs	3.3	3.3
65	450561	R49674	Hs.25909	ESTs	3.3	3.3
	423829	R44107	Hs.240905	ESTs	3.3	4.4
	415527	F11624		gb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
70	425121	AJ797511	Hs.154679	synaptotagmin I	3.2	3.9
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	3.2	10.7
	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.2	3.2
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	3.2	3.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.2	6.7
75	429477	AJ275514	Hs.6658	ESTs	3.2	3.2
	453169	AB037815	Hs.32156	KIAA1394 protein	3.2	5.7
	408039	AA131424	Hs.336636	ESTs	3.2	3.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.2	22.1
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	3.2	10.6
	416874	H98752	Hs.42558	ESTs	3.2	6.0
80	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
	444861	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2	3.2
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.2	3.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	3.2	8.4

	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein		
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	3.2	56.0
	432809	AA565509	Hs.131703	ESTs	3.2	4.1
	445225	AI216555	Hs.202398	ESTs	3.1	9.9
5	424087	N69333	Hs.143434	contactin 1	3.1	5.5
	437924	AI935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODIU	3.1	3.1
	419683	AA248897	Hs.48784	ESTs	3.1	3.2
	420173	AA256151	Hs.22999	ESTs	3.1	5.9
10	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.1	6.6
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	3.1	4.5
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.1	4.2
	445194	AI215667	Hs.175044	ESTs	3.1	3.1
15	438054	AA776626	Hs.169309	ESTs	3.1	3.1
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.1	10.2
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.1	12.2
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.0	3.0
	447673	AI823987	Hs.182285	ESTs	3.0	11.7
20	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	3.0	3.0
	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	3.0	42.3
	429024	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	3.0	3.9
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	3.0	3.7
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fs, clone H	3.0	9.0
25	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0	3.0
	408947	AL080093	Hs.49117	Homo sapiens mRNA: cDNA DKFZp564N1662 (f	3.0	10.0
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	3.0	13.5
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.9	81.1
	410711	AB002316	Hs.65746	KIAA0318 protein	2.9	6.6
30	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	2.9	6.1
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.9	15.7
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.9	3.6
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	2.9	11.5
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.9	3.6
35	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.9	5.1
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	2.9	3.2
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.9	6.1
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.9	5.9
40	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	2.8	28.5
	416836	D54745	Hs.80247	cholecystokinin	2.8	23.1
	449277	AA001064	Hs.43670	ESTs	2.8	6.8
	451952	AL120173	Hs.301663	ESTs	2.8	8.5
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	19.2
45	413408	R51793	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.7	3.7
	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	2.7	3.0
	420489	AA815089	Hs.193513	ESTs	2.7	3.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	2.7	4.1
	423731	T08814		gb:EST06706 Infant Brain, Bento Soares H	2.7	17.2
50	409953	AA332277	Hs.57691	cadherin 18, type 2	2.7	4.0
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.7	5.5
	449714	AB033015	Hs.23941	KIAA1189 protein	2.7	11.5
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.7	7.5
	432447	X92681	Hs.2998	contactin 2 (axonal)	2.7	3.7
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.7	4.1
55	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fs, clone L	2.7	5.1
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.6	5.1
	447761	AF061573	Hs.19492	protocadherin 8	2.6	7.9
	448743	AB032962	Hs.21896	KIAA1136 protein	2.6	6.3
	408547	AA574291	Hs.57837	ESTs	2.6	23.2
60	426380	AI291267	Hs.149990	ESTs	2.6	4.0
	420898	AB002379	Hs.100113	KIAA0381 protein	2.6	6.9
	440357	AA379353	Hs.20950	phosphotyrosine phosphohistidine inorganic	2.6	3.7
	424572	M19650		2',3'-cyclic nucleotide 3' phosphodiester	2.6	3.7
65	418338	NM_002522	Hs.84154	neuronal pentraxin I	2.6	5.9
	427658	H61387	Hs.30868	nogo receptor	2.5	6.1
	410359	R38624	Hs.106313	ESTs	2.5	3.0
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.5	6.3
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.5	4.5
70	450133	AW969769	Hs.105201	ESTs	2.5	10.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.5	40.5
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	2.5	17.4
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fs, clone PL	2.5	9.5
	414883	S78296	Hs.76888	hypothetical protein MGC12702	2.5	3.9
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.5	7.1
75	449568	AI157479	Hs.23740	KIAA1598 protein	2.5	3.0
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 feni	2.5	3.6
	428495	NM_013279	Hs.184640	hypothetical protein MGC10781	2.5	3.6
	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clones TN62 and	2.5	3.2
	452371	R40990	Hs.21658	ESTs	2.4	3.6
80	424997	AL138167	Hs.96920	ESTs	2.4	3.3
	450310	N62341	Hs.94116	ESTs	2.4	6.2
	452898	AA814497	Hs.78792	ESTs	2.4	3.6
	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	2.4	3.9
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	2.4	4.7
					2.4	3.1

5	439428	AA835825	Hs.190490	ESTs	2.4	3.0
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.4	8.1
	436420	AA443966	Hs.31595	ESTs	2.4	3.7
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.4	3.0
	451407	AA131376	Hs.343809	fibroblast growth factor 12B	2.4	7.2
	419757	AA773820	Hs.63970	ESTs	2.4	3.3
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	2.4	3.6
	439199	R40373	Hs.26299	ESTs	2.3	9.5
10	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.3	5.6
	454048	H05626	Hs.6921	ESTs	2.3	9.9
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.3	3.3
	434811	AW971205	Hs.114280	ESTs	2.3	6.7
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	2.3	3.1
15	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.3	3.1
	447028	AI973128	Hs.167257	brain link protein-1	2.3	5.6
	451050	AW937420	Hs.69662	ESTs	2.3	4.4
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	2.3	4.8
	408838	AI669535	Hs.40369	ESTs	2.3	3.0
20	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	2.3	3.8
	453924	R49295	Hs.24886	ESTs	2.3	13.4
	422709	AA315331	Hs.153485	ESTs	2.3	4.4
	438911	AF085841	Hs.301920	ESTs	2.3	3.3
25	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	6.9
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2	4.1
	404819			NM_002688*:Homo sapiens peanut (Drosophi	2.2	5.8
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.2	11.8
	433597	AA708205	Hs.100343	ESTs	2.2	11.0
	440152	AB002376	Hs.7006	KIAA0378 protein	2.2	14.2
30	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2.2	82.9
	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	2.2	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.2	6.0
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	2.2	5.0
	438703	AI803373	Hs.31599	ESTs	2.2	6.2
35	428845	AL157579	Hs.153610	KIAA0751 gene product	2.2	6.7
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.2	3.5
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.2	3.2
	419271	N34901	Hs.238532	ESTs	2.2	7.5
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	2.2	7.3
40	439415	F05538	Hs.4273	ESTs	2.2	31.3
	415170	R44386	Hs.164578	ESTs	2.2	10.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2
	443728	AI083876	Hs.148383	ESTs	2.1	4.1
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	2.1	5.7
45	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	2.1	7.1
	418900	BE207357	Hs.3454	KIAA1821 protein	2.1	4.3
	421268	AI126821	Hs.30514	ESTs	2.1	4.2
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	15.6
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	2.1	6.5
50	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.1	3.3
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	3.5
	447877	AI435184	Hs.164252	ESTs	2.1	5.1
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	2.1	8.3
55	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.1	4.2
	410631	AA086469	Hs.47171	ESTs	2.1	5.8
	407808	AA663559	Hs.279789	histone deacetylase 3	2.1	5.7
	424379	Z42034	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.1	3.2
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	2.1	3.0
60	433932	AW954599	Hs.169330	neuronal protein	2.1	6.9
	425130	AA448208	Hs.99163	ESTs	2.1	3.1
	402027			Target Exon	2.0	3.5
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.0	7.5
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	2.0	10.7
	404541			NM_030795:Homo sapiens stathmin-like 4 (2.0	6.0
65	420050	AL118615	Hs.94653	neurochondrin	2.0	6.5
	417868	AI078534	Hs.122592	ESTs	2.0	5.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	2.0	3.2
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	2.0	4.2
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.0	6.3
70	429900	AA460421	Hs.30875	ESTs	2.0	4.2
	437762	T78028	Hs.154679	synaptotagmin 1	2.0	4.6
	425172	AA447729	Hs.12714	ESTs	2.0	3.1
	419587	S62907	Hs.91343	gamma-aminobutyric acid (GABA) A recepto	2.0	3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.0	4.9
75	423603	AB007880	Hs.129883	Homo sapiens KIAA0420 mRNA, complete cds	2.0	4.3
	438277	AL022326	Hs.6139	synaptogyrin 1	2.0	3.4
	423767	HI8283	Hs.132753	F-box only protein 2	2.0	3.2
	434933	R91095	Hs.4276	KIAA1701 protein	2.0	6.1
80	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.0	4.6

TABLE 18B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408065	103646_1	AW954272 AI003154 AA059300 AA046911
415527	1539393_1	F11624 Z43212 H08936 R56332 H09256 R52303 R13075
415666	1543492_1	H72693 R08673 H72694 F20990 R08580
418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074
418866	179788_1	AW890649
420111	190755_1	T65754 AA229857 AA229658
422890	222707_1	AA255652 AA280911 AW967920 AA262684
423731	231466_1	Z43784 R13382 AWS72911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918
424572	24097_1	AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW204071 AW956110 C15616 D81142 H17038 AW162343
424945	245223_1	T87230 AI3
426919	273507_1	T08814 H19198 AL120536 AA330218 AW961552 N47159
433670	372721_1	M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684
433921	377350_1	AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303
433940	37787_1	AW498662 AA019090 AA001
436773	426857_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227
446692	689623_1	AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655
		AI193667 AI341
		AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601
		AA604405 BE062234 AW748386
		AA518174 AI114549 R36464 R36465
		H05129 N63433 AI651350 AA984734 AI368716 N40915 AI989705 F09042 T03905 R88588 AF112220
		AW078629 AI857375 N64357 AA731069
		Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983

TABLE 18C:

Pkey:

Ref:

Strand:

NT_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
400844	9188605	Plus	24746-24872,25035-25204
402027	7622350	Plus	51645-51888,52917-53005
404541	8318559	Plus	103456-103664
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
405560	183148	Plus	5495-5655,6077-6241,6495-6692
405819	4007557	Plus	2830-2967
406311	9211559	Minus	137114-139033

TABLE 19A: ABOUT 356 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 19A lists about 356 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" non-CNS normal adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: Ratio of CNS to Glioblastoma
 R2: Ratio of CNS to NON-CNS NORMAL ADULT TISSUES

Pkey	ExAccn	UnigenelD	Unigenes Title	R1	R2
425489	M58594	Hs.1905	protactin	24.8	10.5
410330	AW023630	Hs.159425	ESTs	23.4	23.4
430538	AB032435	Hs.242821	differentiation-associated Na-dependent	22.6	22.6
417275	X63578	Hs.295449	parvalbumin	22.4	6.0
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8	21.8
408040	AI266496	Hs.22905	ESTs, Weakly similar to RHG6_HUMAN RHO-G	19.4	19.4
435145	AI277259	Hs.116631	ESTs	18.5	3.8
407039	X00368		gb:Human protactin gene 5' region.	18.1	18.1
409263	AA069573	Hs.50319	ESTs	16.8	16.8
432298	AL118812	Hs.274293	Homo sapiens mRNA: cDNA DKFZp761G1111 (f	15.1	15.1
424645	NM_014682	Hs.151449	KIAA0535 gene product	15.1	15.1
416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	14.0	14.0
405560	AW887701		hypothetical protein FLJ20628	13.9	8.0
452022	AW072330	Hs.293875	ESTs	13.8	13.8
413324	V00571	Hs.75294	corticotropin releasing hormone	13.2	13.2
411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	12.9	19.4
423449	AI497900	Hs.33067	ESTs	12.4	14.5
433940	H05129		cyclic AMP-regulated phosphoprotein, 21	12.0	12.0
410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	11.5	11.5
449078	AK001256	Hs.22975	KIAA1576 protein	11.0	16.1
410635	D58863	Hs.334372	chorionic somatomammotropin hormone 1 (p	11.0	6.6
453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	10.7	10.7
417167	AW206437	Hs.4290	ESTs	10.4	10.4
420033	D59502	Hs.292590	ESTs	10.4	10.4
413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	10.0	10.0

	418207	C14685	Hs.34772	ESTs	9.8	9.8
	417175	R44558	Hs.94002	ESTs	9.6	8.9
	444330	AI597655	Hs.49265	ESTs	9.1	9.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	8.9	8.9
5	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specific	8.6	22.2
	410309	BE043077	Hs.278153	ESTs	8.5	8.5
	416851	AW963951	Hs.85618	ESTs	8.5	8.5
10	427061	AB032971	Hs.173392	KIAA1145 protein	8.4	8.4
	400438	AF185611	Hs.115352	Target	8.3	5.1
	440209	H05049	Hs.247837	neurexin 3	8.2	18.7
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.1	5.8
	435648	H24347	Hs.27524	ESTs	8.1	8.1
15	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	8.0	8.0
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	7.9	8.6
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	7.9	15.7
	436427	AI344378	Hs.143399	ESTs	7.8	7.8
20	434367	AB020700	Hs.3830	KIAA0893 protein	7.8	5.6
	429876	AB028977	Hs.225974	KIAA1054 protein	7.8	16.8
	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7	7.7
	442023	AI187878	Hs.144549	ESTs	7.7	5.6
25	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
	450642	R39773	Hs.7130	copine IV	7.6	5.6
	437073	AI885608	Hs.94122	ESTs	7.5	7.5
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
	424153	AA451737	Hs.141496	MAGE-like 2	7.3	5.1
30	450474	AW872844	Hs.117494	ESTs	7.2	7.2
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.2	7.2
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	7.0	7.0
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0
35	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	6.9	6.1
	457012	R41480	Hs.302754	ESTs	6.9	6.9
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
	409031	AA376836	Hs.288856	ESTs	6.8	6.8
40	453590	AF150278	Hs.33578	KIAA0820 protein	6.6	22.3
	450181	H05254	Hs.201198	ESTs	6.6	7.2
	425580	L11144	Hs.1907	galanin	6.5	3.5
	445279	R41900	Hs.22245	ESTs	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
45	434104	AF116691	Hs.116459	hypothetical protein PRO2198	6.4	4.0
	443244	AI457235	Hs.166479	ESTs	6.3	3.0
	447750	AI422234	Hs.143434	contactin 1	6.2	9.8
	415114	D60468	Hs.94181	ESTs	6.0	6.0
	450600	BE079478	Hs.24880	ESTs	5.9	3.9
50	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	5.9	7.7
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
	414545	AA149287	Hs.76605	ESTs	5.8	3.6
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.6	9.6
55	450590	AI701507	Hs.273740	ESTs	5.6	3.8
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	5.6
	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	5.5	6.5
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	5.3	4.5
60	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.3	3.8
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.2	5.2
	406311			NM_021979*:Homo sapiens heat shock 70kD	5.2	11.5
65	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	5.2	3.3
	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
	416101	R24854	Hs.268806	ESTs	5.2	3.3
	428508	BE252383	Hs.184668	SBB131 protein	5.2	4.1
	419318	AW969742	Hs.291005	ESTs	5.2	3.1
70	439238	N47305	Hs.302161	ESTs	5.1	5.3
	446353	AI290919	Hs.153661	ESTs	5.1	5.1
	412049	N53437	Hs.18268	adenylate kinase 5	5.1	10.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	5.1	5.1
75	408068	AW148652	Hs.167398	ESTs	5.0	5.0
	414631	AW970130	Hs.65406	ESTs	4.9	4.9
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 5 (neurotransmitte	4.9	4.9
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.9	3.9
80	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
	427287	NM_014903	Hs.174188	KIAA0938 protein	4.8	4.8
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	4.7	10.2
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7

	414949	C15314	Hs.323349	ESTs	4.7	3.8
	453534	NM_014796	Hs.33187	KIAA0748 gene product	4.7	4.7
	430537	X82692	Hs.2593	phosphodiesterase 6B, cGMP-specific, rod	4.6	4.6
5	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.6	4.6
	418202	N48521	Hs.26549	KIAA1708 protein	4.6	3.0
	419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.6	5.8
10	459080	AW192083	Hs.290855	ESTs	4.5	4.5
	451783	R42554	Hs.210862	T-box, brain, 1	4.5	13.5
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	11.2
	451050	AW937420	Hs.69662	ESTs	4.4	3.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	4.4
	447746	AW015920	Hs.161359	ESTs	4.4	7.9
15	451301	A1769514	Hs.209890	EST	4.3	9.9
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	4.3
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.3	3.9
20	426365	AA376667	Hs.10283	RNA binding motif protein 8B	4.3	27.9
	423589	AA328082	Hs.209569	ESTs	4.3	4.1
	432453	A1885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	4.2	4.2
	420489	AA815089	Hs.193513	ESTs	4.2	3.9
	427457	AW779105	Hs.164682	ESTs	4.1	4.1
25	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	11.1
	433803	A1823593	Hs.27688	ESTs	4.1	4.1
	407868	NM_000950	Hs.40637	proline-rich Glu (G-carboxyglutamic acid	4.1	4.1
	448117	H49129	Hs.172982	ESTs	4.1	3.3
	442106	AW205881	Hs.326728	ESTs	4.1	4.1
30	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.1	3.2
	442042	A1990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	4.0	3.2
	458694	F12832	Hs.3610	ESTs	4.0	6.2
	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
35	418940	H17739	Hs.288513	Human DNA sequence from clone RPS-899C14	4.0	4.0
	442412	R77677	Hs.346644	ESTs	3.9	7.0
	440293	A1004193	Hs.22123	ESTs	3.9	3.9
	433670	AA604405		gb:nc87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.9	3.9
40	459697	AA406062	Hs.98002	ESTs	3.9	3.9
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.9	5.4
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.3
	424001	W67883	Hs.137476	paternally expressed 10	3.9	3.9
	442676	A1733585	Hs.130897	ESTs	3.8	5.4
	410240	AL157424	Hs.61289	synaptotagmin 2	3.8	3.8
45	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.8	4.6
	434998	AW975157	Hs.26037	ESTs	3.7	3.6
	439450	R51613	Hs.125304	ESTs	3.7	3.7
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.7	8.3
	400844			NM_003105: Homo sapiens sortilin-related	3.7	4.9
50	456765	A1497900	Hs.33067	ESTs	3.7	3.1
	452667	T87219	Hs.13219	ESTs	3.7	3.7
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.6	3.6
55	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.6	19.9
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	12.2
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.6	3.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.6	15.3
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.6	10.0
60	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.5	3.5
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	4.9
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	3.5	3.5
	412266	N59006	Hs.26133	ESTs	3.5	12.5
	452311	AW304029	Hs.252744	ESTs	3.5	30.9
65	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	3.5	3.5
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.5	38.6
	451516	A1800515	Hs.12024	ESTs	3.4	3.4
	400098			Eos Control	3.4	6.3
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	3.4	3.4
70	452238	F01811	Hs.345757	ESTs	3.4	5.3
	417063	N50515	Hs.45061	ESTs	3.3	3.8
	443992	AW022228	Hs.322922	ESTs	3.3	3.3
	412453	R20205	Hs.75236	ESTs	3.3	13.1
	450561	R49674	Hs.25909	ESTs	3.3	3.3
75	415527	F11624		gb:HSC22D101 normalized infant brain cDN	3.3	3.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
	423346	A1267677	Hs.127416	synaptotagmin 1	3.3	3.3
	431342	AW971018	Hs.21659	ESTs	3.2	20.1
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.2	8.0
80	442879	AF032922	Hs.8813	synaptotagmin binding protein 3	3.2	9.6
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	3.2	3.2
	429477	A1275514	Hs.6658	ESTs	3.2	3.2
	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	3.2	3.2
	427317	AB028955	Hs.175780	KIAA1032 protein	3.2	5.3

	408039	AA131424	Hs.336636	ESTs	3.2	3.2
	428976	AL037824	Hs.194695	ras homolog gene family, member I	3.2	17.4
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2	4.1
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	3.2	3.3
	423829	R44107	Hs.240905	ESTs	3.1	4.4
	424087	N69333	Hs.143434	contactin 1	3.1	3.1
	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	3.1	4.1
10	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.1	43.2
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.1	3.1
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	3.1	33.0
	437117	AL049256	Hs.122593	ESTs	3.1	3.8
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
15	452752	AW044058	Hs.33578	KIAA0820 protein	3.1	13.4
	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.1	4.5
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	3.0	3.8
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.0	5.9
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
20	447673	AI823987	Hs.182285	ESTs	3.0	3.0
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.0	3.0
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	3.0	3.0
	408547	AA574291	Hs.57837	ESTs	3.0	4.0
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.0	3.1
25	439274	AF086092	Hs.48372	ESTs	3.0	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	3.0	8.0
	458268	AA428403	Hs.106131	ESTs	3.0	3.9
	424641	AB001106	Hs.151413	glia maturation factor, beta	3.0	5.6
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.0	14.9
30	442593	R39804	Hs.31961	ESTs	2.9	6.7
	426380	AI291267	Hs.149990	ESTs	2.9	6.9
	428536	AI143139	Hs.2288	visinin-like 1	2.9	22.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	2.9	17.1
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.9	11.2
35	422414	AW875237	Hs.13701	ESTs	2.9	5.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.9	3.9
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	2.9	3.6
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.9	9.0
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	2.8	12.4
40	422411	AW749443	Hs.22511	ESTs	2.8	12.0
	416874	H98752	Hs.42568	ESTs	2.8	6.0
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	2.8	21.8
	430456	AA314998	Hs.241503	hypothetical protein	2.8	4.7
45	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor I	2.8	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.8	13.1
	437948	AA772920	Hs.303527	ESTs	2.8	24.8
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.8	8.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.8	3.4
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.8	4.4
50	446574	AI310135	Hs.335933	ESTs	2.8	3.5
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	2.8	3.6
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	2.7	45.2
55	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.7
	434460	AA478486	Hs.3852	KIAA0368 protein	2.7	4.8
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	10.5
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.7	3.4
	437924	AI935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODIU	2.6	3.2
	424945	AI221919		hypothetical protein FLJ10582	2.6	30.5
60	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	2.6	29.3
	447761	AF061573	Hs.19492	protocadherin 8	2.6	6.3
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	2.6	4.2
	436568	H12049	Hs.91564	ESTs	2.6	6.8
65	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	2.6	5.6
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.6	7.6
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	2.6	3.8
	420173	AA256151	Hs.22999	ESTs	2.6	4.1
	429550	AW293055	Hs.119357	ESTs	2.6	6.4
	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.6	5.1
70	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	2.6	7.3
	432809	AA565509	Hs.131703	ESTs	2.6	9.9
	407886	AW969688	Hs.100826	ESTs	2.5	20.2
	445225	AI216555	Hs.202398	ESTs	2.5	5.5
	415257	F03016	Hs.27513	ESTs	2.5	8.6
75	423135	N67655	Hs.26411	ESTs	2.5	8.2
	438283	AI458931	Hs.37282	ESTs	2.5	7.5
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.4	3.6
	443150	AI034467	Hs.34650	ESTs	2.4	7.6
	429956	AI374651	Hs.22542	ESTs	2.4	3.2
80	428392	HI0233	Hs.22665	secretory granule, neuroendocrine protei	2.4	42.3
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	2.4	14.0
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.4	5.1
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.4	3.2
	422949	AA319435		gb:EST121657 Adrenal gland tumor Homo sap	2.4	7.4

	451952	AL120173	Hs.301663	ESTs		
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.4	19.2
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.4	28.5
5	425121	A1797511	Hs.154679	synaptotagmin I	2.4	3.0
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	2.4	3.9
	446377	AW014022	Hs.170953	ESTs	2.4	4.8
	452371	R40990	Hs.21658	ESTs	2.4	3.3
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	2.4	3.3
10	427658	H61387	Hs.30868	nogo receptor	2.4	8.4
	446100	AW967109	Hs.13804	hypothetical protein DJ462023.2	2.4	3.0
	439607	BE540565	Hs.159460	ESTs	2.3	3.6
	412949	AJ471639	Hs.71913	ESTs	2.3	5.6
	419757	AA773820	Hs.63970	ESTs	2.3	3.7
15	410037	AB020725	Hs.58009	KIAA0918 protein	2.3	3.3
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	2.3	12.2
	409953	AA332277	Hs.57691	cadherin 18, type 2	2.3	3.1
	419629	AB020695	Hs.91662	KIAA0888 protein	2.3	5.5
	434792	AA649253	Hs.132458	ESTs	2.3	13.4
20	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.3	3.8
	445194	AJ215667	Hs.175044	ESTs	2.3	6.6
	422491	AA338548	Hs.117546	neuronatin	2.3	3.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	3.6
	434933	R91095	Hs.4276	KIAA1701 protein	2.3	27.4
25	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.2	6.1
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	2.2	3.7
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	2.2	81.1
	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	2.2	56.0
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	2.2	3.9
30	439239	AJ031540	Hs.235331	ESTs	2.2	10.6
	450310	N52341	Hs.94116	ESTs	2.2	49.5
	453924	R49295	Hs.24886	ESTs	2.2	3.6
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.2	13.4
	404819			NM_002688: Homo sapiens peanut (Drosophi	2.2	6.6
35	449568	AL157479	Hs.23740	KIAA1598 protein	2.2	5.8
	419271	N34901	Hs.238532	ESTs	2.2	3.6
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.2	7.5
	438208	AL041224	Hs.65379	ESTs	2.2	3.6
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.2	5.8
40	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	2.2	10.1
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.2	4.1
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (tr	2.1	4.2
	449277	AA001064	Hs.43670	ESTs	2.1	21.4
	420156	AW449258	Hs.6187	ESTs	2.1	8.5
45	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	12.5
	410366	AJ267589	Hs.302689	hypothetical protein	2.1	3.5
	452106	AJ141031	Hs.21342	ESTs	2.1	10.4
	413409	AJ638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.1	3.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	9.4
50	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	2.1	6.2
	410631	AA086469	Hs.47171	ESTs	2.1	12.5
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.1	5.8
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.1	3.3
	444124	R43097	Hs.6818	ESTs	2.1	11.5
55	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	9.3
	432736	AA788898	Hs.179902	transporter-like protein	2.1	8.5
	429024	AJ652297	Hs.119302	complement-c1q tumor necrosis factor-rel	2.1	4.0
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.1	3.7
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.1	5.1
60	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	2.1	3.0
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	2.1	23.1
	425130	AA448208	Hs.99163	ESTs	2.1	14.2
	449714	AB033015	Hs.23941	KIAA1189 protein	2.1	3.1
	439108	AW163034	Hs.6467	synaptogyrin 3	2.0	7.5
65	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.0	6.9
	435040	AJ932350	Hs.152825	ESTs	2.0	10.2
	440152	AB002376	Hs.7006	KIAA0378 protein	2.0	4.7
	445102	AW204610	Hs.22270	ESTs	2.0	14.2
	436734	AJ937612	Hs.273758	hypothetical protein FLJ23112	2.0	19.2
70	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	2.0	4.7
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.0	6.4
	453169	AB037815	Hs.32156	KIAA1394 protein	2.0	7.9
	420050	AL118615	Hs.94653	neurochondrin	2.0	5.7
	429900	AA460421	Hs.30875	ESTs	2.0	6.5
75	432447	X92681	Hs.2998	contactin 2 (axonat)	2.0	4.2
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	2.0	4.1
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor I	2.0	3.1
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.0	10.7
	453754	AW972580	Hs.172753	ESTs	2.0	7.2
80	422544	AB018259	Hs.118140	KIAA0716 gene product	2.0	3.4
	416836	D54745	Hs.80247	cholecystokinin	2.0	11.8
	454048	H05626	Hs.6921	ESTs	2.0	6.8
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	2.0	9.9
					2.0	6.5

TABLE 19B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	408065	103646_1	AW954272 AJ003154 AA059300 AA046911
	415527	1539393_1	F11624 Z43212 H08936 R56332 H09256 R52303 R13075
10	415666	1543492_1	H72693 R08673 H72694 F20990 R08580
	418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074
			AW890649
	418866	179788_1	T65754 AA229857 AA229658
	422890	222707_1	Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918
15			AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW204071 AW956110 C15616 D81142 H17038 AW162343
			T87230 AI3
	422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
	424945	245223_1	AI221919 Z19957 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AJ341345 AW298800 AA724961 AA931158 AI741227
			AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655
			AI193667 AI341
20	426919	273507_1	AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601
	433670	372721_1	AA604405 BE062234 AW748386
	433921	377350_1	AA618174 AI114549 R36464 R36465
	433940	37787_1	H05129 N63433 AI651350 AA984734 AI368716 N40915 AI989705 F09042 T03905 R88588 AF112220
	436773	426857_1	AW078629 AI857375 N64357 AA731069
25	446692	689623_1	Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983

TABLE 19C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

30	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24746-24872,25035-25204
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405560	183148	Plus	5495-5655,6077-6241,6495-6692
	405819	4007557	Plus	2830-2967
35	406311	9211559	Minus	137114-139033

TABLE 20A: ABOUT 328 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 20A lists about 328 CNS-enriched genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

50 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS compared to LOWER GRADE GLIOBLASTOMA
 R2: Ratio of CNS compared to NON-CNS NORMAL ADULT TISSUE

60	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	425580	L11144	Hs.1907	gatanin	33.1	3.5
	425489	MS8594	Hs.1905	prolactin	24.7	10.5
	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	22.6	22.6
	417275	X63578	Hs.295449	parvalbumin	22.4	6.0
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	21.8	21.8
	408040	AI266496	Hs.22905	ESTs, Weakly similar to RHG6_HUMAN RHO-G	19.4	19.4
65	435145	AI277259	Hs.116631	ESTs	18.5	3.8
	407039	X00368		gb:Human prolactin gene 5' region.	18.1	18.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	17.4	17.4
	409263	AA069573	Hs.50319	ESTs	16.8	16.8
	424645	NM_014682	Hs.151449	KIAA0535 gene product	15.1	15.1
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	14.0	14.0
70	405560	AW887701		hypothetical protein FLJ20628	13.9	8.0
	452022	AW072330	Hs.293875	ESTs	13.8	13.8
	433940	H05129		cyclic AMP-regulated phosphoprotein, 21	12.0	12.0
	413324	V00571	Hs.75294	corticotropin releasing hormone	12.0	13.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	11.5	11.5
75	410330	AW023630	Hs.159425	ESTs	11.1	23.4
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	10.7	10.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.5	4.1
	417167	AW206437	Hs.4290	ESTs	10.4	10.4
	420033	D59502	Hs.292590	ESTs	10.4	10.4
80	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	10.0	10.0
	426380	AI291267	Hs.149990	ESTs	9.8	6.9
	410635	D58863	Hs.334372	chorionic somatomammotropin hormone 1 (p	9.5	6.6
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	9.1	5.8

	444330	AI597655	Hs.49265	ESTs		
	427322	AK002017	Hs.176227	hypothetical protein FLJ111155	9.1	9.1
	421633	AF121860	Hs.106260	sorting nexin 10	8.9	8.9
	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	6.7
5	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	410309	BE043077	Hs.278153	ESTs	8.6	8.6
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	8.5	8.5
	417175	R44558	Hs.94002	ESTs	8.5	10.2
10	427061	AB032971	Hs.173392	KIAA1145 protein	8.4	8.9
	400438	AF185611	Hs.115352	Target	8.4	8.4
	418207	C14685	Hs.34772	ESTs	8.3	5.1
	440209	H05049	Hs.247837	neurexin 3	8.2	9.8
	429876	AB028977	Hs.225974	KIAA1054 protein	8.1	18.7
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	8.1	16.8
15	430004	U27768	Hs.227571	regulator of G-protein signalling 4	8.0	8.0
	436427	AI344378	Hs.143399	ESTs	7.9	15.7
	408814	N62499	Hs.176227	hypothetical protein FLJ111155	7.8	7.8
	434367	AB020700	Hs.3830	KIAA0893 protein	7.8	8.6
20	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7	5.6
	416851	AW963951	Hs.85618	ESTs	7.7	7.7
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.7	8.5
	437073	AI885608	Hs.94122	ESTs	7.6	5.5
	441264	AA927170	Hs.23290	ESTs	7.5	7.5
25	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.3	7.3
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.2	7.2
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	7.1	4.8
	423003	AL120077	Hs.122967	ketch (Drosophila)-like 2 (Mayven)	7.1	10.0
	433921	AA618174		gb:ng14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0
30	457012	R41480	Hs.302754	ESTs	7.0	7.0
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	6.9	6.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.1
	409031	AA376836	Hs.288856	ESTs	6.9	6.9
35	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.8	6.8
	445279	R41900	Hs.22245	ESTs	6.5	22.2
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
	434104	AF116691	Hs.116459	hypothetical protein PRO2198	6.4	6.4
40	443244	AI457235	Hs.166479	ESTs	6.4	4.0
	447761	AF061573	Hs.19492	protocadherin 8	6.3	3.0
	450600	BE079478	Hs.24880	ESTs	6.3	6.3
	427457	AW779105	Hs.164682	ESTs	6.2	3.9
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	6.2	11.1
45	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	6.1	8.0
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	6.0	3.9
	415114	D60468	Hs.94181	ESTs	6.0	15.1
	416101	R24854	Hs.268806	ESTs	6.0	6.0
	448958	AB020651	Hs.22653	KIAA0844 protein	5.9	3.3
50	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.9	5.9
	414545	AA149287	Hs.76605	ESTs	5.8	5.8
	424153	AA451737	Hs.141496	MAGE-like 2	5.8	3.6
	424641	AB001106	Hs.151413	glia maturation factor, beta	5.7	5.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIH1U86 salivary	5.6	5.6
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	5.6	9.6
55	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	12.2
	443912	R37257	Hs.184780	ESTs	5.6	5.6
	442023	AI187878	Hs.144549	ESTs	5.5	6.1
	450642	R39773	Hs.7130	copine IV	5.5	5.6
60	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.4	5.6
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	9.8
	438202	AW169287	Hs.22588	ESTs	5.4	5.4
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.3	5.3
65	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.3	3.8
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	5.2	5.2
	415666	H72693		gb:yu03c11.1.r1 Soares fetal liver spleen	5.2	3.3
	428508	BE252383	Hs.184668	S8B131 protein	5.2	5.2
	446353	AI290919	Hs.153661	ESTs	5.2	4.1
70	442106	AW205881	Hs.326728	ESTs	5.1	5.1
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	3.2
	419318	AW969742	Hs.291005	ESTs	5.1	5.1
	408068	AW148652	Hs.167398	ESTs	5.0	3.1
	434149	Z43829	Hs.244624	hypothetical protein MGC5469	5.0	5.0
75	439238	N47305	Hs.302161	ESTs	5.0	5.0
	414631	AW970130	Hs.65406	ESTs	4.9	5.3
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.9	4.9
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	3.0
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	4.9
80	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.9	4.9
	427287	NM_014903	Hs.174188	KIAA0938 protein	4.8	4.8
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	4.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.8	3.2
	414949	C15314	Hs.323349	ESTs	4.7	4.7
					4.7	3.8

	429900	AA460421	Hs.30875	ESTs	4.7	4.2
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	4.7	7.4
	430537	X62692	Hs.2593	phosphodiesterase 6B, cGMP-specific, rod	4.6	4.6
	419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5
5	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	406311			NM_021979: Homo sapiens heat shock 70kD	4.4	11.5
	451050	AW937420	Hs.69662	ESTs	4.4	4.4
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	7.9
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	4.3	19.4
10	451301	AI769514	Hs.209890	EST	4.3	4.3
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.2	3.9
15	420489	AA815089	Hs.193513	ESTs	4.1	4.1
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
	418202	N48521	Hs.26549	KIAA1708 protein	4.1	5.8
	448117	H49129	Hs.172982	ESTs	4.1	4.1
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.0	27.9
20	458694	F12832	Hs.3610	ESTs	4.0	4.0
	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	408547	AA574291	Hs.57837	ESTs	4.0	4.0
	433447	U29195	Hs.3281	neuronal pentraxin II	4.0	3.7
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
25	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	AI004193	Hs.22123	ESTs	3.9	3.9
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.9	4.1
	400844			NM_003105: Homo sapiens sortilin-related	3.9	3.1
30	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.8	3.3
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	3.8	3.8
	442676	AI733585	Hs.130897	ESTs	3.8	3.8
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.8	4.5
35	436476	AA326108	Hs.33829	bHLH protein DEC2	3.8	3.3
	434998	AW975157	Hs.26037	ESTs	3.7	3.7
	412049	N53437	Hs.18268	adenylate kinase 5	3.7	10.7
	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.7	4.5
	459697	AA406062	Hs.98002	ESTs	3.7	5.4
40	435648	H24347	Hs.27524	ESTs	3.7	8.1
	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	3.7	6.2
	456765	AI497900	Hs.33067	ESTs	3.7	3.7
	434933	R91095	Hs.4276	KIAA1701 protein	3.6	6.1
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.6	3.6
45	452667	T87219	Hs.13219	ESTs	3.6	3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	3.6
	453534	NM_014796	Hs.33187	KIAA0748 gene product	3.6	4.7
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
50	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	447746	AW015920	Hs.161359	ESTs	3.5	9.9
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
	447750	AI422234	Hs.143434	contactin 1	3.5	9.8
	453590	AF150278	Hs.33578	KIAA0820 protein	3.5	22.3
55	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.5	3.6
	410240	AL157424	Hs.61289	synaptotagmin 2	3.5	4.6
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4	3.4
	400098			Eos Control	3.4	3.4
	450181	H05254	Hs.201198	ESTs	3.4	7.2
60	459080	AW192083	Hs.290855	ESTs	3.4	13.5
	417063	N50515	Hs.45061	ESTs	3.3	3.3
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	3.3	5.3
	453431	AF094754	Hs.32973	glycine receptor, beta	3.3	4.6
	412453	R20205	Hs.75236	ESTs	3.3	3.3
65	450561	R49674	Hs.25909	ESTs	3.3	3.3
	415527	F11624		gb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.3	15.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
	424001	W67883	Hs.137476	paternally expressed 10	3.2	5.4
70	439450	R51613	Hs.125304	ESTs	3.2	8.3
	442879	AF032922	Hs.8813	syntactin binding protein 3	3.2	3.2
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fs, clone NT	3.2	3.2
	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	3.2	3.2
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	3.2	12.5
75	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
	424087	N69333	Hs.143434	contactin 1	3.1	3.1
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	3.1	3.3
	419852	AW503756	Hs.286184	hypothetical protein dJ55102.5	3.1	4.1
80	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.1	3.1
	423829	R44107	Hs.240905	ESTs	3.1	4.4
	443297	AI049864	Hs.133029	ESTs	3.1	3.1
	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	3.1	4.6
	405819			NM_002578: Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0

	447673	AI823987	Hs.182285	ESTs		
	433670	AA604405		gb.no87h09.s1 NCJ_CGAP_AA1 Homo sapiens	3.0	3.0
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.0	3.9
5	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fs, clone H	3.0	3.2
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.0	3.0
	451032	WQ3692	Hs.323079	Homo sapiens mRNA: cDNA DKFZp564P116 (fr	3.0	3.1
	423346	AI267677	Hs.127416	synaptojanin 1	3.0	4.9
	439274	AF086092	Hs.48372	ESTs	3.0	20.1
10	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	3.0	18.3
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	2.9	38.6
	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	2.9	14.9
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	2.9	3.3
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.9	8.0
15	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	2.8	5.9
	425130	AA448208	Hs.99163	ESTs	2.8	9.6
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8	3.1
	452238	F01811	Hs.345757	ESTs	2.8	3.7
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	2.8	3.8
20	433803	AI823593	Hs.27688	ESTs	2.8	12.4
	407728	AW071502	Hs.175931	ESTs	2.8	4.1
	414931	AK000342	Hs.77646	Homo sapiens mRNA: cDNA DKFZp761M0223 (f	2.7	10.2
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	3.4
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.7	6.1
25	451516	AI800515	Hs.12024	ESTs	2.7	3.5
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.7	6.3
	450474	AW872844	Hs.117494	ESTs	2.7	3.6
	422414	AW875237	Hs.13701	ESTs	2.7	7.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.7	5.3
30	431342	AW971018	Hs.21659	ESTs	2.7	3.9
	423449	AI497900	Hs.33067	ESTs	2.7	8.0
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	2.6	14.5
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.6	3.0
	437117	AL049256		ESTs	2.6	9.0
35	422491	AA338548	Hs.122593	neuronatin	2.6	3.8
	438068	AI927209	Hs.117546	Homo sapiens cDNA: FLJ23133 fs, clone L	2.6	3.6
	432809	AA565509	Hs.131703	ESTs	2.6	5.1
	433551	AI985544	Hs.12450	protocadherin 9	2.5	9.9
	444783	AK001468	Hs.62180	anilin (Drosophila Scraps homolog), act	2.5	18.1
40	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	2.5	43.2
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.5	17.1
	448902	Z45998	Hs.22543	Homo sapiens mRNA: cDNA DKFZp761I1912 (f	2.5	5.7
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	2.5	21.8
	423135	N67655	Hs.26411	ESTs	2.5	14.5
45	452311	AW304029	Hs.252744	ESTs	2.5	8.2
	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	2.5	3.5
	432882	NM_013257	Hs.279696	serum/lyticocorticoid regulated kinase-6	2.5	7.0
	422411	AW749443	Hs.22511	ESTs	2.5	4.2
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.5	12.0
50	404819			NM_002688: Homo sapiens peanut (Drosophi	2.4	3.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.4	5.8
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.4	13.1
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.4	10.5
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (CEBP),	2.4	11.2
55	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.4	45.2
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.4	5.1
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	2.4	7.6
	427658	H61387	Hs.30868	nogo receptor	2.4	3.6
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	2.4	3.0
60	412266	N59006	Hs.26133	ESTs	2.3	3.6
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	2.3	30.9
	420173	AA256151	Hs.22999	ESTs	2.3	4.8
	452371	R40990	Hs.21658	ESTs	2.3	4.1
	430456	AA314998	Hs.241503	hypothetical protein	2.3	3.3
65	409953	AA332277	Hs.57691	cadherin 18, type 2	2.3	4.7
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.3	5.5
	445194	AI215667	Hs.175044	ESTs	2.3	6.6
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	2.3	3.1
	434460	AA478486	Hs.3852	KIAA0368 protein	2.3	42.3
70	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	2.3	4.8
	437924	AI935344	Hs.164118	ESTs, Weakly similar to SLS1_HUMAN SODIU	2.3	12.5
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.3	3.2
	424945	AI221919		hypothetical protein FLJ10582	2.2	16.9
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	2.2	30.5
75	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.2	4.4
	438831	BE263273	Hs.6439	synapsin II	2.2	3.0
	449078	AK001256	Hs.22975	KIAA1576 protein	2.2	3.4
	410631	AA086469	Hs.47171	ESTs	2.2	16.1
	419271	N34901	Hs.238532	ESTs	2.2	5.8
80	452752	AW044058	Hs.33578	KIAA0820 protein	2.2	7.5
	446574	AI310135	Hs.339933	ESTs	2.2	13.4
	452106	AI141031	Hs.21342	ESTs	2.2	3.5
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	2.2	3.4
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	2.2	28.9
					2.2	7.7

5	446692	Z44514	Hs.198416	Homo sapiens mRNA for KIAA1763 protein,	2.2	33.0
	412788	AA120960	Hs.96423	ESTs	2.2	8.5
	419103	Z40229	Hs.148680	hypothetical protein FLJ23033	2.2	8.4
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.2	3.6
	451783	R42554	Hs.210862	T-box, brain, 1	2.1	11.2
	434792	AA649253	Hs.132458	ESTs	2.1	3.8
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.1	3.7
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	2.1	4.9
10	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	2.1	5.1
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	2.1	3.6
	443150	AI034467	Hs.34650	ESTs	2.1	7.6
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	2.1	19.9
	420050	AL118615	Hs.94653	neurochondrin	2.1	6.5
15	408449	NM_004408	Hs.166161	dynamitin 1	2.1	5.1
	423641	AI137256	Hs.130489	ATPase, aminophospholipid transporter-fi	2.1	6.2
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.1	3.2
	449568	AL157479	Hs.23740	KIAA1598 protein	2.1	3.6
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.1	3.3
20	429550	AW293055	Hs.119357	ESTs	2.1	6.4
	446782	AI653048	Hs.144006	ESTs	2.1	9.0
	453924	R49295	Hs.24886	ESTs	2.1	13.4
	437948	AA772920	Hs.303527	ESTs	2.1	24.8
	451952	AL120173	Hs.301663	ESTs	2.0	19.2
25	453754	AW972580	Hs.172753	ESTs	2.0	3.4
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	2.0	3.9
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.0	3.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.0	11.5
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.0	6.6
30	424458	M29273	Hs.1780	myelin associated glycoprotein	2.0	10.1
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.0	28.5
	440152	AB002376	Hs.7006	KIAA0378 protein	2.0	14.2
	429956	AI374651	Hs.22542	ESTs	2.0	3.2
	450590	AI701507	Hs.273740	ESTs	2.0	3.8
35	429024	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	2.0	3.7
	430643	AW970065	Hs.287425	MEGF10 protein	2.0	4.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.0	27.4
	419757	AA773820	Hs.63970	ESTs	2.0	3.3
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	2.0	23.8
40	439607	BE540565	Hs.159460	ESTs	2.0	5.6
	435624	AF218942	Hs.24889	formin 2	2.0	12.2
	425121	AI797511	Hs.154679	synaptotagmin I	2.0	3.9
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	2.0	3.1
	442593	R39804	Hs.31961	ESTs	2.0	6.7
45	410366	AI267589	Hs.302689	hypothetical protein	2.0	10.4
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.0	4.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor I	2.0	10.7
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	2.0	3.8
	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	2.0	3.8
50	436734	AI937612	Hs.273758	hypothetical protein FLJ23112	2.0	4.7
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.0	11.8
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	2.0	8.2
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	2.0	6.5
	450310	N62341	Hs.94116	ESTs	2.0	3.6
55	TABLE 20B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
60	Pkey	CAT Number	Accession			
	415527	1539393_1	F11624 Z43212 H08936 R56332 H09256 R52303 R13075			
	415666	1543492_1	H72693 R08673 H72694 F20990 R08580			
	418866	179788_1	T65754 AA229857 AA229658			
65	422890	222707_1	Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918			
			AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI857447 AW204071 AW956110 C15616 D81142 H17038 AW162343			
			T87230 AI3			
	422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424			
	424945	245223_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227			
70			AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655			
			AI193667 AI341			
	426919	273507_1	AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601			
	433670	372721_1	AA604405 BE052234 AW748386			
	433921	377350_1	AA518174 AI114549 R36464 R36465			
75	433940	37787_1	H05129 N63433 AI651350 AA984734 AI368716 N40915 AI989705 F09042 T03905 R88588 AF112220			
	436773	426857_1	AW078629 AI857375 N64357 AA731069			
	446692	689623_1	Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983			
80	TABLE 20C:					
	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA				
	Strand:	sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	NT_position:	Indicates DNA strand from which exons were predicted.				
		Indicates nucleotide positions of predicted exons.				

	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24746-24872,25035-25204
	404819	4578240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405560	183148	Plus	5495-5655,6077-6241,6495-6692
	405819	4007557	Plus	2830-2967
	406311	9211559	Minus	137114-139033

TABLE 21A: ABOUT 410 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS
 Table 21A lists about 410 genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS to GLIOBLASTOMA MULTIFORMA

	Pkey	ExAccn	UnigenID	Unigene Title	R1
	417275	X63578	Hs.295449	parvalbumin	18.6
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	13.8
	415672	N53097	Hs.193579	ESTs	13.5
	459080	AW192083	Hs.290855	ESTs	12.9
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	11.7
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	10.9
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
	424645	NM_014682	Hs.151449	KIAA0535 gene product	8.2
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	413324	V00571	Hs.75294	corticotropin releasing hormone	7.5
	417167	AW206437	Hs.4290	ESTs	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	6.8
	410330	AW023630	Hs.159425	ESTs	6.5
	450590	AI701507	Hs.273740	ESTs	6.5
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	6.5
	454076	AW204712	Hs.61957	ESTs	6.5
	419956	AL137939	Hs.40096	ESTs	6.3
	416851	AW963951	Hs.85618	ESTs	6.3
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	6.0
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	449078	AK001256	Hs.22975	KIAA1576 protein	5.6
	448072	AI459306	Hs.24908	ESTs	5.6
	412622	AW664708	Hs.171959	ESTs	5.6
	428414	AL049980	Hs.184216	DKFZP564C152 protein	5.5
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	5.4
	453344	BE349075	Hs.44571	ESTs	5.4
	441790	AW294909	Hs.132208	ESTs	5.3
	443037	AW500305	Hs.8906	syntrophin 7	5.3
	445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	5.2
	447750	AI422234	Hs.143434	contactin 1	5.2
	444409	AI792140	Hs.49265	ESTs	5.2
	409031	AA376836	Hs.288856	ESTs	5.1
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	5.0
	452022	AW072330	Hs.293875	ESTs	4.9
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	4.8
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
	443622	AI911527	Hs.11805	ESTs	4.8
	442023	AI187878	Hs.144549	ESTs	4.7
	445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 fis, clone HE	4.6
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	4.5
	414290	AI568801	Hs.71721	ESTs	4.4
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.4
	428508	BE252383	Hs.184668	SBB131 protein	4.4
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	4.3
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.3
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.3
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.1
	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.1
	440736	D56919	Hs.265848	myomegalin	4.1
	407245	X90568	Hs.172004	titin	4.1
	441976	AA428403	Hs.106131	ESTs	4.1
	450642	R39773	Hs.7130	copine IV	4.1
	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferas	4.0
	428465	AW970976	Hs.293653	ESTs	4.0
	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	4.0

5	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypothe	4.0
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
	415666	H72693		gb:yu03c11.1 Soares fetal liver spleen	3.9
	407988	N47760	Hs.285107	hypothetical protein FLJ13397	3.9
	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
10	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	3.8
	431668	AW969610	Hs.151179	ESTs	3.8
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	3.8
	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.8
15	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.8
	450103	R08665	Hs.17244	hypothetical protein FLJ13605	3.7
	426775	AA384564	Hs.3628	ESTs	3.7
	403469			Target Exon	3.7
	450181	H05254	Hs.201198	ESTs	3.7
20	438202	AW169287	Hs.22588	ESTs	3.7
	445279	R41900	Hs.22245	ESTs	3.7
	422546	AB007969	Hs.301478	KIAA0500 protein	3.7
	435712	AA694607	Hs.176956	ESTs	3.6
	417620	R02530	Hs.191198	ESTs	3.6
25	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 H	3.6
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.6
	426365	AA376667	Hs.10283	RNA binding motif protein 88	3.6
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	3.6
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	3.6
30	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	3.6
	414631	AW970130	Hs.65406	ESTs	3.6
	453698	AA037615	Hs.42746	ESTs	3.6
	438704	AI435060	Hs.32825	ESTs	3.5
	437073	AI885608	Hs.94122	ESTs	3.5
35	434460	AA478486	Hs.3852	KIAA0368 protein	3.5
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.5
	423665	BE167153	Hs.24380	ESTs	3.5
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.5
	441264	AA927170	Hs.23290	ESTs	3.5
40	433629	R13140	Hs.13359	ESTs	3.5
	411811	AW864370		gb:PM4-SN0016-100500-004-h09 SN0016 Homo	3.5
	410140	AL134435	Hs.247837	neurexin 3	3.4
	415114	D60468	Hs.94181	ESTs	3.4
	455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	3.4
45	433670	AA604405		gb:nc087h09.s1 NCL_CGAP_AA1 Homo sapiens	3.4
	417175	R44558	Hs.94002	ESTs	3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.4
	457012	R41480	Hs.302754	ESTs	3.3
50	405354			CX000321:gi 6671579 ref NP_031518.1 ari	3.3
	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.3
	433803	AI823593	Hs.27688	ESTs	3.3
	449017	AW002425	Hs.224142	ESTs	3.3
	414545	AA149287	Hs.76605	ESTs	3.3
55	409010	AI648675	Hs.103441	Homo sapiens, Similar to RIKEN cDNA 1700	3.3
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.3
	422411	AW749443	Hs.22511	ESTs	3.3
	428850	AA934975	Hs.185076	ESTs	3.3
	406922	S70284	Hs.119597	gb:stearyl-CoA desaturase [human, adipo	3.2
60	429556	AW139399	Hs.98988	ESTs	3.2
	434104	AF116691	Hs.116459	hypothetical protein PRQ2198	3.2
	427229	AI799751	Hs.5635	ESTs	3.2
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	3.2
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
65	412786	AW900654	Hs.285729	ESTs, Weakly similar to unnamed protein	3.2
	440808	AK001339	Hs.7432	hypothetical protein FLJ10477	3.2
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.1
	429876	AB028977	Hs.225974	KIAA1054 protein	3.1
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.1
70	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypothe	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1
	433582	BE548749	Hs.148016	ESTs	3.1
	452752	AW044058	Hs.33578	KIAA0820 protein	3.0
	439165	AA029517	Hs.95162	KCNQ1 overlapping transcript 1	3.0
75	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.0
	422414	AW875237	Hs.13701	ESTs	3.0
	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AI824977	Hs.145319	ESTs	3.0
80	452990	AA887428	Hs.246970	mitogen-activated protein kinase kinase	3.0
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.0
	429968	AA322503	Hs.227011	G-substrate	3.0
	434348	BE393191	Hs.181795	putative b,b-carotene-9',10'-dioxygenase	2.9
	427115	AW972853	Hs.112237	ESTs	2.9
	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.9
	449561	AI022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	405403			Target Exon	2.9

	452197	AW023595	Hs.232048	ESTs	2.9
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp76202215 (f	2.9
	436427	AI344378	Hs.143399	ESTs	2.9
5	417787	R14948	Hs.23883	ESTs	2.9
	439272	AA832474	Hs.25851	ESTs	2.9
	454247	AJ243950	Hs.46735	deafness locus associated putative guani	2.9
	415839	R40611	Hs.94694	ESTs	2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
10	408468	AI909712	Hs.93837	phosphatidylinositol transfer protein, m	2.9
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	2.9
	410240	AL157424	Hs.61289	synaptotagmin 2	2.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	2.9
	408438	AB011180	Hs.100960	KIAA0608 protein	2.8
15	458793	N80159	Hs.121849	microtubule-associated proteins 1A/1B li	2.8
	429788	U87791	Hs.221040	HBS1 (S. cerevisiae)-like	2.8
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	2.8
	433109	N58907	Hs.162430	EST	2.8
	427974	BE093023	Hs.188767	ESTs	2.8
20	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	2.8
	414764	AW013887	Hs.31522	ESTs	2.8
	411918	AW876354		gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.8
	404563			Target Exon	2.8
25	446468	AI765890	Hs.16341	MAWD binding protein	2.8
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.7
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	2.7
	400138			Eos Control	2.7
30	458676	AI692464	Hs.202263	ESTs	2.7
	459697	AA406062	Hs.98002	ESTs	2.7
	444420	AI148157	Hs.146766	ESTs	2.7
	430371	D87466	Hs.240112	KIAA0276 protein	2.7
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
35	424994	AW954525		gb:EST366595 MAGE resequences, MAGE Homo	2.7
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.7
	417494	AI369494	Hs.222137	ESTs	2.7
	427166	AA431576	Hs.99154	ESTs	2.7
	404746			CX000138:gil7512767 pir T12477 hypothe	2.7
40	411361	AW839073		gb:CM2-L70066-030100-109-d06 L70066 Homo	2.7
	428358	AA993222	Hs.101915	Stargard disease 3 (autosomal dominant)	2.7
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.7
	416101	R24854	Hs.268806	ESTs	2.7
	404606			Target Exon	2.7
45	433921	AA618174		gb:nq14f01.s1 NCL_CGAP_Thy1 Homo sapiens	2.7
	414272	AI651603	Hs.46988	ESTs	2.7
	418047	R37633	Hs.4847	ESTs	2.7
	421089	AB037771	Hs.101799	KIAA1350 protein	2.7
	412244	AW948175		gb:RC0-MT0013-280300-021-c10 MT0013 Homo	2.7
50	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	2.6
	424153	AA451737	Hs.141496	MAGE-like 2	2.6
	427189	H82453	Hs.5635	ESTs	2.6
	454454	AW612264	Hs.131705	ESTs	2.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	2.6
55	456791	H05202	Hs.133968	FGF receptor activating protein 1	2.6
	405715			ENSP00000005198: Mixed lineage kinase ML	2.6
	425494	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr	2.6
	430865	AJ073424	Hs.5232	HSPC125 protein	2.6
	435767	H73505	Hs.117874	ESTs	2.6
	410119	F07841	Hs.13926	ESTs	2.6
60	432146	AW081072	Hs.115960	KIAA0939 protein	2.6
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.6
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypothesi	2.6
	429477	AI275514	Hs.6658	ESTs	2.6
	400269			Eos Control	2.5
65	443692	AW022228	Hs.322922	ESTs	2.5
	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.5
	435145	AI277259	Hs.116631	ESTs	2.5
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
	449709	BE410592	Hs.23918	hypothetical protein PP5395	2.5
70	416530	U62801	Hs.79361	kallikrein-6 (neurosin, zyme)	2.5
	411678	AI907114	Hs.71465	squalene epoxidase	2.5
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypothesi	2.5
	435624	T64297		fatty acid binding protein 1, liver	2.5
75	458268	AA428403	Hs.106131	ESTs	2.5
	451336	AI264643	Hs.3610	ESTs	2.5
	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	2.5
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
	420033	D59502	Hs.292590	ESTs	2.5
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5
80	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5
	408206	AF041853	Hs.43670	kinesin family member 3A	2.5
	440205	T86950	Hs.105448	ESTs, Weakly similar to B34087 hypothesi	2.5
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.5
	420912	AW853156	Hs.90787	ESTs	2.4

	439180	AI393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	2.4
	421025	AW958975	Hs.29387	Homo sapiens cDNA FLJ13226 fis, clone OV	2.4
	439973	AI733308	Hs.124663	ESTs	2.4
5	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.4
	414672	AI218038	Hs.48504	ESTs, Moderately similar to ALU5_HUMAN A	2.4
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	2.4
	433068	NM_006456	Hs.288215	sialyltransferase	2.4
	446520	AA128808	Hs.179902	transporter-like protein	2.4
10	423803	NM_005709	Hs.132945	PDZ-73 protein	2.4
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	2.4
	425907	AA365752	Hs.155965	ESTs	2.4
	433819	AW511097	Hs.112765	ESTs	2.4
	446066	AI343931	Hs.149383	ESTs	2.4
15	430573	AA744550	Hs.136345	ESTs	2.4
	444992	R37658	Hs.21375	ESTs	2.4
	434975	AA657884	Hs.314413	ESTs	2.4
	458227	Z40670	Hs.181340	ESTs	2.4
	443244	AI457235	Hs.166479	ESTs	2.4
20	432408	N39127		ESTs, Weakly similar to A46010 X-linked	2.4
	401600	BE247275		U5 snRNP-specific protein, 116 kD	2.3
	419066	Z98492	Hs.6975	PRO1073 protein	2.3
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.3
	402124			NM_031891:Homo sapiens cadherin 20, type	2.3
25	416678	N80448	Hs.269106	ESTs	2.3
	444897	AW137088	Hs.144857	ESTs	2.3
	425111	BE018485	Hs.30977	ESTs, Weakly similar to B34087 hypothesi	2.3
	400536			NM_000681*:Homo sapiens adrenergic, alph	2.3
	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	2.3
30	459511	AI142379		gb:gg64c01.r1 Soares_testis_NHT Homo sap	2.3
	415111	R39039	Hs.279041	EST	2.3
	433331	AI738815	Hs.117323	ESTs	2.3
	440293	AI004193	Hs.22123	ESTs	2.3
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.3
35	416964	D87467	Hs.80620	guanine nucleotide exchange factor for R	2.3
	419386	AA236867		ESTs, Weakly similar to I38022 hypothesi	2.3
	402493	AI743260		mannosidase, alpha, class 1A, member 1	2.3
	401783			NM_003771*:Homo sapiens keratin, hair, a	2.3
	420548	AA278246	Hs.920	ESTs	2.3
40	419763	AI039691	Hs.127486	ESTs	2.3
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.3
	406023			Target Exon	2.3
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	2.3
	401586			Target Exon	2.3
	404091			Target Exon	2.3
45	456773	AI038192	Hs.129764	EGF-like repeats and discoidin I-like do	2.3
	414106	BE300325	Hs.77135	RNA binding protein	2.3
	454288	BE222648	Hs.241432	ESTs, Highly similar to c380A1.1b [H.sap	2.3
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	2.3
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	2.3
50	415692	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL	2.3
	416282	R86664	Hs.167257	brain link protein-1	2.2
	404659			ENSP00000239999*:HYPOTHETICAL 34.7 kDa P	2.2
	429956	AI374651	Hs.22542	ESTs	2.2
55	429670	L01087	Hs.211593	protein kinase C, theta	2.2
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.2
	458921	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	2.2
	436463	H06502	Hs.6656	ESTs	2.2
	408994	AW299520	Hs.43052	ESTs	2.2
60	413303	AW836130	Hs.75277	hypothetical protein FLJ13910	2.2
	418154	BE165866		nuclear receptor subfamily 1, group I, m	2.2
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.2
	422907	AI879263	Hs.77273	Human glucose transporter pseudogene	2.2
	446377	AW014022	Hs.170953	ESTs	2.2
65	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.2
	449714	AB033015	Hs.23941	KIAA1189 protein	2.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.2
	410066	AL117664	Hs.58419	DKFZP586L2024 protein	2.2
	410912	AW810224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo	2.2
70	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.2
	421709	AA159394	Hs.107056	CED-6 protein	2.2
	403728			Target Exon	2.2
	453359	AA448787	Hs.24872	ESTs	2.2
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.2
75	413427	U31120	Hs.845	interleukin 13	2.2
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	2.2
	413924	AL119964	Hs.75616	setadin-1	2.2
	403463			Target Exon	2.2
	408068	AW148652	Hs.167398	ESTs	2.2
80	407819	R42185	Hs.102720	ESTs	2.2
	414203	BE262170	Hs.78629	ATPase, Na ⁺ transporting, beta 1 polypep	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	449835	AW979300	Hs.293813	ESTs	2.2
	458547	AW204314	Hs.170784	ESTs	2.2

	414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens c	2.2
	427493	H09037		Target CAT	2.2
	458441	AW842283	Hs.288232	cyclin I	2.1
5	410705	BE004107		gb:CM0-BN0102-150300-288-112 BN0102 Homo	2.1
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	2.1
	405502			C7000609*:gij628012[pin]A53933 myosin I	2.1
	400818			Target Exon	2.1
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	2.1
10	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	2.1
	445200	AA084460	Hs.12409	somatostatin	2.1
	453396	AW162768	Hs.22620	ESTs	2.1
	443819	AB033076	Hs.9873	likely homolog of rat kinase D-interacti	2.1
	401929			C17001690:gij6005701[ref]NP_009099.1] AT	2.1
15	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	2.1
	433862	D86960	Hs.3610	KIAA0205 gene product	2.1
	458694	F12832	Hs.3610	ESTs	2.1
	417063	N50515	Hs.45061	ESTs	2.1
	416935	AA190712		gb:zp87109.r1 Stratagene HeLa cell s3 93	2.1
20	414446	AA147534	Hs.142019	ESTs, Weakly similar to 1207289A reverse	2.1
	434681	AA642402	Hs.59142	ESTs	2.1
	413835	A1272727	Hs.249163	fatty acid hydroxylase	2.1
	426137	AL040683	Hs.167031	DKFZP566D133 protein	2.1
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.1
25	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	2.1
	407786	AA687538	Hs.38972	tetraspan 1	2.1
	421296	NM_002666	Hs.103253	perilipin	2.1
	444200	AA327113	Hs.149057	ESTs	2.1
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.1
30	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	2.1
	414759	AW295157	Hs.47587	ESTs	2.1
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.1
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.1
	437924	AI935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODIU	2.1
35	449119	AI631195	Hs.232193	ESTs	2.1
	431568	AW972316	Hs.283703	ESTs	2.1
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.1
	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheli	2.1
	441987	AW452234	Hs.128293	ESTs	2.1
40	414055	AW818687	Hs.5366	hypothetical protein FLJ21522	2.1
	445066	BE178734	Hs.197422	ESTs	2.1
	455546	AW994075		gb:RC3-BN0036-090200-011-g06 BN0036 Homo	2.1
	413607	T64741		gb:yc48f11.r1 Stratagene liver (937224)	2.1
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.0
45	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	425055	AW961959	Hs.96940	ESTs	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	419647	AA348947	Hs.91816	hypothetical protein	2.0
	412266	N59006	Hs.26133	ESTs	2.0
50	449658	AI964033	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEXI	2.0
	424505	AA446131	Hs.124918	KIAA1795 protein	2.0
	438219	AI916151	Hs.257194	ESTs	2.0
	425068	AL048716	Hs.154387	KIAA0103 gene product	2.0
	412949	AJ471639	Hs.71913	ESTs	2.0
55	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.0
	445071	AI280246	Hs.149504	ESTs	2.0
	456529	AF014643	Hs.100072	connexin46.6	2.0
	406475			C15000508*:gij2558825[gb]AAC53387.1] (AF	2.0
60	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kd)	2.0
	431542	H63010	Hs.5740	ESTs	2.0
	452625	AA724771	Hs.61425	ESTs	2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	2.0
	409767	AW501470		gb:UH-HF-BP0p-ajd-b-03-0-UI.r1 NIH_MGC_5	2.0
	446873	AI554439	Hs.30724	ESTs	2.0
65	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	2.0
	420061	AW024937	Hs.29410	ESTs	2.0
	439559	AW364675	Hs.173921	ESTs, Weakly similar to 2109260A B cell	2.0
	449901	AI674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.0
70	428304	AI743177	Hs.98422	ESTs	2.0
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	458480	AI792298		p30 OBC protein	2.0
	404559			Target Exon	2.0
	445831	NM_006055	Hs.13351	LanC (bacterial tetracycline synthetase c	2.0
75	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	2.0
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	2.0
	444904	AW452054	Hs.161139	ESTs	2.0
	443713	AI082810	Hs.204934	ESTs	2.0
	448743	AB032962	Hs.21896	KIAA1136 protein	2.0
80	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.0
	448770	AA326683	Hs.21992	likely ortholog of mouse variant polyade	2.0
	453994	BE180964	Hs.165590	ribosomal protein S13	2.0
	420290	AW977318	Hs.194480	ESTs	2.0
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	2.0

5	447965	AW292577	Hs.94445	ESTs	2.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.0
	459256	AW967468	Hs.95821	hypothetical protein FLJ14547	2.0
	411906	AW875765		gb:QV2-PT0012-020500-186-a08 PT0012 Homo	2.0
	441984	AB037763	Hs.8059	synaptotagmin IV	2.0
	437900	AI763301	Hs.107331	ESTs	2.0
	436092	AI345995	Hs.127383	ESTs	2.0
	416529	AW009370	Hs.115772	ESTs	2.0
10	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.0
	444749	AI190672	Hs.65926	ESTs	2.0
	446277	AI284218	Hs.159204	ESTs	2.0
	452550	AA026735	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	2.0
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.0
15	409265	T78737	Hs.321062	ESTs	2.0
	426736	AA431615	Hs.130722	ESTs	2.0
	447098	AI939409	Hs.157803	ESTs	2.0
	403582			Target Exon	2.0
20	TABLE 21B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
25	Pkey	CAT Number	Accession		
	409767	1154015_1	AW501470 AW502931 AW499500		
	410705	1217235_1	BE004107 BE004105 AW901093 AW797879 AW901094 AW797881 AW797880 BE004108		
	410912	126543_1	AW810224 AW810337 AW810295 AW810333 AW810335 AW810296 AW816053		
	411361	1240611_1	AW839073 AW839234 AW839230 AW878302 AW839109 AW843897		
30	411811	1259427_1	AW864370 AW864319 AW864504		
	411906	1265204_1	AW875765 H50294 AW875444		
	411918	1265807_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198		
	412244	1284692_1	AW948175 AW947637 AW902869 AW947537 AW947531 AW947532 AW947530		
	413607	1379911_1	T64741 BE158393 BE152805		
35	414276	1432115_1	BE297862		
	415666	1543492_1	H72693 R08673 H72694 F20990 R08580		
	416935	163179_1	AA190712 AA190665 AA252564		
	418154	17249_1	BE165866 BE165832 AA319621 AA401166 AI811901 H78857 X56199 R93797 AW896675 AA401072 AW374411 H52942 AW896685 AA348138		
40			AI399764 AA010244 W90159 N90874 AA339496 AW967136 W38705 AA029093 AW444647 BE175700 AV651656 AV651847 AA332039 AV649227		
			AV649164 AV649491 N87956 AA332262 BE001561 H75493 BE218742 AA333298 AA095633 AA091968 M78602 T05342 W17094 AA126501		
			AW374665 AI452905 AW316900 AI185080 AI202928 AI651843 AA693541 AI681019 AV658257 AV658133 BE045335 BE089546 AA300830 AA361376		
			BE218739 AW207622 AA765340 AW612733 BE348741 AI806054 AI817553 AA808552 AI500693 AW342032 AA147066		
	418866	179788_1	T65754 AA229857 AA229658		
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961		
45	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564		
	427493	279541_2	H09037 AW974937 AA657521 H86138 H86513 H09016 AA404410 AA404454		
	431304	331286_1	BE157283 BE157287 AA502438		
	432408	346286_2	N39127 F20776 AI082691 AA865520 F36964 F33894		
	433670	372721_1	AA604405 BE062234 AW748386		
50	433921	377350_1	AA618174 AI114549 R36464 R36465		
	436624	4237_5	T64297 AA894931 NM_001443 M10050 AW843109 AI698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617		
			AI768596 AA101894 W90338 AI742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121		
			AW842284		
	446692	689623_1	Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983		
55	449901	818599_1	AI674072 BE268487		
	454339	1122972_1	AW381980 BE152244 BE152235 BE152238 BE152232		
	455040	1250028_1	AW852286 AW851934 AW852096 AW852274		
	455546	1324614_1	AW994075 AW994386		
	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636		
60	456401	1844649_2	W28146 W28187		
	458480	59843_1	AI792298 H14121 AI375113 AA960851 AA744592 AV648739 AI298360 AW293609		
65	TABLE 21C:				
	Pkey:	Unique number corresponding to an Eos probeset			
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA			
		sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
	Strand:	Indicates DNA strand from which exons were predicted.			
	Nt_position:	Indicates nucleotide positions of predicted exons.			
70	Pkey	Ref	Strand	Nt_position	
	400536	9797380	Minus	170994-172025	
	400818	8569994	Plus	172644-172765,173085-173200	
	401586	9838242	Minus	93974-94099	
	401600	4388746	Minus	27363-27518,28727-28891,29526-29731	
75	401783	7249190	Plus	139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283	
	401929	3810670	Minus	3167-3286,4216-4310	
	402124	4033680	Plus	164206-164459	
	402493	9797670	Minus	205146-205240,205428-205542	
	403463	9929538	Plus	102596-102879	
80	403469	9929739	Minus	4831-7707	
	403582	8101186	Plus	18308-18458	
	403728	7534291	Minus	34481-34671	
	404091	7684554	Minus	82121-83229	
	404559	8748893	Minus	73499-73651,89575-89739	

5	404563	9838310	Plus	100136-100343
	404606	9212936	Minus	22310-23269
	404659	9797068	Minus	65026-67930
	404746	7219894	Minus	32643-32834
	405354	2642452	Plus	52213-53089
10	405403	6850244	Minus	37491-37670,40951-41031
	405502	9211311	Minus	50360-50584
	405715	4156209	Plus	26293-26706
	406023	8272661	Plus	205623-205936
	406475	9797684	Plus	125417-125563,128052-128180

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 22A lists about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exempt Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of CNS to GLIOBLASTOMA

Pkey	ExAccn	UnigeneID	Unigene Title	R1
418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	9.4
415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
417167	AW206437	Hs.4290	ESTs	7.3
453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	6.5
454076	AW204712	Hs.61957	ESTs	6.3
417275	X63578	Hs.295449	parvalbumin	6.2
412636	NM_004415		desmoplakin (DPI, DPII)	6.0
409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
424645	NM_014682	Hs.151449	KIAA0535 gene product	5.6
427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
446390	AA233393	Hs.14992	hypothetical protein FLJ11151	5.2
444409	AI792140	Hs.49265	ESTs	5.2
409031	AA376836	Hs.288856	ESTs	5.1
408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	4.8
428414	AL049980	Hs.184216	DKFZP564C152 protein	4.8
428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	4.6
420605	BE391491	Hs.99291	HSPC156 protein	4.6
445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 fis, clone HE	4.6
450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.4
428508	BE252383	Hs.184668	SBB131 protein	4.4
434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.3
410330	AW023630	Hs.159425	ESTs	4.2
426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
448958	AB020651	Hs.22653	KIAA0844 protein	4.2
428465	AW970976	Hs.293653	ESTs	4.0
429470	AI878901	Hs.203852	guanine nucleotide binding protein (G pr	4.0
432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	3.9
427061	AB032971	Hs.173392	KIAA1145 protein	3.9
430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
435145	AI277259	Hs.116631	ESTs	3.8
416101	R24854	Hs.268806	ESTs	3.8
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.8
438202	AW169287	Hs.22588	ESTs	3.8
433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	3.7
419956	AL137939	Hs.40096	ESTs	3.7
430573	AA744550	Hs.136345	ESTs	3.7
422546	AB007969	Hs.301478	KIAA0500 protein	3.7
453344	BE349075	Hs.44571	ESTs	3.6
417620	R02530	Hs.191198	ESTs	3.6
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511.1 H	3.6
414631	AW970130	Hs.65406	ESTs	3.6
437073	AI885608	Hs.94122	ESTs	3.5
441264	AA927170	Hs.23290	ESTs	3.5
433629	R13140	Hs.13359	ESTs	3.5
415114	D60468	Hs.94181	ESTs	3.4
411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.4
415666	H72693		gb:yu03c11.1 Soares fetal liver spleen	3.4
416851	AW963951	Hs.85618	ESTs	3.4
443037	AW500305	Hs.8906	syntaxin 7	3.4
449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	3.4
427176	AW381569	Hs.40334	ESTs	3.4
438704	AI435060	Hs.32825	ESTs	3.3
417175	R44558	Hs.94002	ESTs	3.3
430865	AI073424	Hs.5232	HSPC125 protein	3.3
457012	R41480	Hs.302754	ESTs	3.3
405354			CX000321:gil[6671579]ref[NP_031518.1] an	3.3
432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferas	3.3

	429876	AB028977	Hs.225974	KIAA1054 protein	3.3
	434348	BE393191	Hs.181795	putative b,b-carotene-9,10'-dioxygenase	3.3
	441071	D79550	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.3
5	445279	R41900	Hs.22245	ESTs	3.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.2
	448072	AI459306	Hs.24908	ESTs	3.2
	402429			Target Exon	3.2
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
	400138			Eos Control	3.1
10	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1
	433582	BE548749	Hs.148016	ESTs	3.1
	434104	AF116691	Hs.116459	hypothetical protein PRO2198	3.0
	404606			Target Exon	3.0
15	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.0
	415672	N53097	Hs.193579	ESTs	3.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AI824977	Hs.145319	ESTs	3.0
20	439165	AA029517	Hs.95162	KCNQ1 overlapping transcript 1	2.9
	449561	AI022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	436427	AI344378	Hs.143399	ESTs	2.9
	405403			Target Exon	2.9
	452197	AW023595	Hs.232048	ESTs	2.9
25	437357	AL359559	Hs.331666	Homo sapiens mRNA: cDNA DKFZp76202215 (f	2.9
	439272	AA832474	Hs.25851	ESTs	2.9
	415839	R40611	Hs.94694	ESTs	2.9
	411906	AW875765		gb:QV2-PT0012-020500-186-a08 PT0012 Homo	2.9
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	2.9
30	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	2.8
	435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	2.8
	433109	N58907	Hs.162430	EST	2.8
	404563			Target Exon	2.8
	427974	BE093023	Hs.188767	ESTs	2.8
35	413324	V00571	Hs.75294	corticotropin releasing hormone	2.7
	409263	AA089573	Hs.50319	ESTs	2.7
	454247	AJ243950	Hs.46735	deafness locus associated putative guani	2.7
	449180	AI633836	Hs.195649	ESTs	2.7
	416004	D11880	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	2.7
40	424994	AW954525		gb:EST366595 MAGC resequences, MAGC Homo	2.7
	430371	D87466	Hs.240112	KIAA0276 protein	2.7
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
	451007	H38108	Hs.32759	ESTs	2.7
	414502	AL133721	Hs.224680	ESTs	2.7
45	458793	N80159	Hs.121849	microtubule-associated proteins 1A/1B li	2.7
	459053	AI807052	Hs.210361	ESTs	2.7
	427229	AI799751	Hs.5635	ESTs	2.7
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	2.7
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	2.7
50	433921	AA618174		gb:ncq14f01.s1 NCL_CGAP_Thy1 Homo sapiens	2.7
	414272	AI651603	Hs.46988	ESTs	2.7
	418047	R37633	Hs.4847	ESTs	2.7
	421089	AB037771	Hs.101799	KIAA1350 protein	2.7
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6
55	414290	AI568801	Hs.71721	ESTs	2.6
	433703	AA210863	Hs.3532	nemo-like kinase	2.6
	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	2.6
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp56481264 (f	2.6
	422137	AJ236885	Hs.112180	zinc finger protein 148 (pH2-52)	2.6
60	442023	AI187878	Hs.144549	ESTs	2.6
	421709	AA159394	Hs.107056	CED-6 protein	2.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	2.6
	412244	AW948175		gb:RC0-MT0013-280300-021-c10 MT0013 Homo	2.6
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	2.6
65	423665	BE167153	Hs.24380	ESTs	2.6
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	2.6
	408468	AI909712	Hs.93837	phosphatidylinositol transfer protein, m	2.6
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	2.6
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.6
70	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.6
	459080	AW192083	Hs.290855	ESTs	2.5
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
	435712	AA694607	Hs.176956	ESTs	2.5
	431662	AA513406	Hs.152307	ESTs	2.5
75	435902	AA701867	Hs.297726	ESTs	2.5
	436624	T64297		fatty acid binding protein 1, liver	2.5
	443155	R54485	Hs.23772	ESTs	2.5
	439183	AW970600	Hs.303261	ESTs	2.5
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.5
80	420033	D59502	Hs.292590	ESTs	2.5
	408438	AB011180	Hs.100960	KIAA0608 protein	2.5
	440205	T86950	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	2.5
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5

	427115	AW972853	Hs.112237	ESTs	
	433670	AA604405		gb:nc087h09.s1 NCI_CGAP_AA1 Homo sapiens	2.4
	452022	AW072330	Hs.293875	ESTs	2.4
5	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.4
	403469			Target Exon	2.4
	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	2.4
	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.4
	443622	AJ911527	Hs.11805	ESTs	2.4
10	456791	H05202	Hs.133968	FGF receptor activating protein 1	2.4
	414672	AJ218038	Hs.48504	ESTs, Moderately similar to ALU5_HUMAN A	2.4
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	2.4
	422414	AW875237	Hs.13701	ESTs	2.4
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	2.4
15	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	2.4
	410240	AL157424	Hs.61289	synaptotagmin 2	2.4
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	2.4
	458227	Z40570	Hs.181340	ESTs	2.4
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	2.4
20	401600	BE247275		U5 snRNP-specific protein, 116 kD	2.4
	422963	M79141	Hs.13234	ESTs	2.3
	444897	AW137088	Hs.144857	ESTs	2.3
	418207	C14685	Hs.34772	ESTs	2.3
	445071	AJ280246	Hs.149504	ESTs	2.3
25	407868	NM_000950		proline-rich Gta (G-carboxyglutamic acid	2.3
	433331	AJ738815	Hs.117323	ESTs	2.3
	440293	AJ004193	Hs.22123	ESTs	2.3
	428850	AA934975	Hs.185076	ESTs	2.3
	401783			NM_003771*:Homo sapiens keratin, hair, a	2.3
30	419763	AJ039691	Hs.127486	ESTs	2.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	2.3
	420912	AW853156	Hs.90787	ESTs	2.3
	442097	AW015799	Hs.128474	ESTs	2.3
	425907	AA365752	Hs.155965	ESTs	2.3
35	404091			Target Exon	2.3
	414106	BE300325	Hs.77135	RNA binding protein	2.3
	454288	BE222648	Hs.241432	ESTs, Highly similar to c380A1.1b [H.sap	2.3
	441040	AW449782	Hs.178803	ESTs	2.3
40	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	2.3
	441879	AJ521936	Hs.107149	novel protein similar to archaeal, yeast	2.3
	407988	N47760	Hs.285107	hypothetical protein FLJ13397	2.2
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	2.2
	458676	AJ692464	Hs.202263	ESTs	2.2
45	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.2
	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.2
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	2.2
	420548	AA278246	Hs.920	ESTs	2.2
	422907	AJ879263	Hs.77273	Human glucose transporter pseudogene	2.2
50	446351	AW444551	Hs.35380	x 001 protein	2.2
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.2
	429598	AA811257	Hs.269710	ESTs	2.2
	408480	AJ350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.2
	411361	AW839073		gb:CM2-LT0066-030100-109-d06 LT0066 Homo	2.2
55	459697	AA406062	Hs.98002	ESTs	2.2
	409856	AW502082		gb:U1-HF-BR0p-ajq-g-04-0-U1.r1 NIH_MGC_5	2.2
	444760	AJ796296	Hs.208062	ESTs	2.2
	443258	AF169301	Hs.9098	sulfate transporter 1	2.2
	428206	AB020643	Hs.183006	KIAA0836 protein	2.2
60	410119	F07841	Hs.13926	ESTs	2.2
	413427	U31120	Hs.845	interleukin 13	2.2
	438021	AV653790	Hs.324275	WW domain-containing protein 1	2.2
	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	2.2
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.2
65	424153	AA451737	Hs.141496	MAGE-like 2	2.2
	413303	AW836130	Hs.75277	hypothetical protein FLJ13910	2.2
	427287	NM_014903	Hs.174188	KIAA0938 protein	2.2
	449658	AJ964033	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEXI	2.2
	441984	AB037763	Hs.8059	synaptotagmin IV	2.2
70	449709	BE410592	Hs.23918	hypothetical protein PPS395	2.2
	408068	AW148652	Hs.167398	ESTs	2.2
	407819	R42185	Hs.102720	ESTs	2.2
	414203	BE262170	Hs.78629	ATPase, Na ⁺ transporting, beta 1 polypep	2.2
	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	2.2
75	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	458480	AJ792298		p30 DBC protein	2.2
	449835	AW979300	Hs.293813	ESTs	2.2
	458547	AW204314	Hs.170784	ESTs	2.2
	411678	AJ907114	Hs.71465	squalene epoxidase	2.2
80	444783	AK001468	Hs.62180	anilin (Drosophila Scraps homolog), act	2.1
	424632	AB014523	Hs.151406	KIAA0623 gene product	2.1
	449901	AJ674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.1
	410538	AW753115		gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.1
	426775	AA384564	Hs.3628	ESTs	2.1

	433862	D86960	Hs.3610	KIAA0205 gene product	2.1
	458694	F12832	Hs.3610	ESTs	2.1
	417063	N50515	Hs.45061	ESTs	2.1
5	416935	AA190712		gb:zcp8709.r1 Stratagene HeLa cell s3 93	2.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	2.1
	431128	AI203545	Hs.296169	S-phase response (cyclin-related)	2.1
	442310	AF033199	Hs.8198	zinc finger protein 204	2.1
	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	2.1
10	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	2.1
	414759	AW295157	Hs.47587	ESTs	2.1
	438219	AI916151	Hs.257194	ESTs	2.1
	451336	AI264643	Hs.3610	ESTs	2.1
15	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.1
	413493	BE144444		gb:MR0-HT0168-141199-002-009 HT0168 Homo	2.1
	428501	AL041162	Hs.98587	ESTs	2.1
	431568	AW972316	Hs.283703	ESTs	2.1
	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	2.1
20	441976	AA428403	Hs.106131	ESTs	2.1
	421311	N71848	Hs.283609	hypothetical protein PRO2032	2.1
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.1
	439973	AI733308	Hs.124663	ESTs	2.1
	446185	AI279191	Hs.149454	ESTs, Weakly similar to DSR6_HUMAN DOWN	2.1
25	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.1
	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypothe	2.1
	441987	AW452234	Hs.128293	ESTs	2.1
	457140	AI279960	Hs.178140	ESTs	2.1
	414055	AW818687	Hs.5366	hypothetical protein FLJ21522	2.1
30	445066	BE178734	Hs.197422	ESTs	2.1
	459265	AJ003616		gb:AJ003616 Selected chromosome 21 cDNA	2.0
	425337	AA355442	Hs.169054	ESTs	2.0
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.0
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.0
35	425055	AW961959	Hs.96940	ESTs	2.0
	425068	AL048716	Hs.154387	KIAA0103 gene product	2.0
	444700	NM_003645	Hs.11729	fatty acid-Coenzyme A ligase, very long-	2.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.0
	450103	R08665	Hs.17244	hypothetical protein FLJ13605	2.0
40	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	2.0
	440808	AK001339	Hs.7432	hypothetical protein FLJ10477	2.0
	429968	AA322503	Hs.227011	G-substrate	2.0
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.0
	433068	NM_006456	Hs.288215	sialyltransferase	2.0
45	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.0
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	2.0
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	452625	AA724771	Hs.61425	ESTs	2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	2.0
50	409767	AW501470		gb:U1-HF-BP0p-ajd-b-03-0-U1.r1 NIH_MGC_5	2.0
	415925	HD9474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	2.0
	405670			C2000627:gi12034653 gb AA045951.1 AF22	2.0
	408206	AF041853	Hs.43670	kinesin family member 3A	2.0
	458660	AI299739	Hs.99601	hypothetical protein FLJ12553	2.0
55	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	404559			Target Exon	2.0
	403728			Target Exon	2.0
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	2.0
60	407786	AA687538	Hs.38972	tetraspan 1	2.0
	413266	BE300352		gb:000944231F1 NIH_MGC_17 Homo sapiens c	2.0
	453994	BE180964	Hs.165590	ribosomal protein S13	2.0
	451583	AI653797	Hs.24133	ESTs	2.0
	443244	AI457235	Hs.166479	ESTs	2.0
	453396	AW162768	Hs.22620	ESTs	2.0
65	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	2.0
	459511	AI142379		gb:ag64c01.r1 Soares_testis_NHT Homo sap	2.0
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	2.0
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	2.0
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypothe	2.0
70	444647	H14718	Hs.11506	Human clone Z3589 mRNA sequence	2.0
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.0
	444749	AI190672	Hs.65926	ESTs	2.0
	446277	AI284218	Hs.159204	ESTs	2.0
	452550	AA026735	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	2.0
75	453843	D25215	Hs.35804	hect domain and RLD 3	2.0
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.0
	409265	T78737	Hs.321062	ESTs	2.0

TABLE 22B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

5	409767	1154015_1	AW501470 AW502931 AW499500
	409856	1156268_1	AW502082 AW502979 AW502807 AW501876
	410538	1207341_1	AW753115 AW753113 R45779
	411361	1240611_1	AW839073 AW839234 AW839230 AW878302 AW839109 AW843897
	411906	1265204_1	AW875765 H50294 AW875444
	412244	1284592_1	AW948175 AW947637 AW902869 AW947537 AW947531 AW947532 AW947530
	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413
10			AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985
			BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047
			AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935 AW747877 AW748114 BE148516
			AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145
			BE001925 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090 BE184941 AW804674 BE184924 C04715 W39488
15			AW995615 BE184948 BE159646 AW606653 AA098891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859
			AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690
			T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767
			H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AJ022662 BE091653 AW376811 AW848592
20			AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181
			BE167165 N84767 H27408 H30146 AJ190590 C03378 AJ554403 AJ205263 AA128470 AJ392926 AF139065 AW370813 AW370827 AW798417
			AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AJ760816 AJ439101 AW879451
			A1700963 AA451923 AJ340326 AJ590975 T48793 AJ568096 AJ142882 AA039975 AJ470146 AA946936 BE067737 BE067786 W19287 AA644381
			AJ702424 AJ417612 AJ306554 AJ686869 AJ568892 AW190555 AJ571075 AJ220573 AA056527 AJ471874 AJ304772 AW517828 AJ915596 AJ627383
25			AJ270345 AW021347 AW166807 AW105614 AJ346078 AA552300 W95070 AJ494069 AJ911702 AA149191 AA026864 AJ830049 AJ887258 AW780435
			AJ910434 AJ819984 AJ858282 AJ078449 AJ025932 AJ860584 AJ635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892
			T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AJ927207 AA782109 AW473233 AJ804485 AW169216 AJ572669 AA602182
			AW015480 AW771865 AJ270027 AA961816 AA283207 AJ076962 AJ498487 AJ348053 AJ783914 H44405 AW799118 AA128330 AA515500 AA918281
			W02156 AJ059527 AA022701 W38382 R20795 T77861 AW860878
30	413266	1356260_1	BE300352 BE299274 BE075351 BE297444
	413493	1373555_1	BE144444 BE144430
	415666	1543492_1	H72693 R08673 H72694 F20990 R08580
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	424994	245786_1	AW954525 AJ372685 AA349501 AJ372687 H10564
	432408	346286_2	N39127 F20776 AJ082691 AA865520 F36964 F33894
35	433670	372721_1	AA604405 BE062234 AW748386
	433921	377350_1	AA618174 AJ114549 R36464 R36465
	436624	4237_5	T64297 AA894931 NM_001443 M10050 AW843109 AJ698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
40	449901	818599_1	AJ785996 AA101894 W90338 AJ742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AJ343047 AJ345671 T68235 T68121
	454339	1122972_1	AW842284
	455040	1250028_1	AJ674072 BE268487
	458480	59843_1	AW381980 BE152244 BE152235 BE152238 BE152232
	459265	966590_1	AW852286 AW851934 AW852096 AW852274
			AJ792298 H14121 AJ375113 AA960851 AA744592 AV648739 AJ298360 AW293609
			AJ003616 AJ003654 AJ003617
45	TABLE 22C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA	
	Strand:	sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
50	NL_position:	Indicates DNA strand from which exons were predicted.	
		Indicates nucleotide positions of predicted exons.	
55	Pkey	Ref	Strand
	401600	4388746	Minus
	401783	7249190	Plus
	402429	9796372	Minus
	403469	9929739	Minus
	403728	7534291	Minus
	404091	7684554	Minus
60	404559	8748893	Minus
	404563	9838310	Plus
	404606	9212936	Minus
	405354	2642452	Plus
	405403	6850244	Minus
65	405670	4662655	Plus
70	TABLE 23A: ABOUT 441 GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS		
	Table 23A lists about 441 genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets		
	on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2.5. The "average" normal CNS level was set		
	to the 75 th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 95 th percentile amongst various tumor samples. In order to remove gene-specific		
	background levels of non-specific hybridization, the 10 th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before		
	the ratio was evaluated.		
75	Pkey:	Unique Eos probeset identifier number	
	ExAccn:	Exemplar Accession number, Genbank accession number	
	UnigenelD:	Unigene number	
	Unigene Title:	Unigene gene title	
	R1:	Ratio of CNS to LOWER GRADE GLIOBLASTOMA	
80	Pkey	ExAccn	UnigenelD
	415388	AF018081	Hs.78409
	418318	U47732	Hs.84072
	445529	H14421	Hs.180513
	417433	BE270266	Hs.82128
			collagen, type XVIII, alpha 1
			transmembrane 4 superfamily member 3
			ATP-binding cassette, sub-family A (ABC1
			ST4 oncofetal trophoblast glycoprotein
			R1
			10.3
			10.1
			9.9
			7.8

	422746	NM_004484	Hs.119651	glypican 3	7.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	7.7
	430573	AA744550	Hs.136345	ESTs	7.6
5	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	7.4
	424670	W61215	Hs.116651	epithelial V-like antigen 1	7.3
	417167	AW206437	Hs.4290	ESTs	7.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	7.3
10	424632	AB014523	Hs.151406	KIAA0623 gene product	6.9
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	6.5
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	6.5
	439272	AA832474	Hs.25851	ESTs	6.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	6.4
	454076	AW204712	Hs.61957	ESTs	6.3
15	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	6.3
	430865	AI073424	Hs.5232	HSPC125 protein	6.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	6.2
	417458	NM_005655	Hs.82173	TGFB inducible early growth response	6.1
20	412636	NM_004415		desmoplakin (DPI, DP1)	6.0
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	5.8
	434725	AK000796	Hs.4104	hypothetical protein	5.6
	417175	R44558	Hs.94002	ESTs	5.6
25	417275	X63578	Hs.295449	parvalbumin	5.5
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	5.4
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.4
	412472	AW975398	Hs.293836	ESTs	5.4
30	443258	AF169301	Hs.9098	sulfate transporter 1	5.3
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	5.3
	442064	AI422867	Hs.88594	ESTs	5.2
	438868	AW246243	Hs.334800	hypothetical protein FLJ20974	5.2
	444409	AI792140	Hs.49265	ESTs	5.2
35	442310	AF033199	Hs.8198	zinc finger protein 204	5.1
	409031	AA376836	Hs.288856	ESTs	5.1
	438460	AB020702	Hs.6224	KIAA0895 protein	5.1
	411939	AI365585	Hs.146246	ESTs	5.0
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	5.0
40	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	5.0
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, acti	4.9
	448960	AF006513	Hs.22670	chromodomain helicase DNA binding protei	4.9
	416101	R24854	Hs.268806	ESTs	4.9
45	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	4.9
	424645	NM_014682	Hs.151449	KIAA0535 gene product	4.8
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	4.8
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	4.8
	414502	AL133721	Hs.224680	ESTs	4.8
50	442572	AI001922	Hs.135121	hypothetical protein FLJ22415	4.8
	412700	BE222433	Hs.239208	ESTs, Weakly similar to I38022 hypotheti	4.8
	422503	BE242587	Hs.118651	hematopoietically expressed homeobox	4.8
	420605	BE391491	Hs.99291	HSPC156 protein	4.7
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	4.7
55	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.7
	409263	AA069573	Hs.50319	ESTs	4.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.6
	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	4.6
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	4.6
60	449901	AI674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	4.6
	445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 fs, clone HE	4.6
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	4.5
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	4.5
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	4.5
65	401600	BE247275		U5 snRNP-specific protein, 116 kD	4.5
	447135	T58148		gb:yb98g06.s1 Stratagene lung (937210) H	4.5
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	4.4
	429598	AA811257	Hs.269710	ESTs	4.4
	428206	AB020643	Hs.183006	KIAA0836 protein	4.4
70	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.4
	428508	BE252383	Hs.184668	SBB131 protein	4.4
	435145	AI277259	Hs.116631	ESTs	4.4
	405670			C2000627:gb:12034653[gb]AAG45951.1[AF22	4.4
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (4.3
75	427670	BE612888	Hs.180224	myosin regulatory light chain	4.3
	428465	AW970976	Hs.293653	ESTs	4.3
	449180	AI633836	Hs.195649	ESTs	4.3
	402364	AV653231		CCAAT/enhancer binding protein (C/EBP),	4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
80	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	4.2
	441408	AI733249	Hs.126897	ESTs	4.2
	419631	AW188117	Hs.303154	popeye protein 3	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2

5	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.2
	459053	AJ807052	Hs.210361	ESTs	4.1
	450600	BE079478	Hs.24880	ESTs	4.1
	415839	R40611	Hs.94694	ESTs	4.1
10	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	4.1
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proti	4.1
	405674			NM_022775:Homo sapiens hypothetical prot	4.1
	453906	AW444952	Hs.257054	ESTs	4.1
	419318	AW969742	Hs.291005	ESTs	4.1
15	456382	NM_001126	Hs.90011	adenylosuccinate synthase	4.0
	435902	AA701867	Hs.297726	ESTs	4.0
	449483	AK001971	Hs.23607	hypothetical protein FLJ11109	4.0
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.0
	403890			CS002036*:gij10241574[emb]CAC09416.1 (A	4.0
20	429470	AJ878901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
	409856	AW502082		gb:U1-HF-BR0p-ajq-g-04-0-U1.r1 NH_MGC_5	4.0
	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	4.0
	420230	AL034344	Hs.284186	forkhead box C1	4.0
	410509	AW840743		gb:QV1-CN0002-080300-102-f07 CN0002 Homo	4.0
25	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.9
	400138			Eos Control	3.9
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.9
	436521	AW203986	Hs.213003	ESTs	3.9
	401507			C15000810*:gij11131272[sp]P79331[ATS2_BO	3.9
30	449785	AJ225235	Hs.288300	hypothetical protein FLJ23231	3.9
	434815	AF155582	Hs.46744	core1 UDP-galactose-4-epimerase	3.9
	411906	AW875765		gb:QV2-PT0012-020500-186-a08 PT0012 Homo	3.9
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypoteti	3.9
	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
35	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
	449658	AJ964033	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEX	3.9
	429876	AB028977	Hs.225974	KIAA1054 protein	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (3.8
40	437659	AB007944	Hs.5737	KIAA0475 gene product	3.8
	438171	AW976507	Hs.293515	ESTs	3.8
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.8
	405586			NM_000299:Homo sapiens plakophilin 1 (ec	3.8
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	3.8
45	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.8
	438202	AW169287	Hs.22588	ESTs	3.8
	404606			Target Exon	3.8
	425329	AJ961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	3.8
	407604	AW191962	Hs.288061	collagen, type VIII, alpha 2	3.8
50	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	3.7
	430868	W93178	Hs.5232	HSPC125 protein	3.7
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	3.7
	458660	AJ299739	Hs.99601	hypothetical protein FLJ12553	3.7
	408732	AL117490	Hs.47225	Ras-associated protein Rap1	3.7
55	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.7
	413493	BE144444		gb:MR0-HT0168-141199-002-f09 HT0168 Homo	3.7
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	3.7
	445797	AJ253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.7
	457121	AJ743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	3.6
60	417620	R02530	Hs.191198	ESTs	3.6
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 H	3.6
	454247	AJ243950	Hs.46735	deafness locus associated putative guani	3.6
	431662	AA513406	Hs.152307	ESTs	3.6
	426908	AW815163	Hs.172851	arginase, type II	3.6
65	438519	AJ186033	Hs.147025	ESTs, Weakly similar to C57785 zinc fing	3.6
	415606	W70022		gb:zd51e10.r1 Soares_fetal_heart_NbHH19W	3.6
	444859	AW449137	Hs.157487	ESTs	3.6
	414631	AW970130	Hs.65406	ESTs	3.6
	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	3.5
70	437073	AJ885608	Hs.94122	ESTs	3.5
	427287	NM_014903	Hs.174188	KIAA0938 protein	3.5
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	3.5
	450235	AA007512	Hs.17538	ESTs	3.5
	447263	AW965667	Hs.322406	hypothetical protein FLJ14494	3.5
75	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	427254	AL121523	Hs.97774	ESTs	3.5
	434348	BE393191	Hs.181795	putative b,b-carotene-9',10'-dioxygenase	3.5
	441264	AA927170	Hs.23290	ESTs	3.5
	433629	R13140	Hs.13359	ESTs	3.5
80	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
	441585	AJ760755	Hs.202383	ESTs	3.5
	438704	AJ435060	Hs.32825	ESTs	3.5
	445279	R41900	Hs.22245	ESTs	3.4
	415114	D60468	Hs.94181	ESTs	3.4
	449561	AJ022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.4
	416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26S subu	3.4

5	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.4
	450928	AJ744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	3.4
	457012	R41480	Hs.302754	ESTs	3.3
10	405354			CX000321:gil6671579[ref]NP_031518.1] ari	3.3
	408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	3.3
	418525	AW450369	Hs.86937	ESTs	3.3
	420174	AJ824144	Hs.23912	ESTs	3.3
	437124	AA554458	Hs.279860	KIAA0666 protein	3.3
15	419211	BE270817	Hs.37617	ESTs, Weakly similar to A53933 myosin I	3.3
	424335	AW021508	Hs.28170	ESTs	3.3
	453344	BE349075	Hs.44571	ESTs	3.3
	428065	AJ634046	Hs.157313	ESTs	3.3
	417248	AA329449	Hs.247302	twisted gastrulation	3.3
20	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.3
	411393	AW797437	Hs.69771	B-factor, properdin	3.3
	406976	M60299		gb:Human alpha-1 collagen type II gene,	3.3
	441071	D79550	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.3
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	3.3
25	433703	AA210863	Hs.3532	nemo-like kinase	3.3
	418880	N87353	Hs.89421	CBF1 interacting corepressor	3.3
	445947	AW612084	Hs.298494	ESTs	3.3
	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	3.3
	434795	BE620794	Hs.4147	translocating chain-associating membrane	3.2
30	400127			Eos Control	3.2
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	3.2
	402429			Target Exon	3.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.2
	427699	AW965076	Hs.180378	hypothetical protein 669	3.2
35	403442			Target Exon	3.2
	419272	AA663904	Hs.89862	TNFRSF1A-associated via death domain	3.2
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	3.2
	407581	R48402	Hs.173508	P3ECSL	3.2
	412633	AF001691	Hs.74304	periplakin	3.2
40	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
	449294	AJ651786	Hs.195045	ESTs	3.1
	442799	AJ564739	Hs.68505	ESTs	3.1
	434045	AJ065133	Hs.152316	hypothetical protein PRO0971	3.1
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.1
45	420033	D59502	Hs.292590	ESTs	3.1
	422137	AJ236885	Hs.112180	zinc finger protein 148 (pH2-52)	3.1
	444760	AJ796296	Hs.208062	ESTs	3.1
	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	3.1
	411359	H86088	Hs.22635	ESTs	3.1
50	443037	AW500305	Hs.8906	syntaxin 7	3.1
	407127	R45970	Hs.236349	EST	3.1
	416851	AW963951	Hs.85618	ESTs	3.1
	416838	D84109	Hs.80248	RNA-binding protein gene with multiple s	3.1
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.1
55	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1
	433582	BE548749	Hs.148016	ESTs	3.1
	431128	AJ203545	Hs.296169	S-phase response (cyclin-related)	3.1
	420411	AJ581085	Hs.24678	sphingosine-1-phosphatase	3.1
60	459584	AJ910884	Hs.346429	ESTs	3.1
	449883	AJ004464	Hs.344156	gb:ot56e06.s1 Soares_testis_NHT Homo sap	3.1
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	3.1
	410786	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	3.1
	418207	C14685	Hs.34772	ESTs	3.0
65	420521	AJ915734	Hs.87298	ESTs	3.0
	425890	H24530	Hs.273294	hypothetical protein FLJ20069	3.0
	416749	AW068550.comp	Hs.79732	fibulin 1	3.0
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.0
	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.0
70	415672	N53097	Hs.193579	ESTs	3.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AJ824977	Hs.145319	ESTs	3.0
	404091			Target Exon	3.0
	406085			Target Exon	3.0
75	438825	BE327427	Hs.79953	ESTs	3.0
	457441	BE467737	Hs.146125	ESTs	3.0
	403512			C3000579:gil12643308[sp]Q9Y4K1[AI]M1_HUM	3.0
	416866	AA297356	Hs.80324	serine/threonine protein phosphatase cat	3.0
	439877	H39685	Hs.250700	tryptase beta 1	3.0
80	441984	AB037763	Hs.8059	synaptotagmin IV	3.0
	436765	AB028952	Hs.5307	synaptopodin	3.0
	445071	AJ280246	Hs.149504	ESTs	3.0
	404333			C7001735:gil7768636[dbj]BAA95483.1] (AB	3.0
	422907	AJ879263	Hs.77273	Human glucose transporter pseudogene	3.0
	413266	BE300352		gb:600944231F1 NIH_MGC_17 Homo sapiens c	3.0
	429393	AA383024	Hs.201603	Homo sapiens mRNA: cDNA DKFZp434D0917 (f	3.0
	415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	3.0

	415044	AA419108	Hs.77840	annexin A4	2.9
	403469			Target Exon	2.9
5	416928	AA190573	Hs.85902	ESTs, Weakly similar to MCHU catmodulin	2.9
	430195	AW969308	Hs.188594	ESTs	2.9
	458544	AB310336	Hs.196843	ESTs	2.9
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.9
	424641	AB001106	Hs.151413	gla maturation factor, beta	2.9
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	2.9
10	405403			Target Exon	2.9
	452197	AW023595	Hs.232048	ESTs	2.9
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp76202215 (f	2.9
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	2.9
	404559			Target Exon	2.9
15	406270			Target Exon	2.9
	422190	H17399	Hs.11506	Human clone 23589 mRNA sequence	2.9
	431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	420286	A1796395	Hs.111377	ESTs	2.9
	422964	AW439476	Hs.256895	ESTs	2.9
20	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.9
	428595	AB037795	Hs.186547	KIAA1374 protein	2.9
	402198			NM_024323:Homo sapiens hypothetical prot	2.9
	416246	U47413	Hs.79101	cyclin G1	2.9
	427593	AK001132	Hs.179752	Homo sapiens cDNA FLJ10270 fis, clone HE	2.9
25	446351	AW444551	Hs.35380	x 001 protein	2.9
	440432	A239637	Hs.202653	ESTs, Weakly similar to T14267 Xln prote	2.9
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	2.8
	400965			C11002190:gi12737279[ref]XP_012163.1]	2.8
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	2.8
30	458793	N80159	Hs.121849	microtubule-associated proteins 1A/18 li	2.8
	406810	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	2.8
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	2.8
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis 1	2.8
	418745	AW882645	Hs.88044	sprouty (Drosophila) homolog 1 (antagoni	2.8
35	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	2.8
	425580	L11144	Hs.1907	galanin	2.8
	416233	AA176633		gb:zp13g01.s1 Stratagene fetal retina 93	2.8
	438219	AB16151	Hs.257194	ESTs	2.8
40	404661			C9000306:gi12737280[ref]XP_006682.2] k	2.8
	435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	2.8
	423665	BE167153	Hs.24380	ESTs	2.8
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	2.8
	401783			NM_003771*:Homo sapiens keratin, hair, a	2.8
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	2.8
45	447271	AL041747	Hs.170261	ESTs	2.8
	438913	AI380429	Hs.172445	ESTs	2.8
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.8
	444385	BE278964	Hs.11085	CGI-111 protein	2.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.8
50	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	2.8
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	2.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.8
	439556	AI623752	Hs.163603	ESTs	2.8
	405474			NM_001093*:Homo sapiens acetyl-Coenzyme	2.8
55	426208	AI370379	Hs.132216	ESTs	2.8
	419461	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	2.8
	428501	AL041162	Hs.98587	ESTs	2.8
	413427	U31120	Hs.845	interleukin 13	2.8
	433109	N58907	Hs.162430	EST	2.8
60	427974	BE093023	Hs.188767	ESTs	2.8
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.8
	453994	BE180964	Hs.165590	ribosomal protein S13	2.8
	459171	AW967801	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	2.8
	404845			C22000163:gi10242166[gb]AAG15318.1[AF2	2.8
65	408182	AA047854		gb:z49g04.r1 Soares retina N2b4HR Homo	2.8
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibitor	2.7
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.7
	432815	Z30045	Hs.293676	ESTs	2.7
	404036			Target Exon	2.7
70	418157	W99382	Hs.283709	lipopolysaccharide specific response-7 p	2.7
	426403	NM_000361	Hs.2030	thrombomodulin	2.7
	439659	AW970780	Hs.59483	Homo sapiens cDNA FLJ14471 fis, clone MA	2.7
	443932	AW888222	Hs.9973	tensin	2.7
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	2.7
75	419269	AA235838		gb:zs41b04.s1 Soares_NhHMPu_S1 Homo sapi	2.7
	416004	D11880	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	2.7
	430371	D87466	Hs.240112	KIAA0276 protein	2.7
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
	451007	H38108	Hs.32759	ESTs	2.7
80	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	2.7
	406308			NM_025192:Homo sapiens hypothetical prot	2.7
	413208	BE071799		gb:RC0-BT0522-071299-011-b10 BT0522 Homo	2.7
	421420	AI024236	Hs.123296	ESTs, Weakly similar to PEC1_HUMAN PLATE	2.7
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	2.7

	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	2.7
	410538	AW753115		gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.7
	448072	AA459306	Hs.24908	ESTs	2.7
5	420912	AW853156	Hs.90787	ESTs	2.7
	453830	AA534296	Hs.20953	ESTs	2.7
	457791	AW117431	Hs.191906	ESTs	2.7
	417735	AA188175	Hs.82506	KIAA1254 protein	2.7
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.7
10	417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.7
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.7
	440945	AW505345	Hs.7540	I-box and leucine-rich repeat protein 3A	2.7
	425826	U97698		mucin 6, gastric	2.7
	422795	AB033109	Hs.120866	KIAA1283 protein	2.7
15	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
	414272	AI651603	Hs.46988	ESTs	2.7
	418047	R37633	Hs.4847	ESTs	2.7
	421089	AB037771	Hs.101799	KIAA1350 protein	2.7
	419763	AI039691	Hs.127486	ESTs	2.7
20	459265	AJ003616		gb:AJ003616 Selected chromosome 21 cDNA	2.7
	410970	AW812151		gb:RC5-ST0178-081099-011-A06 ST0178 Homo	2.7
	401925	N98378		sialyltransferase 1 (beta-galactoside al	2.7
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (I	2.6
	433789	AA220977		gb:zr01a08.r1 Stratagene NT2 neuronal pr	2.6
25	418308	AA215738	Hs.182514	ESTs, Weakly similar to A46010 X-linked	2.6
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO	2.6
	406299			Target Exon	2.6
	422963	M79141	Hs.13234	ESTs	2.6
	441244	BE612935	Hs.184052	PP1201 protein	2.6
30	439954	AL046748	Hs.6790	DnaJ (Hsp40) homolog, subfamily B, membe	2.6
	405088			Target Exon	2.6
	404741			Target Exon	2.6
	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.6
	439103	AF085959	Hs.38705	ESTs	2.6
35	437241	AL137318	Hs.306450	Homo sapiens mRNA; cDNA DKFZp434L171 (fr	2.6
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	2.6
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.6
	427229	AI799751	Hs.5635	ESTs	2.6
	414630	BE410857	Hs.16064	gb:601301177F1 NIH_MGC_21 Homo sapiens c	2.6
40	406744	AA554082	Hs.279860	tumor protein, translationally-controlled	2.6
	443984	AI424415	Hs.143719	ESTs	2.6
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	2.6
	421709	AA159394	Hs.107056	CED-6 protein	2.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	2.6
45	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.6
	419567	AW339890	Hs.128187	ESTs	2.6
	421922	AW295043	Hs.109590	genethonin 1	2.6
	421859	AA356620	Hs.108947	KIAA0050 gene product	2.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.6
50	444843	AA400172		gb:zu69e01.r1 Soares_testis_NHT Homo sap	2.6
	416729	U46165	Hs.1027	Ras-related associated with diabetes	2.6
	439238	N47305	Hs.302161	ESTs	2.6
	439183	AW970600	Hs.303261	ESTs	2.6
	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	2.6
55	412061	AA833763	Hs.330211	ESTs	2.6
	432114	AL036021	Hs.8934	ESTs	2.6
	425337	AA355442	Hs.169054	ESTs	2.6
	424299	AK000377	Hs.82294	homolog of mouse C2PA	2.6
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.6
60	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.6
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	2.6
	410429	AA310600	Hs.63657	peptide:N-glycanase similar to yeast PNG	2.6
	449251	AW151660	Hs.31444	ESTs	2.6
	436546	AW023329	Hs.132743	ESTs	2.6
65	450546	AA010200	Hs.175551	ESTs	2.6
	437255	R58970	Hs.9887	ESTs	2.6
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.6
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	2.5
	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	2.5
70	423763	R98203	Hs.132724	nuclear transcription factor Y, alpha	2.5
	413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo	2.5
	415590	T74068	Hs.170081	gb:yc81f07.r1 Soares infant brain 1N1B H	2.5
	406215			Target Exon	2.5
	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.5
75	424310	AA338648	Hs.50334	testes development-related NYD-SP22	2.5
	442097	AW015799	Hs.128474	ESTs	2.5
	456650	AA620501	Hs.106773	ESTs, Weakly similar to T42689 hypotheti	2.5
	413231	D87461	Hs.75244	BCL2-like 2	2.5
	457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	2.5
80	444942	AW293458	Hs.283807	chromosome 11 open reading frame 16	2.5
	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fs, clone MA	2.5
	435712	AA694607	Hs.176956	ESTs	2.5
	436624	T64297		fatty acid binding protein 1, liver	2.5
	443155	R54485	Hs.23772	ESTs	2.5

5	425907	AA365752	Hs.155965	ESTs	
	414759	AW295157	Hs.47587	ESTs	2.5
	414899	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	2.5
	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	2.5
	404492			C80000677:gi10432400 embjCAC10290.1 (A	2.5
	425153	AW023193	Hs.27046	ESTs	2.5
	426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.5
	434803	AW974640	Hs.303413	ESTs	2.5
10	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.5
	433069	X76732	Hs.3164	nucleobindin 2	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	424823	NM_006226	Hs.153322	phosphatase C, epsilon	2.5
	456972	AI054347	Hs.2017	ribosomal protein L38	2.5
15	431405	AI470895	Hs.334895	ribosomal protein L10a	2.5
	427982	NM_016156	Hs.181326	KIAA1073 protein	2.5
	412831	AA121352	Hs.143314	ESTs	2.5
	437114	AA836641	Hs.163085	ESTs	2.5
	426157	AA370977	Hs.345728	STAT induced STAT inhibitor 3	2.5
20	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fs, clone HE	2.5
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	2.5
	453572	AA382590	Hs.46366	KIAA0948 protein	2.5
25	TABLE 23B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
30	Pkey	CAT Number	Accession		
	408182	104479_1	AA047854 AA057506 AA053841		
	409856	1156268_1	AW502082 AW502979 AW502807 AW501876		
	410509	1206699_1	AW840743 AW752404 HA3469		
	410538	1207341_1	AW753115 AW753113 R45779		
35	410786	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422		
	410970	1228131_1	AW812151 AW812186 AW812166		
	411426	1245515_1	BE141714 AW845993 AW845989		
	411906	1265204_1	AW875765 H50294 AW875444		
40	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413		
			AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985		
			BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW866475 BE160433 J05211 BE082576 BE082584 BE004047		
			AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516		
			AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145		
45			BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 CD4715 W39488		
			AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859		
			AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690		
			T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767		
			H93284 AA026863 AW177787 AA026854 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592		
50			AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181		
			BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417		
			AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451		
			AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381		
			AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383		
55			AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435		
			AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892		
			T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182		
			AW015480 AW771865 AI270027 AA961816 AA263207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281		
			W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878		
60	413208	1353610_1	BE071799 BE071804 BE071798		
	413266	1356260_1	BE300352 BE299274 BE075351 BE297444		
	413282	1358147_1	BE078159 BE078276 BE078163 BE078277 BE078279 BE078158		
	413493	1373555_1	BE144444 BE144430		
	415606	1540470_1	W70022 R35201 F12763 T74725 H63485 Z45782 H61126		
	415666	1543492_1	H72693 R08673 H72694 F20990 R08580		
65	416233	158010_1	AA176633 AW961842 AA309418		
	419269	183444_1	AA235838 BE180775		
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961		
	425826	25682_1	U97698 AW815264 AI791966 AI732669 AA588236 AI521662 AI804760 AI955717 AW292169 AI468227 AI420483 AA603459 AI868225 AI919551		
	431300	331217_1	AA502346 BE159863		
	433789	37421_1	AA220977 AF091029 AA701227		
70	433921	377350_1	AA618174 AI114549 R36464 R36465		
	436624	4237_5	T64297 AA894931 NM_001443 M10050 AW843109 AI698516 T53219 T48785 T64166 AA706930 T29613 T55913 T56518 T64679 R29666 M10617		
			AI768596 AA101894 W90338 AI742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121		
			AW842284		
75	444843	62260_1	AA400172 AA400146 AV651691		
	445797	650943_1	AI253414 AI366014 R34822		
	447135	70963_1	T58148 AW516579 AW059603		
	449901	818599_1	AI674072 BE268487		
	450928	851593_1	AI744417 R91614 H77365		
80	452351	91233_1	AA025647 R45716 AW753786		
	455040	1250028_1	AW852286 AW851934 AW852096 AW852274		
	456235	168686_1	AA203637 AA832266 H67452		
	457297	313764_1	AW968188 AA468196 AA468269 AA468298		
	459265	966590_1	AJ003616 AJ003654 AJ003617		

TABLE 23C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400965	7770576	Minus	173043-173564
401507	7534110	Plus	71055-71259
401600	4388746	Minus	27363-27518,28727-28891,29526-29731
401783	7249190	Plus	139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283
401925	3892083	Minus	138252-138469,140239-140364,140437-140598,141037-141193,141925-142007,142787-143230
402198	8576116	Plus	79041-79191
402364	9454515	Minus	54983-55240,56507-56785,56982-57365
402429	9796372	Minus	57622-57793,59282-59402,59624-59827
403442	7210003	Plus	174560-175270
403469	9929739	Minus	4831-7707
403488	9966615	Minus	12450-12753
403512	7656757	Minus	114487-114610
403890	7710561	Plus	83165-83350
404036	8567760	Minus	65247-67529,112537-114863
404091	7684554	Minus	82121-83229
404333	9802821	Minus	137948-138024,138111-138300
404492	8123400	Minus	138612-138803
404559	8748893	Minus	73499-73651,89575-89739
404606	9212936	Minus	22310-23269
404661	9797073	Plus	33374-33675,33769-34008
404741	8574139	Plus	143025-143467
404845	7958980	Minus	47174-47326,52928-53146,53312-53602
405088	8072518	Minus	115690-117621
405354	2642452	Plus	52213-53089
405403	6850244	Minus	37491-37670,40951-41031
405474	8439781	Plus	172005-172175
405586	5002511	Plus	38810-39017
405670	4662655	Plus	96543-96870
405674	4589984	Plus	68302-68429
406085	9123888	Plus	18665-18843
406215	7342161	Plus	310-432
406270	7534217	Plus	13136-13591
406299	5686278	Minus	35655-36119
406308	9211532	Plus	358408-358651

TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile tumor to 85th percentile normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
431917	D16181	Hs.2868	peripheral myelin protein 2	75.2
427343	A1880044	Hs.176977	protein kinase C binding protein 2	74.6
455601	A1368680	Hs.816	SRY (sex determining region Y)-box 2	74.2
428321	A1699994	Hs.2868	peripheral myelin protein 2	71.6
412719	AW016610	Hs.129911	ESTs	70.7
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	66.3
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-l	64.3
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	60.1
456759	BE259150	Hs.127792	delta (Drosophila)-like 3	52.3
435147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFp761C1712 (f	46.7
425842	A1587490	Hs.159623	NK-2 (Drosophila) homolog B	40.1
412733	AA984472	Hs.74554	KIAA0080 protein	39.0
418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	38.7
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	37.2
423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFp761J1324 (f	36.8
413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	31.8
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	31.8
436878	BE465204	Hs.47448	ESTs	31.4
426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	30.9
425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	30.4
446711	AF169692	Hs.12450	protocadherin 9	30.2
439415	F05538	Hs.12825	ESTs	28.3
430838	N46664	Hs.169395	hypothetical protein FLJ12015	26.9
429466	M85835	Hs.12827	ESTs	25.9

	447004	AW296968	Hs.157539	ESTs	
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	25.3
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (tr	24.8
5	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.8
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	24.3
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	24.3
	450133	AW969769	Hs.105201	ESTs	24.2
	408562	AI436323	Hs.311141	Homo sapiens mRNA for KIAA1568 protein,	23.3
10	448672	AI955511	Hs.225106	ESTs	22.7
	435708	AI362949	Hs.75169	ESTs	22.0
	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	21.9
	407168	R45175	Hs.117183	ESTs	21.7
	431019	NM_005249	Hs.2714	forkhead box G1B	21.5
15	409049	AI423132	Hs.146343	ESTs	21.4
	433896	AW294729	Hs.274461	ESTs	21.1
	445041	T64183	Hs.282982	solute carrier	21.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	20.4
	444378	R41339	Hs.12569	ESTs	20.0
20	411305	BE241596	Hs.69547	myelin basic protein	19.9
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	19.8
	441016	AW138653	Hs.25845	ESTs	19.6
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	18.5
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	18.4
25	452461	N78223	Hs.108106	transcription factor	18.1
	409395	U46745	Hs.54435	dystrobrevin, alpha	18.0
	417183	R52089	Hs.172717	ESTs	18.0
	409638	AW450420	Hs.21335	ESTs	17.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	16.9
30	449611	AI970394	Hs.197075	ESTs	16.6
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	16.6
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.8
	444471	AB020684	Hs.11217	KIAA0877 protein	16.7
	421659	NM_014459	Hs.106511	protocadherin 17	16.6
35	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	16.6
	428276	AF056085	Hs.198612	G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
	441440	AI807981	Hs.30495	ESTs	15.7
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	15.7
40	421264	AL039123	Hs.103042	microtubule-associated protein 1B	15.5
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885	Hs.117183	ESTs	15.1
	424945	AI221919	Hs.173438	hypothetical protein FLJ10582	14.9
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	14.9
45	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
	416857	AA188775	Hs.292453	ESTs	14.7
	419721	NM_001650	Hs.288650	aquaporin 4	14.6
	411078	AI222020	Hs.182364	CocoaCrisp	14.4
	453924	R49295	Hs.24886	ESTs	14.4
50	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	14.3
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266	N59006	Hs.26133	ESTs	14.0
	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	14.0
55	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	14.0
	439239	AI031540	Hs.235331	ESTs	14.0
	441497	RS1064	Hs.23172	ESTs	14.0
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypothesi	14.0
	414245	BE148072	Hs.75850	WAS protein family, member 1	13.7
60	429900	AA460421	Hs.30875	ESTs	13.6
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	449605	AW138581	Hs.198416	ESTs	13.6
	452526	W38537	Hs.280740	hypothetical protein MGC3040	13.6
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	13.3
65	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	13.3
	420077	AW512260	Hs.87767	ESTs	13.2
	424120	T80579	Hs.290270	ESTs	13.2
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	13.2
	423361	AW170055	Hs.47628	ESTs	13.1
70	428409	AW117207	Hs.98523	ESTs	12.9
	417160	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	12.6
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	12.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
	436954	AA740151	Hs.130425	ESTs	12.4
75	430691	C14187	Hs.103538	ESTs	12.4
	433551	AI985544	Hs.12450	protocadherin 9	12.2
	422544	AB018259	Hs.118140	KIAA0716 gene product	12.2
	427540	R12014	Hs.20976	ESTs	12.1
	435624	AF218942	Hs.24889	formin 2	12.1
80	415849	R20529	Hs.6806	ESTs	12.1
	428845	AL157579	Hs.153610	KIAA0751 gene product	11.9
	442671	AI005668	Hs.134779	EST	11.9
	444396	T65213	Hs.4257	ESTs	11.8
	452752	AW044058	Hs.33578	KIAA0820 protein	

	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
5	428976	AL037824	Hs.194695	ras homolog gene family, member 1	11.6
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	11.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	11.6
	414214	D49958	Hs.75819	glycoprotein MGA	11.5
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
	405238				11.4
10	420362	U79734	Hs.97206	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	11.4
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
	451952	AL120173	Hs.301663	ESTs	11.3
15	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AJ381028	Hs.118769	ESTs	11.3
	429918	AW873986	Hs.119383	ESTs	11.3
	443912	R37257	Hs.184780	ESTs	11.3
20	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092	AA814043	Hs.88045	ESTs	11.2
	408081	AW451597	Hs.167409	ESTs	11.2
	411642	NM_014932	Hs.71132	neurotigin 1	10.9
25	415170	R44386	Hs.164578	ESTs	10.9
	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	10.7
30	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	10.7
	447773	AJ423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
	440684	AJ253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	10.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
35	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3
	440471	AA886146	Hs.307944	ESTs	10.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.1
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	10.1
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AJ538323	Hs.52620	integrin, beta 8	9.8
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
45	436511	AA721252	Hs.291502	ESTs	9.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	9.7
	449539	W80363	Hs.58446	ESTs	9.7
	412959	D87458	Hs.75090	KIAA0282 protein	9.6
	412811	H06382	Hs.21400	ESTs	9.6
50	449300	AJ656959	Hs.222165	ESTs	9.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
	451516	AJ800515	Hs.12024	ESTs	9.4
55	422656	AJ870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	9.3
	414175	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	9.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	9.2
60	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
	424641	AB001106	Hs.151413	glia maturation factor, beta	9.1
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9.1
	408508	AJ806109	Hs.135736	KIAA1580 protein	9.0
65	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	9.0
	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	8.9
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
70	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	8.8
	400292	AA250737	Hs.72472	ESTs	8.7
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	8.7
	420345	AW295230	Hs.25231	ESTs	8.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	8.7
75	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	400780				8.6
	434891	AA814309	Hs.123583	ESTs	8.6
80	449277	AA001064	Hs.172976	ESTs	8.6
	415709	AA649850	Hs.278558	ESTs	8.5
	439947	AB006627	Hs.6788	astrotactin	8.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11650 fis, clone HE	8.4

	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	8.4
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothe	8.4
	415796	R87548	Hs.78854	ATPase, Na ⁺ /K ⁺ transporting, beta 2 poly	8.3
5	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	8.3
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	8.3
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	8.3
	433447	U29195	Hs.3281	neuronal pentraxin II	8.3
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	8.3
10	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
	414300	AI304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
15	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	8.1
	442710	AI015631	Hs.23210	ESTs	8.1
	425048	H05468	Hs.164502	ESTs	8.1
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypothe	8.0
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neurodigin	7.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
25	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
	435501	AW051819	Hs.129908	KIAA0591 protein	7.8
	423600	AI633559	Hs.310359	ESTs	7.8
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	7.8
	415314	N88802	Hs.5422	glycoprotein M6B	7.7
30	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	7.7
	427687	AIW003867	Hs.1570	histamine receptor H1	7.7
	449328	AI962493	Hs.197647	ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.7
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
35	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
	438779	NM_003787	Hs.6414	nucleolar protein 4	7.6
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	7.6
	448555	AI536697	Hs.159863	ESTs	7.5
	439662	H97552	Hs.269060	ESTs	7.5
40	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	7.5
	410099	AA081630	Hs.169387	KIAA0036 gene product	7.5
	431592	R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	405819				7.4
45	407886	AW969688	Hs.100826	ESTs	7.4
	437416	AL359605	Hs.283851	Homo sapiens mRNA; cDNA DKFZp547G036 (fr	7.4
	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	7.4
	408604	D51408	Hs.21925	ESTs	7.4
50	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
	447499	AW262580	Hs.147674	protocadherin beta 16	7.3
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.2
	410037	AB020725	Hs.58009	KIAA0918 protein	7.2
	419318	AW969742	Hs.291005	ESTs	7.2
55	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.2
	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52620	integrin, beta 8	7.2
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	7.2
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	7.2
60	407182	AA312551	Hs.230157	ESTs	7.1
	415293	R49462	Hs.106541	ESTs	7.1
	422764	AI767727	Hs.47522	ESTs	7.1
	451592	AI805416	Hs.213897	ESTs	7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0
65	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
	434149	Z43829	Hs.19574	hypothetical protein MGC5469	7.0
	436726	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypothe	7.0
	417632	R20855	Hs.5422	glycoprotein M6B	7.0
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	6.9
70	435267	N23797	Hs.110114	ESTs	6.9
	437117	AL049256	Hs.122593	ESTs	6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
	445745	AB007924	Hs.13245	KIAA0455 gene product	6.9
75	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.9
	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	6.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.7
	443297	AI049864	Hs.133029	ESTs	6.7
80	443992	AW022228	Hs.322922	ESTs	6.7
	453096	AW294631	Hs.11325	ESTs	6.7
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	6.7
	443761	AI525743	Hs.160603	ESTs	6.6
	429609	AF002246	Hs.210883	cell adhesion molecule with homology to	6.6

	435056	AW023337	Hs.5422	glycoprotein M6B	6.5
	453431	AF094754	Hs.32973	glycine receptor, beta	6.5
	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	6.5
5	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.5
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805	L10333	Hs.99947	reticulin 1	6.4
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	6.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407866	AW088232	Hs.89506	paired box gene 6 (aniridia, keratitis)	6.3
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
	445102	AW204610	Hs.22270	ESTs	6.2
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	6.2
15	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	6.2
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
20	419347	C15944	Hs.90005	superiorocervical ganglia, neural specifi	6.1
	424997	AL138167	Hs.96920	ESTs	6.1
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (-)	6.1
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.1
25	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0
	437034	AA742643		gb:my91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.0
	444170	AW613879	Hs.102408	ESTs	6.0
30	457183	H91882	Hs.118569	DNA-binding protein IDAX (inhibition of	6.0
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H05626	Hs.6921	ESTs	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.9
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.9
35	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	5.9
	438993	AA828995		gb:cd77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9
	447350	AJ375572	Hs.172634	ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9
40	447101	N72185	Hs.44189	ESTs	5.9
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.9
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	5.9
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	5.8
45	437036	A1571514	Hs.133022	ESTs	5.7
	412225	AW902042		gb:QVD-NN1022-170400-193-c02 NN1022 Homo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	5.7
	445828	F05802	Hs.81907	ESTs	5.7
50	447198	D61523	Hs.283435	ESTs	5.7
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	5.6
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	5.6
55	435718	R06569	Hs.269534	ESTs	5.6
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW514021	Hs.245510	ESTs	5.6
	422411	AW749443	Hs.22511	ESTs	5.6
60	438328	AJ492261	Hs.32450	ESTs	5.6
	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	5.5
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
	400859				5.5
65	413625	AW451103	Hs.71371	ESTs	5.5
	421863	AJ952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	AJ879064	Hs.54618	ESTs	5.5
	452055	AJ377431	Hs.141693	hypothetical protein MGC10858	5.5
70	430979	AJ479755	Hs.129010	ESTs	5.5
	412709	AL022327	Hs.74518	KIAA0027 protein	5.5
	439920	H05430	Hs.288433	neurotrophin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
75	419235	AW470411	Hs.288433	neurotrophin	5.4
	418030	BE207573	Hs.83321	neuromedin B	5.4
	410330	AW023630	Hs.46786	ESTs	5.4
	410781	AJ375672	Hs.165028	ESTs	5.4
	420658	AW965215	Hs.336656	ESTs	5.4
80	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4
	443740	R56434	Hs.21062	ESTs	5.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	5.4
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	5.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4

5	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.4
	424432	AB037821	Hs.146858	protocadherin 10	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
10	404584				5.3
	430091	AB032958	Hs.233023	KIAA1132 protein	5.3
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	5.3
	424001	W67883	Hs.137476	paternally expressed 10	5.3
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitter)	5.3
15	426625	T78300	Hs.300642	serologically defined colon cancer antigen	5.3
	428137	AA421792	Hs.170999	ESTs	5.3
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.3
	438176	AW138970	Hs.122113	ESTs	5.3
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.3
20	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340	N31772	Hs.79226	fasciculation and elongation protein zeta	5.3
	435244	N77221	Hs.187824	ESTs	5.3
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
25	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillator	5.3
	430437	A1768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.2
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian)	5.2
	453941	U39817	Hs.36820	Bloom syndrome	5.2
	424998	U58515	Hs.154138	chitinase 3-like 2	5.2
30	423419	R55336	Hs.23539	ESTs	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	5.2
	408206	AF041853	Hs.43670	kinesin family member 3A	5.2
	421013	M62397	Hs.1345	mutated in colorectal cancers	5.2
35	429443	AB028967	Hs.202687	potassium voltage-gated channel, Shal-re	5.2
	434367	AB020700	Hs.3830	KIAA0893 protein	5.2
	444861	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	5.2
	446142	A1754693	Hs.145968	ESTs	5.2
	448816	AB033052	Hs.22151	KIAA1226 protein	5.2
40	451050	AW937420	Hs.69662	ESTs	5.2
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related	5.2
	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
	416737	AF154335	Hs.79691	LIM domain protein	5.2
	424800	AL035588	Hs.153203	MyoD family inhibitor	5.2
45	443695	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	5.2
	415257	F03016	Hs.27513	ESTs	5.2
	433929	A1375499	Hs.27379	ESTs	5.1
	415651	A1207162	Hs.3815	stathmin-like-protein RB3	5.1
	451027	AW519204	Hs.40808	ESTs	5.1
50	409172	Z99399	Hs.118145	ESTs	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	429172	AA447417	Hs.285491	ESTs	5.1
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	5.1
	451270	AW341392	Hs.235795	ESTs	5.1
55	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 f1	5.1
	420560	AW207748	Hs.59115	ESTs	5.1
	418097	R45137	Hs.21868	ESTs	5.1
	442910	A1365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.1
	434849	AW292765	Hs.8053	ESTs	5.1
60	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.1
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	5.0
	413627	BE182082	Hs.246973	ESTs	5.0
	418661	NM_001949	Hs.1189	E2F transcription factor 3	5.0
65	422438	AA445925	Hs.270896	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
	435087	AW975241	Hs.23567	ESTs	5.0
	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (5.0
70	410434	AF051152	Hs.63668	tol-like receptor 2	4.9
	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	4.9
	407808	AA663559	Hs.279789	histone deacetylase 3	4.9
	418940	H17739	Hs.288513	Human DNA sequence from clone RPS-899C14	4.9
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.9
75	426814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
	447112	H17800	Hs.7154	ESTs	4.9
	449574	F05048	Hs.175373	ESTs	4.9
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	4.9
	423869	BE409301	Hs.134012	C1q-related factor	4.9
80	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.9
	449176	A1633545	Hs.198072	ESTs	4.9
	448451	AW015994		gb:UH-H-B10p-abh-g-09-0-UI.s1 NCI_CGAP_S	4.8
	402604				4.8
	436039	AW023323	Hs.121070	ESTs	4.8
	448769	N66037	Hs.38173	ESTs	4.8
	423678	AW963357	Hs.7847	ESTs	4.8
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.8

	425870	R13406	Hs.56782	ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
	413409	AJ638418	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.8
5	413623	AA825721	Hs.246973	ESTs	4.8
	417246	AI760098	Hs.21411	ESTs	4.8
	420900	AL045633	Hs.44269	ESTs	4.8
	424153	AA451737	Hs.141496	MAGE-like 2	4.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALLU6_HUMAN A	4.8
	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
10	454030	AW021429	Hs.231980	ESTs	4.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.8
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	4.8
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956	AI374651	Hs.22542	ESTs	4.7
	435060	AI422719	Hs.233349	ESTs, Weakly similar to fork head like p	4.7
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7
	449353	AA001220	Hs.271369	ESTs	4.7
	452022	AW072330	Hs.293875	ESTs	4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
	404541				4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125	R17268	Hs.259873	axonal transport of synaptic vesicles	4.7
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.6
30	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.6
	413492	D87470	Hs.75400	KIAA0280 protein	4.6
	419629	AB020695	Hs.91662	KIAA0888 protein	4.6
	407638	AJ040467	Hs.334483	hypothetical protein FLJ23571	4.6
	436140	W87355	Hs.269587	ESTs	4.6
35	439169	AI912122	Hs.41095	ESTs	4.6
	443150	AI034467	Hs.34650	ESTs	4.6
	451073	AI758905	Hs.206063	ESTs	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
	452106	AI141031	Hs.21342	ESTs	4.6
40	451407	AA131376	Hs.326401	fibroblast growth factor 12B	4.6
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	4.6
	437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	4.6
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.5
45	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5
	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	4.5
	419343	AA456245	Hs.85603	down-regulated by Ctnnb1, a	4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
	429399	AA452244	Hs.16727	ESTs	4.5
50	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
	453118	AW195849	Hs.252757	ESTs	4.5
	443455	AB001025	Hs.9349	ryanodine receptor 3	4.4
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	4.4
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
55	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.4
	435202	AI971313	Hs.170204	KIAA0551 protein	4.4
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4
	451254	AI571016	Hs.172967	ESTs	4.4
60	439039	AI656707	Hs.48713	ESTs	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	AI742434	Hs.169911	ESTs	4.4
	410611	AW954134	Hs.20924	KIAA1628 protein	4.4
65	402605				4.4
	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222	AI061301	Hs.164773	ESTs	4.4
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.4
70	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	4.4
	442832	AW206560	Hs.253569	ESTs	4.4
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279	AW959861	Hs.290943	ESTs	4.3
	427194	AA399018	Hs.250835	ESTs	4.3
	419723	AL120193	Hs.92614	longevity assurance (LAG1, S. cerevisiae	4.3
75	445810	AW265700	Hs.155660	ESTs	4.3
	409734	BE161664	Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	4.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.3
	433024	AA573847	Hs.26549	KIAA1708 protein	4.3
80	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	4.3
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.3
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3
	444600	R41398	Hs.6996	ESTs	4.3

	454042	H22570	Hs.172572	hypothetical protein FLJ20093	4.3
	441899	AI372588	Hs.8022	TU3A protein	4.3
	425256	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
5	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
	430291	AV660345	Hs.238126	CGI-49 protein	4.2
	433597	AA708205	Hs.100343	ESTs	4.2
	444127	N63620	Hs.13281	ESTs	4.2
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	4.2
10	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833.1 noncl	4.2
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.2
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	4.2
	428536	AI143139	Hs.2288	visinin-like 1	4.2
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
15	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	4.2
	447138	AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.2
	450648	AI703366	Hs.26766	ESTs	4.2
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2
	421686	AB011156	Hs.106794	KIAA0584 protein	4.2
20	452776	AA194540	Hs.13522	ESTs, Weakly similar to I38022 hypotheti	4.2
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp43480650 (f	4.2
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.2
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.2
25	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
	439607	BE540565	Hs.159460	ESTs	4.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	4.1
	446936	H10207	Hs.47314	ESTs	4.1
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.1
30	412446	AI768015	Hs.92127	ESTs	4.1
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.1
	419683	AA248897	Hs.48784	ESTs	4.1
	426071	AW138057	Hs.163835	ESTs	4.1
35	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.1
	432809	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039	AI922988	Hs.172510	ESTs	4.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.1
40	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433932	AW954599	Hs.169330	neuronal protein	4.1
	436537	AI783629	Hs.26766	ESTs	4.1
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.1
45	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	4.1
	410486	AW235094	Hs.69233	zinc finger protein	4.0
	413916	N49813	Hs.75615	apolipoprotein C-II	4.0
50	438703	AI803373	Hs.31599	ESTs	4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	405771				4.0
	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	4.0
	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.0
55	424176	AL137273	Hs.142307	hypothetical protein	4.0
	425773	N21279	Hs.237749	ESTs	4.0
	427304	AA761526	Hs.163853	ESTs	4.0
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	4.0
	452834	AI638627	Hs.105685	KIAA1688 protein	4.0
60	453745	AA952989	Hs.63908	hypothetical protein MGC14726	4.0
	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
65	439199	R40373	Hs.26299	ESTs	4.0
	439450	R51613	Hs.125304	ESTs	4.0
	446782	AI653048	Hs.144006	ESTs	4.0
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	4.0
	402408				3.9
70	453362	H14988	Hs.107375	ESTs	3.9
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	3.9
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	3.9
	425010	T16837	Hs.4241	ESTs	3.9
	444230	H95537	Hs.146067	ESTs	3.9
75	441736	AW292779	Hs.169799	ESTs	3.9
	418951	F07809	Hs.89506	paired box gene 6 (aniridia, keratitis)	3.9
	406311				3.9
	408460	AA054726	Hs.285574	ESTs	3.9
	410658	AW105231	Hs.192035	ESTs	3.9
80	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.9
	418849	AW474547	Hs.53565	Homo sapiens PTG-M mRNA for mannosyltran	3.9
	429477	AI275514	Hs.6658	ESTs	3.9
	433766	AA609234	Hs.112669	ESTs	3.9
	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	3.9

	447891	R41754	Hs.6496	ESTs	3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9
	404283				3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.9
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.9
	445314	AI689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.9
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9
10	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.9
	438054	AA776626	Hs.62183	ESTs	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157646	Hs.153506	ESTs	3.9
	432590	AI609273	Hs.110783	ESTs	3.9
15	453331	AI240665	Hs.8895	ESTs	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.8
	447247	AW368351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.8
20	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	3.8
	417355	D13168	Hs.82002	endothelin receptor type B	3.8
	446727	AB011095	Hs.16032	KIAA0523 protein	3.8
	424340	AA339036	Hs.7033	ESTs	3.8
25	423346	AI267677	Hs.127416	synaptotagmin 1	3.8
	412788	AA120960	Hs.198416	ESTs	3.8
	404593				3.8
	416856	N27833	Hs.269028	ESTs, Weakly similar to I38022 hypotheti	3.8
	429896	AA460367	Hs.224223	ESTs, Moderately similar to I38022 hypot	3.8
30	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	3.8
	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
	440322	AA879430		gb:q91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	447761	AF061573	Hs.19492	protocadherin 8	3.8
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	3.8
35	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.8
	447028	AI973128	Hs.167257	brain link protein-1	3.8
	449458	AI805078	Hs.208261	ESTs	3.8
40	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.8
	428841	AI418430	Hs.104935	ESTs	3.8
	430643	AW970065	Hs.287425	MEGF10 protein	3.8
	422263	AA307639	Hs.129908	KIAA0591 protein	3.8
45	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.8
	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN !	3.8
	441928	AI370188	Hs.211454	ESTs	3.8
	441797	AI936933	Hs.214635	ESTs	3.7
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.7
	425588	F07396	Hs.46751	ESTs	3.7
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
	425741	AF052152	Hs.159412	Homo sapiens clone 24528 mRNA sequence	3.7
55	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.7
	440080	AW051597	Hs.143707	ESTs	3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.7
	409234	AI879419	Hs.27206	ESTs	3.7
60	420489	AA815089	Hs.193513	ESTs	3.7
	426890	AA393167	Hs.41294	ESTs	3.7
	438849	W28948	Hs.10762	ESTs	3.7
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.7
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.7
65	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.7
	459518	AI937419	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	3.7
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL135740	Hs.102447	TSC-22-like	3.7
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.7
70	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.7
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.7
	420807	AA280627	Hs.57846	ESTs	3.7
	449961	AW265634	Hs.133100	ESTs	3.7
	422634	NM_016010	Hs.118821	CGI-62 protein	3.7
75	421030	AW161357	Hs.101174	microtubule-associated protein tau	3.7
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	3.7
	440483	AI200836	Hs.150386	ESTs	3.7
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.7
80	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.6
	425187	AW014486	Hs.22509	ESTs	3.6
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	3.6
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.6
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.6

	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	3.6
	429239	AA448419	Hs.45209	ESTs	3.6
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.6
5	446659	AJ335361	Hs.226376	ESTs	3.6
	426757	AW205640	Hs.158206	ESTs	3.6
	418819	AA228776	Hs.191721	ESTs	3.6
	458332	AJ000341	Hs.220491	ESTs	3.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.6
10	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	3.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.6
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	3.6
	425305	AA363025	Hs.155572	Human clone Z3801 mRNA sequence	3.6
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	3.6
15	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	3.6
	430530	AA480870	Hs.47660	ESTs	3.6
	436425	AB913146	Hs.318725	CGI-72 protein	3.6
	438078	AJ016377	Hs.131693	ESTs	3.6
	442927	AJ024347	Hs.131519	ESTs	3.6
20	446242	N66336	Hs.7360	ESTs	3.6
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.6
	450474	AW872844	Hs.201919	ESTs	3.6
	452198	AJ097560	Hs.61210	ESTs, Weakly similar to I38022 hypothe	3.6
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
25	436443	AW138211	Hs.128746	ESTs	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.6
	456038	AA203285	Hs.294141	ESTs, Weakly similar to alternatively sp	3.6
	408902	AW014869	Hs.5510	ESTs	3.6
	442950	AJ500417	Hs.46764	ESTs	3.6
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.6
	425478	AB007953	Hs.268840	ESTs	3.6
	453884	AA355925	Hs.36232	KIAA0186 gene product	3.6
	404721				3.6
	408453	AJ369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
35	440553	AA889416	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.5
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	3.5
	413999	N46124	Hs.34460	ESTs	3.5
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.5
	425017	AL119305	Hs.288405	ESTs	3.5
40	435958	H98180	Hs.117975	ESTs	3.5
	415101	R45531	Hs.144534	ESTs	3.5
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.5
	430290	AJ734110	Hs.136355	ESTs	3.5
	416836	D54745	Hs.80247	cholecystokinin	3.5
45	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.5
	419412	AW161058	Hs.90297	synuclein, beta	3.5
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.5
	452689	F33868	Hs.284176	transferrin	3.5
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	3.5
50	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypothe	3.5
	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.5
	444584	AJ168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5
	408296	AL117452	Hs.44155	DKFZP585G1517 protein	3.5
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.5
55	412659	AW753855	Hs.74376	olfactomedin related ER localized protei	3.5
	429077	AB028983	Hs.2352	adenylate cyclase 2 (brain)	3.5
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	3.5
	450784	AW246803	Hs.47289	ESTs	3.5
	446827	AW451243	Hs.157069	ESTs	3.5
60	436434	N50465	Hs.92927	putative 47 kDa protein	3.5
	412777	AJ335773	Hs.270123	ESTs	3.5
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.5
	408601	U47928	Hs.86122	protein A	3.5
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	3.4
65	448425	AJ500359	Hs.233401	ESTs	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	451729	AW160725	Hs.312469	ESTs	3.4
	435910	AJ084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.4
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.4
70	414598	AJ094221	Hs.135150	lung type-I cell membrane-associated gly	3.4
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.4
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	3.4
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (f	3.4
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.4
75	426958	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.4
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.4
	435061	AJ651474	Hs.163944	ESTs	3.4
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.4
	449714	AB033015	Hs.23941	KIAA1189 protein	3.4
80	443392	AJ055821	Hs.293420	ESTs	3.4
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.4
	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.4
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.4
	432731	R31178	Hs.287820	fibronectin 1	3.4

	448758	AB018311	Hs.21917	KIAA0768 protein	3.4
	432613	AW081698	Hs.80712	KIAA0202 protein	3.4
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
5	410108	AA081659	Hs.318775	OSBP-related protein 6	3.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	3.4
	402855				3.3
	422170	AI791949	Hs.112432	anti-Mullerian hormone	3.3
	445034	AW293376	Hs.143659	ESTs	3.3
10	424378	W28020	Hs.167988	neural cell adhesion molecule 1	3.3
	423611	AB011163	Hs.129908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	3.3
	404819				3.3
	436607	AW661783	Hs.211061	ESTs	3.3
15	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.3
	452693	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW850180		gb:FL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	3.3
20	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.3
	421192	AA833718	Hs.204529	KIAA1806 protein	3.3
	426695	AW118191	Hs.112729	ESTs	3.3
	438885	AI886558	Hs.184987	ESTs	3.3
25	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypothe	3.3
	453590	AF150278	Hs.33578	KIAA0820 protein	3.3
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.3
30	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.3
	436045	AB037723	Hs.5028	DKFZP564O0423 protein	3.3
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.3
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.3
	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3
35	443898	AW804296	Hs.9950	Sec61 gamma	3.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3
	445953	AI612775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3
40	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.3
	420549	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
	436556	AI364997	Hs.7572	ESTs	3.2
45	424369	R87622	Hs.26714	KIAA1831 protein	3.2
	457065	AI476318	Hs.192480	ESTs	3.2
	440210	AW674562	Hs.125296	ESTs	3.2
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
50	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	3.2
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
	439924	AI985897	Hs.125293	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	3.2
55	415115	AA214228	Hs.127751	hypothetical protein	3.2
	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437762	T78028	Hs.154679	synaptotagmin I	3.2
	438944	AA302517	Hs.92732	KIAA1444 protein	3.2
60	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2
	410953	AW811766	Hs.334858	hypothetical protein MGC12250	3.2
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin tyrosine ligase-like 1	3.2
65	429496	AA453800	Hs.192793	ESTs	3.2
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
	439274	AF086092	Hs.48372	ESTs	3.2
70	440847	AA907511	Hs.130178	ESTs	3.2
	447750	AI422234	Hs.143434	contactin 1	3.2
	455350	AW901809		gb:QV0-NN1020-170400-195-b02 NN1020 Homo	3.2
	430890	X54232	Hs.2699	glypican 1	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
75	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450	AB014526	Hs.178121	KIAA0626 gene product	3.2
	430456	AA314998	Hs.241503	hypothetical protein	3.2
	430181	AF065314	Hs.234785	cyclic nucleotide gated channel alpha 3	3.2
	418512	AW498974	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.2
80	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (3.2
	450689	AI389275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.2
	424899	AL119387	Hs.119062	ESTs	3.2
	436277	R88520	Hs.120917	ESTs	3.2

	451455	AI937227	Hs.8821	hepoidin antimicrobial peptide	3.2
	445078	AI869975	Hs.4775	junctophilin 3	3.2
	447746	AW015920	Hs.161359	ESTs	3.2
5	435458	F11872	Hs.4892	Homo sapiens clone 24841 mRNA sequence	3.2
	427729	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	3.2
	417417	F05745	Hs.89512	ATPase, Ca ⁺⁺ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	3.1
	421988	AW450481	Hs.161333	ESTs	3.1
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
	408786	AA773187	Hs.294027	ESTs	3.1
15	433494	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	3.1
	412723	AA648459	Hs.335951	hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439456	AI752409	Hs.109314	hypothetical protein FLJ20980	3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1
20	452780	BE171598	Hs.13522	ESTs, Weakly similar to I38022 hypothe	3.1
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1
	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.1
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	3.1
	404299				3.1
25	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.1
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566I133	3.1
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1
35	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.1
	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	3.1
	410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.1
	425491	AA883316	Hs.255221	ESTs	3.1
40	456273	AF154846	Hs.1148	zinc finger protein	3.1
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	3.1
	445255	NM_014841	Hs.12477	synaposomal-associated protein, 91 kDa	3.1
	432154	AI701523	Hs.112577	ESTs	3.1
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.1
45	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.1
	448616	AF035621	Hs.21611	kinesin family member 3C	3.0
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	3.0
	443906	AA348031	Hs.7913	ESTs	3.0
	417318	AW953937	Hs.12891	ESTs	3.0
50	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.0
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.0
55	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	422758	AF152329	Hs.284180	protocadherin gamma subfamily C, 3	3.0
	421633	AF121860	Hs.106260	sorting nexin 10	3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.0
	416805	F13271	Hs.79981	Human clone Z3560 mRNA sequence	3.0
60	419518	U79289	Hs.90798	Human clone Z3695 mRNA sequence	3.0
	422709	AA315331	Hs.153485	ESTs	3.0
	423135	N67655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	3.0
65	426617	W58006	Hs.266258	endonuclease G-like 1	3.0
	427386	AW836261	Hs.337717	ESTs	3.0
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor 1	3.0
	435071	D60683	Hs.35495	ESTs	3.0
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.0
70	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.0
	436936	AL134451	Hs.197478	ESTs	3.0
	445855	BE247129	Hs.145569	ESTs	3.0
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypothe	3.0
75	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	3.0
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.0
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.0
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	3.0
80	416874	H98752	Hs.42568	ESTs	3.0
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	424066	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypothe	3.0
	404048				3.0

	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.0
	418196	A1745649	Hs.26549	KIAA1708 protein	3.0
	434131	A1858275	Hs.143659	ESTs	3.0
5	441255	R06350	Hs.171635	ESTs	2.9
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.9
	453905	NM_002314	Hs.36566	UIM domain kinase 1	2.9
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	2.9
10	431173	AW971198	Hs.294068	ESTs	2.9
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	436401	A1087958	Hs.29088	ESTs	2.9
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.9
15	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	2.9
	433149	BE257672	Hs.42949	hypothetical protein HES6	2.9
	434811	AW971205	Hs.114280	ESTs	2.9
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
20	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.9
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.9
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	2.9
	441707	R42637	Hs.21963	hypothetical protein DKFZp76180514	2.9
25	435741	A1240668	Hs.113099	ESTs	2.9
	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypotheti	2.9
	422939	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	2.9
	439376	AA883521	Hs.222064	ESTs	2.9
	439935	S75105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
30	437267	AW511443	Hs.258110	ESTs	2.9
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	2.9
	400250				2.9
	400992				2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
35	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	2.9
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	450203	AF097994	Hs.301528	L-tyrosine/alpha-aminoadipate aminotra	2.9
40	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.9
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9
	428500	A1815395	Hs.184641	fatty acid desaturase 2	2.9
	421641	A1638184	Hs.106334	Homo sapiens clone 23836 mRNA sequence	2.9
	421141	AW117261	Hs.125914	ESTs	2.9
45	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	2.9
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.9
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9
	412190	R16180	Hs.274461	ESTs	2.9
50	446131	NM_000929	Hs.290	phospholipase A2, group V	2.9
	441668	A1611973	Hs.127525	ESTs	2.9
	437387	A1198874	Hs.28847	AD026 protein	2.9
	423420	A1571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	2.9
55	427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	2.9
	447067	R42098	Hs.21964	ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
	424126	AA335635	Hs.96917	ESTs	2.9
60	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	2.9
	447422	BE618703	Hs.98258	orthopedia (Drosophila) homolog	2.9
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.9
	446997	AA383439	Hs.16758	Spir-1 protein	2.9
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type reco	2.9
65	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.9
	419586	A1088485	Hs.144759	ESTs, Weakly similar to I38022 hypotheti	2.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	2.8
	408432	AW195262		gb:am67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.8
	420320	AB002361	Hs.96633	KIAA0363 protein	2.8
70	425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	2.8
	428670	AA431682	Hs.134832	ESTs	2.8
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.8
	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	2.8
	411555	AF113537	Hs.70669	HMP19 protein	2.8
75	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	2.8
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	2.8
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.8
	424572	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.8
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.8
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	2.8
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.8
	440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	2.8
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8
	403056	R58624	Hs.2186	eukaryotic translation elongation factor	2.8

	423449	AI497900	Hs.33067	ESTs	
	424188	AW954552	Hs.142634	zinc finger protein	2.8
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.8
5	434981	AW182577	Hs.293077	ESTs	2.8
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	2.8
	442748	AI016713	Hs.135787	ESTs	2.8
	443312	NS2025	Hs.46616	ESTs	2.8
	450940	AI744943	Hs.143209	ESTs, Weakly similar to I38022 hypothe	2.8
10	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.8
	409182	AA064970	Hs.118145	ESTs	2.8
	439793	AA018825	Hs.7934	Kruppel-like factor 4 (gut)	2.8
	432683	AW995441	Hs.10475	ESTs	2.8
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	2.8
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	2.8
15	433290	R20077	Hs.302185	Homo sapiens clone Z3618 mRNA sequence	2.8
	434276	AF123659	Hs.53605	leucine zipper, putative tumor suppresso	2.8
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.8
20	425168	R96366		gb:q37d04.s1 Soares fetal liver spleen	2.8
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.8
	409348	AI401535	Hs.146090	ESTs	2.8
	409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.8
25	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	2.8
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothesi	2.8
	434008	AA740878	Hs.112982	ESTs	2.8
	446776	AW293417	Hs.156455	ESTs	2.8
30	408838	AI669535	Hs.40369	ESTs	2.8
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	2.8
	447397	BE247676	Hs.18442	E-1 enzyme	2.8
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.8
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	2.8
35	446377	AW014022	Hs.170953	ESTs	2.8
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	2.8
	447710	AI420523	Hs.328241	ESTs	2.8
	404049				2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8
40	426400	M78361	Hs.169743	Homo sapiens clone 25121 neuronal octact	2.8
	413264	W26456	Hs.134757	hypothetical protein FLJ20033	2.8
	458997	AW937420	Hs.69662	ESTs	2.7
	422864	AA318323		gb:EST20390 Retina II Homo sapiens cDNA	2.7
45	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
	452023	AB032999	Hs.27566	KIAA1173 protein	2.7
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
	452438	BE514230	Hs.29595	JM4 protein	2.7
	435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypothesi	2.7
	418791	AA935633	Hs.194628	ESTs	2.7
50	438821	AA826425	Hs.291829	ESTs	2.7
	423464	NM_016240	Hs.128856	CSR1 protein	2.7
	442091	AW770493	Hs.182874	guanine nucleotide binding protein (G pr	2.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.7
55	412436	AA665089		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.7
	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	2.7
	416404	AA180138	Hs.107924	ESTs	2.7
	441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	2.7
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	2.7
60	426304	AA374532	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	2.7
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	2.7
	449701	AW952323	Hs.129908	KIAA0591 protein	2.7
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.7
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	2.7
	414603	RS8394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
65	416096	H18577	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.7
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.7
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.7
	436304	AA339622	Hs.108887	ESTs	2.7
	441027	AI911412	Hs.126444	ESTs	2.7
70	452545	N31940	Hs.14434	ESTs, Weakly similar to I38022 hypothesi	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	448560	BE613183	Hs.23213	ESTs	2.7
	426807	AA385315	Hs.156682	ESTs	2.7
	425825	AI929508	Hs.159590	lymphocyte antigen 6 complex, locus H	2.7
75	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.7
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.7
	427624	AA406245	Hs.24895	ESTs	2.7
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.7
80	422491	AA338548	Hs.117546	neuronatin	2.7
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	2.7
	415827	H17462	Hs.23079	ESTs	2.7
	445568	H00918	Hs.268744	KIAA1796 protein	2.7

	433315	R96754	Hs.239706	GRB2-associated binding protein 1	2.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	2.7
5	426420	BE383808	Hs.322430	NDRG family, member 4	2.7
	436899	AA764852	Hs.291567	ESTs	2.7
	444100	AA383343	Hs.221116	CDC14 (cell division cycle 14, S. cerevi	2.7
	426501	AW043782	Hs.293616	ESTs	2.7
	449092	U91641	Hs.22985	alpha2,8-sialyltransferase	2.7
10	427311	AB020672	Hs.175411	KIAA0865 protein	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	404029				2.7
	416289	W26333	Hs.337438	ESTs	2.7
	439108	AW163034	Hs.6467	synaptogyrin 3	2.6
15	418746	AI955289	Hs.300759	ribosomal protein L36	2.6
	412046	Y07847	Hs.73088	RAS-related on chromosome 22	2.6
	435040	AI932350	Hs.152825	ESTs	2.6
	453083	U87223	Hs.31622	contactin associated protein 1	2.6
	428167	AA770021	Hs.16332	ESTs	2.6
20	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.6
	443715	AI583187	Hs.9700	cyclin E1	2.6
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
	415056	AB004662	Hs.77867	adenosine A1 receptor	2.6
25	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	2.6
	433701	AW445023	Hs.15155	ESTs	2.6
	457358	AI479755	Hs.129010	ESTs	2.6
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.6
	418027	AB037807	Hs.83293	hypothetical protein	2.6
30	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16365	ESTs	2.6
	459335	AW298545	Hs.250726	EST	2.6
	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	2.6
	453169	AB037815	Hs.32156	KIAA1394 protein	2.6
35	433647	AA603367	Hs.222294	ESTs	2.6
	450414	AI907735	Hs.21446	KIAA1716 protein	2.6
	446233	AI282028	Hs.25205	ESTs	2.6
	415446	F08898	Hs.66075	ESTs	2.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	2.6
40	413012	D83777	Hs.75137	KIAA0193 gene product	2.6
	428671	BE297851	Hs.189482	zinc finger protein 179	2.6
	427158	AA935603	Hs.166231	ESTs	2.6
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.6
	459516	AI049662	Hs.246858	EST	2.6
	402693				2.6
45	408039	AA131424	Hs.50340	ESTs	2.6
	422896	AW961489	Hs.154116	ESTs	2.6
	423130	AW897586	Hs.21213	ESTs	2.6
	438796	W67821	Hs.109590	genethonin 1	2.6
50	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.6
	440192	AA872282	Hs.190596	ESTs	2.6
	419708	AK000753	Hs.92374	hypothetical protein	2.6
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434i2117	2.6
	436870	AW204219	Hs.155560	calnexin	2.6
55	448424	AW009892	Hs.31924	ESTs	2.6
	401324				2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	2.6
60	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.6
	429139	F09092	Hs.66087	ESTs	2.6
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.6
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.6
	412049	NS3437	Hs.18268	adenylate kinase 5	2.6
65	441783	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence	2.6
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.6
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.6
	453478	AF083898	Hs.33021	neuro-oncological ventral antigen 2	2.6
70	418962	AA714835	Hs.271863	ESTs	2.6
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.6
	443257	AI334040	Hs.11614	HSPC065 protein	2.6
	428748	AW593206	Hs.98785	Ksp37 protein	2.6
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.6
75	433404	T32982	Hs.102720	ESTs	2.6
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	2.6
	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	2.6
80	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	2.6
	433216	AF217412	Hs.47320	neuroigin 3	2.6
	435380	AA679001	Hs.192221	ESTs	2.6
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.6
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.6

5	419304	AI271326	Hs.146101	ESTs, Weakly similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.6
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	2.6
	435370	AI964074	Hs.225838	ESTs	2.6
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.6
	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	2.5
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	2.5
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.5
10	427951	AI826125	Hs.43546	ESTs	2.5
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.5
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451422	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-f	2.5
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.5
	428826	AL048842	Hs.194019	atractin	2.5
15	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	2.5
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.5
	429560	AW293055	Hs.119357	ESTs	2.5
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.5
20	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.5
	427513	AI476318	Hs.192480	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2.5
	417123	BE326521	Hs.159450	ESTs	2.5
25	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	412980	AI815750	Hs.20977	hypothetical protein MGC3129 similar to	2.5
	427209	H06509	Hs.92423	KIAA1566 protein	2.5
	424327	AA431707	Hs.31209	ESTs	2.5
	436340	R42246	Hs.21606	ESTs	2.5
30	450650	T65617	Hs.101257	hypothetical protein MGC3295	2.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	2.5
	400777				2.5
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.5
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.5
35	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	2.5
	432558	R97268	Hs.177269	ESTs	2.5
	400860				2.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.5
	416063	BE047699	Hs.93454	ESTs	2.5
40	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.5
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.5
	417791	AW965339	Hs.111471	ESTs	2.5
	418079	R40058	Hs.6911	ESTs	2.5
	408495	W68796	Hs.237731	ESTs	2.5
45	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.5
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.5
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.5
50	408955	BE315170	Hs.8087	NAG-5 protein	2.5
	415261	T40928	Hs.8346	ESTs	2.5
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.5
	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ111364 fis, clone HE	2.5
55	421002	AF116030	Hs.100932	transcription factor 17	2.5
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.5
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLL_HUMAN CYTOP	2.5
	427961	AW293165	Hs.143134	ESTs	2.5
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	2.5
60	428508	BE252383	Hs.184668	SBB131 protein	2.5
	428858	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.5
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	2.5
	432427	AL037630	Hs.6638	Homo sapiens cDNA FLJ11602 fis, clone HE	2.5
	435347	AW014873	Hs.116963	ESTs	2.5
65	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.5
	438208	AL041224	Hs.65379	ESTs	2.5
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	2.5
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	2.5
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
70	442337	AI371029	Hs.129257	ESTs, Weakly similar to TC17_HUMAN TRANS	2.5
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.5
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.5
	449086	AI628357	Hs.208037	ESTs	2.5
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
75	TABLE 24B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
80	Pkey	CAT Number	Accession		
	408432	1058667_1	AW195262 R27868 AW811262		
	412225	1284108_1	AW902042 N77591		
	412436	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765		

5	416120	1571266_1	H46739 H51513 H19779
	416871	1626761_1	H98716 N90792 N24283
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	422864	222336_1	AA318323 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821
	422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424
	422977	223410_1	AA631498 AJ017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642
			AW853758 H56414
10	423756	231725_1	AA828125 AA834883 AA330555
	425168	247552_1	R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194
	425517	252729_1	AF121179 BE162736 AA358827
	426413	266650_1	AA377823 AW954494 AI022688
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	428679	294049_1	AA431765 AA432015
15	428858	296453_1	AA436760 AW237453 BE327496 N47347 N56967
	429007	298301_1	D80642 AA443145 AL119015 AW904500
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	433532	368950_1	AW975367 AA598607 AA742735
	436190	41555_1	AK001059 AA633055
20	437034	431713_1	AA742643 AA808575 AW976668
	438458	457837_1	AW975186 AA807807 D29548
	438993	467651_1	AA828995 AA834879 AI926361
	439566	47387_1	AF086387 W77884 W72711
	440322	491966_1	AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400
25	444584	611496_1	AI168422 D80113 T59074
	447197	711623_1	R36075 AI366546 R36167
	448451	764066_1	AW015994 R39898 AW000978 AI598202 AI521706
	450625	84032_1	AW970107 AA513951 AA010406
	452453	918300_1	AI902519 AI902518 AI902516
30	454996	1248640_1	AW850180 AW850326
	455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798

TABLE 24C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

40	Pkey	Ref	Strand	Nt_position
	400777	8131663	Plus	70745-71121
	400780	8131663	Minus	118372-118619
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400860	9757499	Minus	151830-152104,152649-152744
45	400992	8096828	Plus	140390-140822
	401324	9863791	Plus	234057-234174
	402408	9796239	Minus	110326-110491
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973
50	402693	8569863	Minus	82366-82515
	402855	9662953	Minus	59763-59909
	404029	7671252	Plus	108716-111112
	404048	3688074	Minus	54421-56808
	404049	3688074	Minus	75765-78155
55	404283	2276311	Minus	99460-99564
	404299	5738652	Minus	3826-4025
	404541	8318559	Plus	103456-103664
	404584	9857511	Plus	138651-139153
	404593	9944086	Minus	74922-75788
60	404721	9856648	Minus	173763-174294
	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405238	7249119	Minus	51728-51836
	405771	7018349	Plus	91191-91254,91510-91589
	405819	4007557	Plus	2830-2967
65	406311	9211559	Minus	137114-139033

TABLE 25A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 25A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue

80	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	452461	N78223	Hs.108106	transcription factor	20.1
	436895	AF037335	Hs.5338	carbonic anhydrase XII	15.2
	453941	U39817	Hs.36820	Bloom syndrome	14.2
	443247	BE614387	Hs.333893	c-Myc target JPO1	12.4

	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.0
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	11.7
	422163	AF027208	Hs.112350	prominin (mouse)-like 1	11.4
5	439451	AF086270	Hs.278554	heterochromatin-like protein 1	11.2
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.2
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A {	10.0
	444190	AB78918	Hs.10526	cysteine and glycine-rich protein 2	9.9
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.9
10	449340	AW235786	Hs.195359	hypothetical protein MGC10954	9.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	9.4
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	8.9
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.2
15	420092	AA814043	Hs.88045	ESTs	7.9
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	7.9
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.9
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.8
20	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	7.8
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	7.7
	409638	AW450420	Hs.21335	ESTs	7.5
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	7.5
25	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	7.5
	412777	AI335773	Hs.270123	ESTs	7.4
	436607	AW661783	Hs.211061	ESTs	7.3
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.3
	417061	AI675944	Hs.186691	Homo sapiens cDNA FLJ12033 fis, clone HE	7.3
30	428976	AL037824	Hs.194695	ras homolog gene family, member 1	7.2
	433244	AB040943	Hs.271285	KIAA1510 protein	7.1
	436726	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypotheti	7.1
	408432	AW195262		gb:u67b05.x1 NCI_CGAP_CML1 Homo sapiens	7.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	7.0
35	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	7.0
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	7.0
	432656	NM_000246	Hs.3076	MHC class II transactivator	6.8
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.8
	453387	AI990741	Hs.252809	ESTs	6.8
40	418821	AA436002	Hs.183161	ESTs	6.6
	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.6
	411252	AB018549	Hs.69328	MD-2 protein	6.5
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.4
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	6.3
45	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	6.3
	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.3
	418097	R45137	Hs.21868	ESTs	6.2
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	6.2
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.1
50	449448	D60730	Hs.57471	ESTs	6.1
	403790				6.0
	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	6.0
	435542	AA687376	Hs.269533	ESTs	5.9
55	418216	AA662240	Hs.283099	AF15q14 protein	5.8
	439086	AF085947		gb:Homo sapiens full length insert cDNA	5.8
	408037	AW271720	Hs.42233	hypothetical protein FLJ10300	5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
60	435005	U80743	Hs.306094	trinucleotide repeat containing 12	5.7
	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti	5.7
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.6
	405558				5.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
65	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.5
	420560	AW207748	Hs.59115	ESTs	5.5
	408096	BE250162	Hs.83765	dihydrofolate reductase	5.5
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	5.4
70	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, clone H	5.4
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	5.3
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.3
	444168	AW379879		gb:RC1-HT0256-081199-011-r01 HT0256 Homo	5.3
	432789	D26361	Hs.3104	KIAA0042 gene product	5.3
75	437036	AI571514	Hs.133022	ESTs	5.2
	421247	BE391727	Hs.102910	general transcription factor IIIH, polype	5.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	5.1
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	454157	AW162906	Hs.312481	ESTs, Weakly similar to S66668 hydrogen	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.1
	406679	AA070786		gb:zm66b07.r1 Stratagene neuroepithelium	5.1
	442671	AI005668	Hs.134779	EST	5.1

	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	5.0
	418819	AA228776	Hs.191721	ESTs	5.0
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	4.9
	420730	NM_002691	Hs.99890	polymerase (DNA directed), delta 1, cata	4.9
5	441217	AI922183	Hs.213246	ESTs	4.9
	453385	AW296101	Hs.252806	ESTs	4.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.7
	450813	AI739525	Hs.203376	ESTs	4.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.7
10	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	4.7
	405771				4.6
	457065	AM76318	Hs.192480	ESTs	4.6
15	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	400859				4.6
	435267	N23797	Hs.110114	ESTs	4.6
	443454	AI057494	Hs.133421	ESTs	4.5
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5
20	437267	AW511443	Hs.258110	ESTs	4.5
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.5
	454269	AI961060	Hs.129908	KIAA0591 protein	4.5
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
25	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.5
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	4.5
	417308	H60720	Hs.81892	KIAA0101 gene product	4.5
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.4
30	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	4.4
	406568	AF088886	Hs.11590	cathepsin F	4.4
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	4.4
	402516				4.4
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothe	4.4
35	413625	AW451103	Hs.71371	ESTs	4.4
	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
40	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	4.3
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	441020	W79283	Hs.35962	ESTs	4.3
45	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	405701				4.3
	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2
50	433323	AA805132	Hs.30701	ESTs	4.2
	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282FBR Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.1
	441269	AW015206	Hs.178784	ESTs	4.1
55	418727	AA227609	Hs.94834	ESTs	4.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	4.1
	430786	AA486144	Hs.31293	ESTs	4.1
	445372	N36417	Hs.144928	ESTs	4.1
60	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.0
	457465	AW301344	Hs.122908	DNA replication factor	4.0
	422094	AF129535	Hs.272027	F-box only protein 5	4.0
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
	459321	AW044477	Hs.299538	ESTs	4.0
65	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.0
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	4.0
	447004	AW296968	Hs.157539	ESTs	4.0
	448295	AI381911	Hs.334859	KIAA1814 protein	3.9
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.9
70	440704	M69241	Hs.162	insulin-like growth factor binding prote	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
	457026	AA397620	Hs.48692	ESTs	3.9
	404642				3.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9
75	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	3.9
	437718	AI927288	Hs.196779	ESTs	3.9
	438490	AW593272	Hs.301299	ESTs	3.9
	429919	AA460692	Hs.278945	hypothetical protein FLJ23024	3.9
	413604	R51767		gb:yg73g11.r1 Soares infant brain 1N1B H	3.9
80	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.9
	449300	AI656959	Hs.222165	ESTs	3.8
	452203	X57522	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.8

	404295				
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.8
	428728	NM_016625	Hs.191381	hypothetical protein	3.8
5	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.8
	430172	AA468591	Hs.161889	ESTs	3.8
	447499	AW262580	Hs.147674	protocadherin beta 16	3.8
	405884				3.8
	437236	AW137817	Hs.244353	ESTs	3.8
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.7
	425529	NM_014656	Hs.158282	KIAA0040 gene product	3.7
	425502	R98895	Hs.125823	ESTs	3.7
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
	402424				3.7
15	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.7
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.7
	414872	U82010	Hs.77513	COX10 (yeast) homolog, cytochrome c oxid	3.7
	426071	AW138057	Hs.163835	ESTs	3.7
20	419078	M93119	Hs.89584	insulinoma-associated 1	3.7
	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.7
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	3.7
	436899	AA764852	Hs.291567	ESTs	3.7
	436722	AW975977		gb:EST388086 MAGE resequences, MAGN Homo	3.6
25	440652	AI216751	Hs.143977	ESTs	3.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypothe	3.6
	409048	H59990	Hs.37699	ESTs	3.6
	439546	AF088056		gb:Homo sapiens full length insert cDNA	3.6
30	443544	AI076315	Hs.16359	ESTs	3.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
	435889	AI249107	Hs.269901	ESTs	3.6
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.6
	438078	AI016377	Hs.131693	ESTs	3.6
35	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	3.6
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.5
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.5
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.5
40	436123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5
	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo	3.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	3.5
	435065	BE064391		gb:RC4-BT0310-110300-015-b08 BT0310 Homo	3.5
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.5
45	447101	N72185	Hs.44189	ESTs	3.5
	410530	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	3.5
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	3.5
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.5
50	439743	AL389956	Hs.283858	Homo sapiens mRNA full length insert cDN	3.5
	453884	AA359925	Hs.36232	KIAA0186 gene product	3.5
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.5
	420721	AA927802	Hs.159471	ZAP3 protein	3.5
	426764	AA732524	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.5
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.4
55	448831	AL080123	Hs.22182	zinc finger protein 23 (K0X 16)	3.4
	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604				3.4
	442407	AW469584	Hs.32353	mitogen-activated protein kinase kinase	3.4
60	414300	AI304870	Hs.188680	ESTs	3.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	3.4
	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4
	452211	AI985513	Hs.233420	ESTs	3.4
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.4
	449961	AW265634	Hs.133100	ESTs	3.4
65	413257	BE075035		gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.4
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.4
	446189	H85224	Hs.214013	ESTs	3.4
70	437385	AA757055	Hs.164060	ESTs	3.4
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	3.4
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.4
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
	417546	H65569	Hs.18845	ESTs	3.3
75	412471	M63193	Hs.73946	endothelial cell growth factor 1 (plate	3.3
	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	3.3
	454294	AB000734	Hs.50640	JAK binding protein	3.3
	457131	AC002310	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	3.3
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
80	449676	AW380579	Hs.209657	ESTs	3.3
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.3
	453745	AL120611		gb:DKFZp761H119_r1 761 (synonym: hamy2)	3.3
	452799	AI948829	Hs.213786	ESTs	3.3
	435380	AA679001	Hs.192221	ESTs	3.3

5	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	3.3
	453362	H14988	Hs.107375	ESTs	3.3
	456473	AJ202788	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	3.3
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.3
	445777	AI580371	Hs.145384	ESTs	3.3
10	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299				3.3
	404108				3.3
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1MIB H	3.3
15	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.3
	450193	AJ916071	Hs.15607	Homo sapiens Fanconi anemia complementat	3.2
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.2
	418968	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	3.2
20	449248	M33782	Hs.23391	Homo sapiens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2
	401596	AA172106	Hs.110950	Rag C protein	3.2
	408380	AF123050	Hs.44532	diubiquitin	3.2
	450325	AF935962	Hs.26289	ESTs	3.2
25	428730	AA625947	Hs.25750	ESTs	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2
	442710	AI015631	Hs.23210	ESTs	3.2
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.2
30	430970	AI018210	Hs.144083	ESTs	3.2
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	3.2
	446676	H09380	Hs.300965	ESTs	3.2
	451459	AJ797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
35	413840	AI301558	Hs.146381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	3.2
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.2
	458786	AI457098	Hs.280848	ESTs	3.2
	455909	BE156417	Hs.278798	ESTs	3.2
40	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	439710	AF086543		gb:Homo sapiens full length insert cDNA	3.2
	434559	AF147315		gb:Homo sapiens full length insert cDNA	3.1
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.1
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1
45	414799	AJ752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.1
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.1
50	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.1
	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	3.1
	404589				3.1
	421764	AI681535	Hs.148135	serine/threonine kinase 33	3.1
55	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.1
	416941	BE000150	Hs.48778	niban protein	3.1
	414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	449611	AJ970394	Hs.197075	ESTs	3.1
	434746	AA648368	Hs.295368	ESTs	3.1
60	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum amyloid A1	3.1
	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.1
	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
65	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	3.1
	426531	AA381071		gb:EST94100 Activated T-cells XJ1 Homo s	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
	406267				3.1
	447039	AV661798	Hs.282915	ESTs	3.1
70	404802				3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
	419314	AW971924	Hs.87280	ESTs	3.0
	435894	AI076667	Hs.188011	ESTs	3.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.0
75	43426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.0
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	3.0
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0
	418241	M26682	Hs.1149	LIM domain only 1 (thrombosin 1)	3.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse	3.0
80	412950	BE018581	Hs.245342	hypothetical protein FLJ14642	3.0
	428670	AA431682	Hs.134832	ESTs	3.0
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0
	437756	AA767537	Hs.197096	ESTs	3.0
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.0
	402374	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.0
	443885	H91806	Hs.15284	ESTs	3.0
	434008	AA740878	Hs.112982	ESTs	3.0

5	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	3.0
	414239	AI288330	Hs.182330	ESTs	3.0
	421013	M52397	Hs.1345	mutated in colorectal cancers	3.0
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.0
	410276	AI554545	Hs.68301	ESTs	3.0
10	433865	N29862	Hs.44104	ESTs	3.0
	406028				3.0
	401626				3.0
	415949	H10562	Hs.21691	ESTs	3.0
	418583	AA604379	Hs.86211	hypothetical protein	3.0
15	417933	X02308	Hs.82962	thymidylate synthetase	3.0
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.0
	430437	AJ768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.0
	427940	AA417812	Hs.38775	ESTs	3.0
	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	2.9
20	421988	AW450481	Hs.161333	ESTs	2.9
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	2.9
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.9
	451189	AA016019	Hs.40905	ESTs	2.9
25	401558				2.9
	426207	BE390657	Hs.30026	HSPC182 protein	2.9
	404721				2.9
	401384				2.9
	417288	AI984792	Hs.108812	hypothetical protein FLJ22004	2.9
30	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.9
	435928	H64345	Hs.183961	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	2.9
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.9
	439972	AI348100	Hs.124662	ESTs	2.9
35	433112	AA973801	Hs.144553	ESTs, Weakly similar to unnamed protein	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	406748	AW339106	Hs.217493	annexin A2	2.9
	422154	T79045	Hs.126927	ESTs	2.9
	405588				2.9
40	440911	AA909536	Hs.143562	ESTs	2.9
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066	ESTs	2.9
	410114	AW590540	Hs.271280	ESTs	2.9
	419217	AA504571		gb:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens	2.9
45	415849	R20529	Hs.6806	ESTs	2.9
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.9
	453331	AI240665	Hs.8895	ESTs	2.9
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.9
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	2.9
50	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTs	2.9
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.8
	415446	F08898	Hs.66075	ESTs	2.8
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.8
55	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.8
	419451	AI907117	Hs.90535	synaptobrevin binding protein 2	2.8
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.8
	424126	AA335635	Hs.96917	ESTs	2.8
60	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypothesi	2.8
	418973	AA233056	Hs.191518	ESTs	2.8
	440471	AA886146	Hs.307944	ESTs	2.8
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
	433647	AA603367	Hs.222294	ESTs	2.8
65	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.8
	421723	AA620400	Hs.300717	sodium channel, voltage-gated, type III,	2.8
	434964	AI638850	Hs.130746	ESTs	2.8
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
	400517	AF242388	Hs.149585	lengsin	2.8
70	433023	AW864793	Hs.87409	thrombospondin 1	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	406736	AI254733	Hs.182426	ribosomal protein S2	2.8
	409207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	2.8
	440196	N72847	Hs.125221	ESTs	2.8
75	403961				2.8
	425193	AW965689	Hs.22509	ESTs	2.8
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.8
	440483	AI200836	Hs.150386	ESTs	2.8
	412391	AW947710		gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
80	448769	M66037	Hs.38173	ESTs	2.8
	411632	AW854829		gb:QV2-CT0261-201099-011-01 CT0261 Homo	2.8
	438221	AI798853	Hs.122224	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.8
	457578	AA578027		gb:nl20h01.s1 NCI_CGAP_HSC1 Homo sapiens	2.8
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	2.8
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.8
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.8
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.8

	439662	H97552	Hs.269060	ESTs	2.8
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.8
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	2.8
5	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.8
	447752	M73700	Hs.105938	lactotransferrin	2.8
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	2.8
	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	2.7
	456629	AW891965	Hs.279789	histone deacetylase 3	2.7
10	439538	AA837323	Hs.164047	ESTs	2.7
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	2.7
	456029	BE255990	Hs.218329	hypothetical protein	2.7
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	2.7
	456412	AW749617	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	2.7
15	453536	AA137000	Hs.62578	ESTs	2.7
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.7
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
	446322	N23033	Hs.155814	ESTs	2.7
	451592	AI805416	Hs.213897	ESTs	2.7
20	429466	M85835	Hs.12827	ESTs	2.7
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.7
	455514	AW983871		gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.7
	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.7
25	427421	AA402414	Hs.3059	coatamer protein complex, subunit beta	2.7
	449655	AI021987	Hs.59970	ESTs	2.7
	422648	D86983	Hs.118893	Melanoma associated gene	2.7
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	2.7
	406895	X60648	Hs.172550	polypyrimidine tract binding protein (he	2.7
30	453255	AA278167	Hs.19215	Homo sapiens, clone IMAGE:3605822, mRNA	2.7
	427348	NM_014137	Hs.177258	PRO0650 protein	2.7
	435370	AI964074	Hs.225838	ESTs	2.7
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV	2.7
	411874	AA096106	Hs.20403	ESTs	2.7
35	421192	AA833718	Hs.204529	KIAA1806 protein	2.7
	435899	W89093	Hs.189914	ESTs	2.7
	414603	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
	453462	AL037291	Hs.236605	ESTs, Moderately similar to ALLU4_HUMAN A	2.7
	436554	AI985810	Hs.301173	ESTs	2.7
40	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7
	403881				2.7
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.7
	404984				2.7
45	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.7
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.7
	404756				2.7
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.7
	422176	H80977		gb:yu89a11.s1 Soares fetal liver spleen	2.7
50	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.7
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	2.7
	412833	AW960547	Hs.298262	ribosomal protein S19	2.7
	457245	AI745498	Hs.204579	ESTs	2.7
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
55	453263	R91778	Hs.99369	ESTs	2.7
	459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo sapiens c	2.7
	438764	AA824524	Hs.336452	ESTs	2.7
	429285	AI971081	Hs.20432	ESTs, Weakly similar to I38022 hypotheti	2.7
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	2.7
60	430037	BE409649	Hs.227789	mitogen-activated protein kinase-activat	2.7
	449892	N73608	Hs.50309	ESTs	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.7
	427954	J03060	Hs.247551	metaxin 1	2.7
65	400371	U80740			2.7
	452449	AW068658	Hs.20943	ESTs	2.7
	431114	AA492400	Hs.291015	ESTs	2.7
	417088	M54915	Hs.81170	pim-1 oncogene	2.7
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.7
70	403680				2.7
	454679	AW813110		gb:CM4-ST0189-051099-021-r05 ST0189 Homo	2.7
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	2.6
	422240	R60594	Hs.29002	KIAA1706 protein	2.6
	424368	AB037766	Hs.146085	KIAA1345 protein	2.6
75	405808				2.6
	419700	AF084935	Hs.92357	galactokinase 1	2.6
	435972	W95088	Hs.114198	ESTs	2.6
	453568	S70782	Hs.557	adrenergic, alpha-1D-, receptor	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
80	444156	AW500059	Hs.86437	ESTs, Highly similar to AF219140 1 gastr	2.6
	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin I	2.6
	437640	AA764893	Hs.272155	ESTs, Weakly similar to I38022 hypotheti	2.6
	453948	AI970797	Hs.64859	ESTs	2.6
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	2.6

	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.6
	418228	AA962181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	401324				2.6
5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.6
	443210	AJ692649	Hs.9451	hypothetical protein MGC13168	2.6
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I38022 hypotheti	2.6
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	2.6
	433933	AJ754389	Hs.133494	Homo sapiens clone TCC01A00164 mRNA sequ	2.6
10	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.6
	400992				2.6
	455530	AW984744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	2.6
	436139	AA765786	Hs.120936	ESTs	2.6
15	448330	AL036449	Hs.207163	ESTs	2.6
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	2.6
	433430	AI863735	Hs.186755	ESTs	2.6
	436693	AW973223	Hs.303197	B-cell CLL/lymphoma 7C	2.6
20	429482	AF076974	Hs.203952	transformation/transcription domain-asso	2.6
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	2.6
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.6
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	2.6
	414835	AA156720	Hs.185342	ESTs	2.6
25	424489	T48851	Hs.149250	D-siglec precursor,	2.6
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797				2.6
	434573	AW372340	Hs.159717	ESTs	2.6
	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
30	415785	RB2419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6
	450608	AA010365	Hs.193229	ESTs	2.6
	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.6
	432268	BE311856	Hs.274230	3'-phosphoadenosine 5'-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
35	427343	AI880044	Hs.176977	protein kinase C binding protein 2	2.6
	420917	AW135716	Hs.117330	ESTs	2.6
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	2.6
	446089	AJ860021	Hs.270651	ESTs, Moderately similar to A47582 B-cel	2.6
	440829	AF136407	Hs.7446	chromosome 6 open reading frame 5	2.6
40	408475	AA315514	Hs.47986	hypothetical protein MGC10940	2.6
	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	2.6
	421462	AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	2.6
	422887	AJ751848	Hs.49215	ESTs	2.6
45	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	2.6
	408981	AW500797	Hs.49427	Gem-interacting protein	2.5
	432180	Y18418	Hs.272822	RuvB (E. coli homolog)-like 1	2.5
	418079	R40058	Hs.6911	ESTs	2.5
50	437820	AA769062	Hs.323836	ESTs, Weakly similar to alternatively sp	2.5
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	2.5
	425681	AB018297	Hs.159183	KIAA0754 protein	2.5
	435177	AI018174	Hs.42936	ESTs	2.5
	437323	AA371145	Hs.226627	leptin receptor	2.5
55	422114	AW194851	Hs.111801	arsenate resistance protein ARS2	2.5
	448478	AI523218	Hs.203456	ESTs	2.5
	426623	AA382826	Hs.132793	ESTs	2.5
	448764	AI568607	Hs.182112	ESTs	2.5
	458385	AJ051489	Hs.246214	ESTs	2.5
60	403726	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
	444888	AI651039	Hs.148559	ESTs	2.5
	456179	H75490	Hs.271930	ESTs	2.5
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.5
	406273	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	2.5
65	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	2.5
	454967	AW848276		gb:IL3-CT0214-150200-074-E06 CT0214 Homo	2.5
	442303	AA989289	Hs.129169	ESTs	2.5
	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	2.5
70	434263	N34895	Hs.44648	ESTs	2.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	2.5
	406038	Y14443	Hs.88219	zinc finger protein 200	2.5
	413495	Y12395	Hs.315177	interferon-related developmental regulat	2.5
75	423098	AA321980	Hs.204682	ESTs	2.5
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	2.5
	439841	AF038961	Hs.6710	mannose-6-phosphate utilization defect 1	2.5
	453828	AW970960	Hs.293821	ESTs	2.5
	445034	AW293376	Hs.143659	ESTs	2.5
80	449620	BE407797	Hs.23794	checkpoint with forkhead and ring finger	2.5
	406876	AI382286	Hs.180842	ribosomal protein L13	2.5
	412370	AW946614		gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.5
	430357	AW976789	Hs.165607	ESTs	2.5

5	414853	U31116	Hs.77501	saroglycan, beta (43kD dystrophin-assoc	2.5
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.5
	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	2.5
	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.5
	445223	AW291553	Hs.254983	ESTs	2.5
10	423926	X03833	Hs.1722	interleukin 1, alpha	2.5
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	2.5
	406474				2.5
	433908	AW298141	Hs.157975	ESTs	2.5
	439755	AW748482	Hs.77873	B7 homolog 3	2.5
15	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	ESTs	2.5
	415346	Z43108		gb:HSC13E071 normalized infant brain cDN	2.5
	419337	AW291112	Hs.209978	ESTs	2.5
	444606	R09478	Hs.18041	ESTs	2.5
20	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
	411965	BE467339	Hs.280115	ESTs	2.5
	409278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5
	403142				2.5
25	401714				2.5
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.5
	416505	H66470	Hs.16004	ESTs	2.5
	431518	AA743462	Hs.165337	ESTs	2.5
	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
30	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	2.5
	404366				2.5
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HE	2.5
	455853	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
	402856	AW939659		gb:RCD-OT0076-110100-031-c09 DT0076 Homo	2.5
35	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	2.4
	436805	AA731533	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.4
	453853	AL040600	Hs.188083	ESTs	2.4
40	407909	AW103986		gb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	2.4
	454630	BE142075		gb:CM3-HT0137-170999-012-402 HT0137 Homo	2.4
	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	2.4
	420779	L12398	Hs.99922	dopamine receptor D4	2.4
	438322	AA804170	Hs.221349	ESTs	2.4
45	455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	2.4
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4
	440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	2.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
50	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.4
	451802	AI817711	Hs.209374	ESTs	2.4
	419417	R92491	Hs.39429	ESTs	2.4
	407094	AF000574	Hs.22405	leukocyte immunoglobulin-like receptor,	2.4
	423567	BE252949	Hs.69331	hypothetical protein FLJ13633	2.4
55	427501	AI369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2.4
	436845	AA732297	Hs.113928	ESTs	2.4
	431584	AW296121	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	2.4
	440614	AA781530	Hs.127236	hypothetical protein FLJ12879	2.4
60	423721	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotroph	2.4
	452125	BE312642	Hs.28077	GDP-mannose pyrophosphorylase B	2.4
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.4
	453446	BE299996		gb:600944574F1 NIH_MGC_17 Homo sapiens c	2.4
	419792	AA250890	Hs.190037	ESTs	2.4
65	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.4
	410447	AW816134		gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.4
	402408				2.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.4
70	414625	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403048				2.4
	432088	AA525454		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo sapiens	2.4
	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	2.4
	455023	AW850907		gb:ILL3-CT0220-310100-065-H11 CT0220 Homo	2.4
75	426249	F05422	Hs.168352	nucleoporin-like protein 1	2.4
	446795	AI797713	Hs.156471	ESTs	2.4
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
	414252	AA346483	Hs.126191	ESTs	2.4
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.4
80	427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DE	2.4
	404020				2.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.4
	417222	AI525424	Hs.42053	hypothetical protein MGC2383	2.4
	443639	BE269042	Hs.9561	proteasome (prosome, macropain) subunit,	2.4
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	401676				2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4

	436277	R88520	Hs.120917	ESTs	
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
	405353				2.4
5	409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithelium	2.4
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	453335	AW857376	Hs.169238	fucosyltransferase 3 (galactoside 3(4)-L	2.4
	450621	AW297288	Hs.55918	hypothetical protein FLJ11354	2.4
10	419652	AL157485	Hs.91973	hypothetical protein	2.4
	421151	BE174431	Hs.63386	ESTs	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
	405288				2.4
15	453527	R49570	Hs.180236	ESTs	2.4
	429875	A091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	2.4
	436360	A1962796	Hs.136754	ESTs	2.4
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.4
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.4
20	449539	W80363	Hs.58446	ESTs	2.4
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.4
	404584				2.4
	454276	AW294996	Hs.255374	ESTs	2.4
	423746	AW361817	Hs.132370	NADPH oxidase 1	2.4
25	415558	AA885143	Hs.125719	ESTs	2.4
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
	406953	L36847		gb:Human (clone p1790) rearranged iduro	2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4
	451031	A1360187	Hs.4254	ESTs	2.4
30	455302	AW997641		gb:RC6-BN0052-170200-011-D06 BN0052 Homo	2.4
	449063	A1627352	Hs.236547	Homo sapiens, clone IMAGE:2905978, mRNA,	2.4
	401048				2.4
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.4
35	449086	A1628357	Hs.208037	ESTs	2.4
	415238	R37780	Hs.21422	ESTs	2.4
	448337	AW206453	Hs.3782	ESTs	2.4
	416991	N36389	Hs.141296	KIAA0226 gene product	2.3
	412600	L28824	Hs.74101	spleen tyrosine kinase	2.3
40	418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
	440769	BE561793	Hs.21446	KIAA1716 protein	2.3
	450437	X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3
	406739	A1566709	Hs.182426	ribosomal protein S2	2.3
45	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.3
	410286	A1739159	Hs.61898	DKFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	ESTs	2.3
	405605				2.3
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
50	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	2.3
	445828	F05802	Hs.81907	ESTs	2.3
	457195	AB011099	Hs.196647	KIAA0527 protein	2.3
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.3
	423198	M81933	Hs.1634	cell division cycle 25A	2.3
55	457730	AW753613		gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	412014	A1620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	2.3
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.3
	446288	AW189209	Hs.149708	ESTs	2.3
60	436954	AA740151	Hs.130425	ESTs	2.3
	411658	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
	404240				2.3
	456094	H95091		gb:yw57a09.r1 Soares_placenta_8to9weeks_	2.3
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.3
	406737	A1356586		gb:qy15h09.x1 NCI_CGAP_Bm23 Homo sapien	2.3
65	458453	A1097452	Hs.135095	ESTs	2.3
	452330	A1879127	Hs.191979	KIAA1733 protein	2.3
	408523	AW833259	Hs.314287	ESTs	2.3
	455470	AW947992		gb:PM0-MT0011-240300-001-c09 MT0011 Homo	2.3
70	436323	R17697	Hs.140963	ESTs, Weakly similar to I38022 hypotheti	2.3
	450000	A1952797	Hs.10888	hypothetical protein FLJ21709	2.3
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.3
	419134	T89863	Hs.221771	ESTs	2.3
	445933	AV655733	Hs.293860	spinster-like protein	2.3
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.3
75	449911	A1262106	Hs.12653	ESTs	2.3
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.3
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.3
	423491	AA191765	Hs.129673	eukaryotic translation initiation factor	2.3
80	407182	AA312551	Hs.230157	ESTs	2.3
	411448	AA178955	Hs.271439	ESTs, Weakly similar to I38022 hypotheti	2.3
	438644	A126162	Hs.129037	ESTs	2.3
	432691	U29725	Hs.3080	mitogen-activated protein kinase 7	2.3
	452198	A1097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	2.3

	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3
	404054				2.3
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	2.3
	440210	AW674562	Hs.125296	ESTs	2.3
5	446727	AB011095	Hs.16032	KIAA0523 protein	2.3
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.3
	449919	AJ674685	Hs.200141	ESTs	2.3
	415293	R49462	Hs.106541	ESTs	2.3
10	441126	NM_000429	Hs.323715	methionine adenosyltransferase I, alpha	2.3
	408203	AA053137	Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
	450748	AI733093	Hs.130016	ESTs	2.3
	404185				2.3
15	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
	451370	AI791929	Hs.300782	ESTs	2.3
	400034				2.3
	407723	AW071161	Hs.252873	ESTs	2.3
	431320	AW969474	Hs.183070	ESTs	2.3
20	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.3
	419225	U70073		gb:HSU70073 Human Homo sapiens cDNA clon	2.3
	444656	AJ277924	Hs.145199	ESTs	2.3
	405741				2.3
25	400917				2.3
	432567	AA736777	Hs.293770	ESTs	2.3
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.3
	450514	AC005785	Hs.25059	A kinase (PRKA) anchor protein 8	2.3
30	418400	BE243026	Hs.301989	KIAA0246 protein	2.3
	444019	BE173977	Hs.10098	putative nucleolar RNA helicase	2.3
	406326				2.3
	412077	N51107	Hs.47199	ESTs, Weakly similar to FLJ00004 protein	2.3
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.3
	414528	AA148950	Hs.188836	ESTs	2.3
35	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.3
	439467	AW292275	Hs.158365	ESTs	2.3
	402627				2.3
40	451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	2.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.3
	423869	BE409301	Hs.134012	C1q-related factor	2.3
	405915				2.3
	431503	NM_012129	Hs.258576	claudin 12	2.3
45	423306	W88562	Hs.108198	ESTs	2.3
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	2.3
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	2.3
	434437	AI912566	Hs.187813	ESTs	2.3
	436191	BE407866	Hs.170253	hypothetical protein FLJ23282	2.3
50	420006	H14429	Hs.94300	serologically defined colon cancer antig	2.3
	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3
	403166				2.3
	422119	AI277829	Hs.111862	KIAA0590 gene product	2.3
	403751				2.3
55	426451	AI908165	Hs.169946	GATA-binding protein 3	2.3
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.3
	409091	AW970386	Hs.269423	ESTs	2.3
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.3
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.3
60	405747				2.3
	438210	AA780519	Hs.311601	EST	2.3
	404652				2.3
	423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
	426793	X89887	Hs.172350	HiR (histone cell cycle regulation defec	2.2
65	444424	AI654684	Hs.196377	ESTs	2.2
	434031	BE384165	Hs.23723	pseudouridylylase synthase 1	2.2
	427650	AW501245	Hs.252259	ribosomal protein S3	2.2
	435220	D50030	Hs.104	HGF activator	2.2
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	2.2
70	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
	429961	BE246829	Hs.226770	DKFZP566C0424 protein	2.2
	442065	AI831229	Hs.128417	hypothetical protein FLJ14009	2.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.2
	420536	AL117455	Hs.275438	histone deacetylase 7A	2.2
75	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
	443753	AW367578	Hs.134749	ESTs	2.2
	423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	2.2
	446572	AV659151	Hs.282961	ESTs	2.2
	412247	AF022375	Hs.73793	vascular endothelial growth factor	2.2
80	421040	AA715026	Hs.135280	ESTs	2.2
	426212	S71824	Hs.167988	neural cell adhesion molecule 1	2.2
	455584	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	406851	AA609784	Hs.180255	major histocompatibility complex, class	2.2
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.2

	419575	U43431	Hs.91175	topoisomerase (DNA) III alpha	2.2
	418672	L44284	Hs.159743	ESTs	2.2
	456261	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0894 protein	2.2
	415737	AA167626	Hs.118743	ESTs	2.2
5	447554	AJ391598	Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	405159				2.2
	442177	AW661820	Hs.211413	ESTs	2.2
	446139	H77395	Hs.39749	ESTs	2.2
10	458339	AW976853	Hs.172843	ESTs	2.2
	401876				2.2
	439566	AF086387		gb:Homo sapiens full length insert cDNA	2.2
	425079	H09963	Hs.2257	vitronectin (serum spreading factor, som	2.2
	441837	AA361743	Hs.179881	core-binding factor, beta subunit	2.2
15	430644	AB015419	Hs.247710	preprolactin-releasing peptide	2.2
	431474	AL133990	Hs.190642	ESTs	2.2
	407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2.2
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	2.2
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	2.2
20	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.2
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2.2
	404170				2.2
	406902	M32074		gb:Human retinoic acid receptor gamma 2	2.2
	437902	AA770599	Hs.144055	ESTs	2.2
	401012				2.2
25	446502	AI302654	Hs.208024	ESTs	2.2
	442554	AW467376	Hs.129640	ESTs	2.2
	443021	AA368546	Hs.8904	Ig superfamily protein	2.2
	421141	AW117261	Hs.125914	ESTs	2.2
30	443070	BE388662	Hs.8984	Homo sapiens chromosome 14 BAC 98L12	2.2
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.172862	ESTs	2.2
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	2.2
	431468	AW248431	Hs.256526	nuclear prelamin A recognition factor	2.2
35	416185	AW975861	Hs.47367	KIAA1785 protein	2.2
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	2.2
	402064				2.2
	413335	AJ613318	Hs.48442	ESTs	2.2
	408212	AA297567	Hs.43728	hypothetical protein	2.2
40	406169				2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.2
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fis, clone NT	2.2
	409715	W42591	Hs.23892	ESTs	2.2
	431921	N46466	Hs.58879	ESTs	2.2
45	443823	BE089782	Hs.9877	hypothetical protein	2.2
	432458	AI968598	Hs.78768	malignant cell expression-enhanced gene/	2.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	2.2
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	2.2
	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	2.2
50	415216	AI825905	Hs.193211	Homo sapiens cDNA FLJ11421 fis, clone HE	2.2
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.2
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2.2
	406660	X65371	Hs.172550	polypyrimidine tract binding protein (he	2.2
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2.2
55	432558	R97268	Hs.177269	ESTs	2.2
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.2
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.2
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	2.2
	438407	AI457122	Hs.129673	eukaryotic translation initiation factor	2.2
60	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447394, mRNA,	2.2
	409130	BE076601	Hs.75658	phosphorylase, glycogen; brain	2.2
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.2
	429489	AF008203	Hs.204039	aristless-like homeobox 3	2.2
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	2.2
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.2
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	2.2
	427498	NM_003926	Hs.178728	methyl-CpG binding domain protein 3	2.2
	408006	H57654	Hs.303345	ESTs, Weakly similar to I38022 hypotheti	2.2
	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	2.2
70	431446	AW294929	Hs.255369	Homo sapiens cDNA FLJ10265 fis, clone HE	2.2
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	2.2
	433099	NM_002504	Hs.3187	nuclear transcription factor, X-box bind	2.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.2
	415245	N59650	Hs.27252	ESTs	2.2
75	443657	R14973		gb:yf4210.s1 Soares fetal liver spleen	2.2
	402521	AW501216	Hs.108945	KIAA0515 protein	2.2
	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	2.2
	446530	AV658909	Hs.282642	ESTs	2.2
	415797	AI291896	Hs.72800	ESTs	2.2
80	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.2
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.2
	437033	AW248364	Hs.5409	RNA polymerase I subunit	2.2

	422732	AA577455	Hs.24937	transformer-2 alpha (htra-2 alpha)	2.2
	416388	AJ417358	Hs.73577	ESTs	2.2
	452849	AF044924	Hs.30792	hook2 protein	2.2
5	446615	BE513202	Hs.15589	PPAR binding protein	2.2
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.2
	446279	AA490770	Hs.182382	ESTs	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.2
	403969				2.2
10	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	2.2
	447091	AW089648	Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.2
15	438726	AB033103	Hs.6385	KJAA1277 protein	2.2
	453315	BE544203	Hs.24831	ESTs	2.2
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.2
	433610	AA806822	Hs.112547	ESTs	2.2
	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.2
20	417980	R32235		gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
	406347				2.2
	414406	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	2.2
	401827				2.2
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tet	2.2
25	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.2
	404084				2.2
	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI632091	Hs.116877	ESTs	2.2
	442609	AL020996	Hs.8518	selenoprotein N	2.1
30	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	2.1
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.1
	439253	AF086064	Hs.332252	ESTs	2.1
	409669	AW177551	Hs.220255	hypothetical protein MGC13098	2.1
	429574	BE268321	Hs.208912	hypothetical protein MGC861	2.1
35	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.1
	408945	AW015089	Hs.4964	DKFZP586J1624 protein	2.1
	447687	AI627947	Hs.150186	hypothetical protein DKFZp566K1946	2.1
	459584	AI910884	Hs.207898	ESTs	2.1
	439130	AA306090	Hs.124707	ESTs	2.1
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.1
	442028	AI239437	Hs.48945	ESTs	2.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	2.1
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	2.1
	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.1
45	444534	AW271626	Hs.42294	ESTs	2.1
	438391	AI262248	Hs.25027	ESTs	2.1
	442003	AW297497	Hs.201891	ESTs	2.1
	456278	BE300369	Hs.289308	hypothetical protein MGC4126	2.1
50	416976	BE243985	Hs.80680	major vault protein	2.1
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	2.1
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	2.1
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	2.1
	421564	AB007864	Hs.105850	KIAA0404 protein	2.1
55	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1
	432742	AA564453	Hs.162339	ESTs	2.1
	435958	H98180	Hs.117975	ESTs	2.1
	421531	AA713505	Hs.291769	ESTs	2.1
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.1
60	426503	AI570943	Hs.337546	ESTs	2.1
	448127	AI478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452897	BE066058	Hs.269233	ESTs, Moderately similar to I78885 serin	2.1
	447112	H17800	Hs.7154	ESTs	2.1
	406577				2.1
65	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
	451460	AI797550	Hs.209652	ESTs	2.1
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	2.1
	435828	AA700705	Hs.13852	ESTs	2.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.1
70	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.1
	452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN	2.1
	415586	Z45481		gb:HSC2QE041 normalized infant brain cDN	2.1
	452620	AA436504	Hs.119286	ESTs	2.1
	457066	BE244613	Hs.158272	ESTs, Weakly similar to CA13 MOUSE COLLA	2.1
75	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.1
	431741	AA514783	Hs.191701	ESTs	2.1
	446840	AW294828	Hs.209203	ESTs	2.1
	440818	AI147060	Hs.146726	ESTs	2.1
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.1
	400822				2.1
80	412760	AW379030	Hs.41324	ESTs	2.1
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein binding pr	2.1
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fls, clone H	2.1
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	2.1

	452560	BE077084	Hs.336432	ESTs	2.1
	456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferr	2.1
	458922	BE501831	Hs.282053	ESTs	2.1
5	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.1
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	2.1
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	2.1
	457192	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.1
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	2.1
10	452571	W31518	Hs.34665	ESTs	2.1
	423699	H41850	Hs.131846	PCAF associated factor 65 alpha	2.1
	406610				2.1
	453638	AW814996		gb:MR1-ST0206-170400-024-h09 ST0206 Homo	2.1
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	2.1
15	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.1
	410908	AA121686	Hs.10592	ESTs	2.1
	420221	N25991	Hs.43725	ESTs	2.1
	424739	AA346108	Hs.221610	ESTs	2.1
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.1
20	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	418181	U37012	Hs.83727	cleavage and polyadenylation specific fa	2.1
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.1
25	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1
	400021				2.1
	439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	2.1
	456505	AA504595	Hs.111418	ESTs	2.1
	405258				2.1
30	444645	AI184564	Hs.101654	ESTs	2.1
	430246	AI269069	Hs.109268	hypothetical protein FLJ12552	2.1
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	2.1
	403857				2.1
	400258				2.1
35	422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.1
	441054	AA913591	Hs.126480	ESTs	2.1
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.1
	454806	AW809752		gb:MR4-ST0124-181299-020-b06 ST0124 Homo	2.1
	448954	AB014564	Hs.22616	KIAA0664 protein	2.1
40	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.1
	453486	AL039201	Hs.173554	ubiquinol-cytochrome c reductase core pr	2.1
	437695	AA769202	Hs.192142	ESTs	2.1
	425449	X52056	Hs.157441	spleen focus forming virus (SFFV) provir	2.1
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	2.1
45	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	2.1
	436382	AW977063	Hs.250181	ESTs	2.1
	435837	AI689210	Hs.187276	Homo sapiens cDNA FLJ11431 fis, clone HE	2.1
	458287	AA987556	Hs.12867	ESTs	2.1
	423794	BE551781	Hs.231895	ESTs	2.1
50	408049	AW076098	Hs.74316	desmoplakin (DPI, DPPI)	2.1
	402721				2.1
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.1
	417541	AI992191	Hs.180040	hypothetical protein FLJ22439	2.1
	414857	AW402389	Hs.920	modulator recognition factor I	2.1
55	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.1
	428086	AL110193	Hs.224137	hypothetical protein	2.1
	447853	AI434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.1
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.1
	431019	NM_005249	Hs.2714	forkhead box G1B	2.1
60	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.1
	416435	AI431301	Hs.179703	KIAA0129 gene product	2.1
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	2.1
	459369	T83080		gb:yd40e03.r1 Soares fetal liver spleen	2.1
	402239				2.1
65	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	2.1
	426012	AA367507	Hs.75874	pregnancy-associated plasma protein A	2.1
	438885	AI886558	Hs.184987	ESTs	2.1
	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	2.1
	404561				2.1
70	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.1
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	2.1
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.1
	458604	W37944	Hs.4007	Sarcolemmal-associated protein	2.1
	409650	T08490	Hs.288969	HSCARG protein	2.1
	401729				2.1
75	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.1
	456741	W37608	Hs.184492	ESTs	2.1
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibod	2.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	2.1
80	439262	AA832333	Hs.333045	ESTs	2.1
	403108				2.1
	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	2.1
	440696	AI762757	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	2.1

	453485	BE620712	Hs.33026	hypothetical protein PP2447	2.1
	418177	N44967	Hs.5663	ESTs	2.1
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.1
	454434	AA083558	Hs.261286	ESTs	2.1
5	406085				2.1
	424441	X14850	Hs.147097	H2A histone family, member X	2.1
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	2.1
	424576	BE154142	Hs.96833	ESTs	2.1
10	423660	AL045228	Hs.130831	Homo sapiens mRNA; cDNA DKFZp434L137 (fr	2.1
	403509	AF231919	Hs.18759	KJAA0539 gene product	2.1
	441940	AW298115	Hs.128152	ESTs	2.1
	439190	AW978693	Hs.293811	ESTs	2.1
	417791	AW965339	Hs.111471	ESTs	2.1
	423701	AA329856	Hs.143022	ESTs	2.1
15	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.1
	459642	BE243103		gb:TCAAP2E0949 Pediatric acute myelogeno	2.1
	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	2.1
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.1
20	425591	AW294734	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	2.1
	412811	H06382	Hs.21400	ESTs	2.1
	426369	AF134157	Hs.169487	Kreiser (mouse) maf-related leucine zip	2.1
	435924	AW029203	Hs.191952	ESTs	2.1
25	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.1
	452235	AL039743	Hs.28514	testes development-related MYD-SP21	2.1
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	2.1
	450704	H85157	Hs.40696	ESTs	2.1
	427539	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box	2.1
30	402028				2.1
	405362				2.1
	414718	H95348	Hs.107987	ESTs	2.1
	433424	R68252	Hs.163566	ESTs	2.1
	444875	AI200759	Hs.44737	ESTs	2.0
35	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.0
	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen	2.0
	436331	AI239495	Hs.120189	ESTs	2.0
	448418	Z43704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
40	448192	R43915	Hs.4958	ESTs	2.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.0
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.0
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	2.0
	436872	X15624		gb:Human H1 RNA	2.0
45	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	2.0
	446307	T50083	Hs.9094	ESTs	2.0
	436588	AA759233	Hs.126506	ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	2.0
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.0
50	432036	AF224266	Hs.272373	interleukin 20	2.0
	414460	L00727	Hs.898	dystrophin myotonic-protein kinase	2.0
	433507	AI817336	Hs.191791	ESTs	2.0
	427964	AA418082	Hs.98286	ESTs, Weakly similar to T20655 hypothesi	2.0
	443108	W86975	Hs.203707	ESTs	2.0
55	434504	AI887341	Hs.121590	hypothetical protein FLJ12827	2.0
	454310	AW818390	Hs.175613	homolog of Xenopus Caspase	2.0
	443566	AI290284	Hs.159872	ESTs	2.0
	449722	BE280074	Hs.23960	cyclin B1	2.0
	452682	AA456193	Hs.9071	progesterone membrane binding protein	2.0
60	412362	AW945484	Hs.184252	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.0
	435863	AF255346	Hs.62919	Jun dimerization protein p21SNFT	2.0
	400774	R58624	Hs.2186	eukaryotic translation elongation factor	2.0
	453944	AW975369	Hs.292570	Homo sapiens, clone IMAGE:3502107, mRNA,	2.0
65	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.0
	448529	T26460	Hs.22550	ESTs	2.0
	443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	2.0
	439360	AA448488	Hs.336629	ribosomal protein L44	2.0
	436660	AI658870	Hs.184513	ESTs	2.0
70	449030	AI365582	Hs.57100	Homo sapiens mRNA for FLJ00016 protein,	2.0
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	2.0
	406624	AF052762		gb:Homo sapiens clone csneg8-1 immunoglo	2.0
	450666	T99968	Hs.18799	ESTs, Weakly similar to I38022 hypothesi	2.0
	446143	BE245342	Hs.306079	sec61 homolog	2.0
75	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	2.0
	426607	AA382330	Hs.124223	ESTs	2.0
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	2.0
	422564	AI148006	Hs.222120	ESTs	2.0
	432682	AI376400	Hs.159588	ESTs	2.0
80	422140	BE295918	Hs.112193	mutS (E. coli) homolog 5	2.0
	408215	BE614290	Hs.43812	syntaxin 10	2.0
	417129	AI381800	Hs.300684	calcitonin gene-related peptide-receptor	2.0
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.0
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	2.0

	411380	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	2.0
	430603	AA148164	Hs.247280	HBV associated factor	2.0
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	2.0
5	401125				2.0
	412939	AW411491	Hs.2186	eukaryotic translation elongation factor	2.0
	448740	BE250632	Hs.8026	sestrin 2	2.0
	454390	AB020713	Hs.56966	KIAA0906 protein	2.0
	415012	NM_004383	Hs.77793	c-src tyrosine kinase	2.0
10	410407	X66839	Hs.63287	carbonic anhydrase IX	2.0
	403478				2.0
	455485	AJ393037	Hs.97871	Homo sapiens, clone IMAGE:3845253, mRNA,	2.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	2.0
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	2.0
15	451944	AW445218	Hs.210876	ESTs	2.0
	436395	AJ227900		gb:Homo sapiens partial mRNA; ID EE2-16B	2.0
	456457	AA252905	Hs.194477	E3 ubiquitin ligase SMURF2	2.0
	449123	D50920	Hs.23106	KIAA0130 gene product	2.0
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957135, mRNA,	2.0
20	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	2.0
	453348	BE272318	Hs.8595	hypothetical protein FLJ12438	2.0
	424382	AA351898	Hs.23539	ESTs	2.0
	447079	AA280057	Hs.105280	ESTs, Weakly similar to dJ963K23.2 [Hsa]	2.0
25	449501	AJ652924	Hs.231942	ESTs	2.0
	422893	X98411	Hs.121555	myosin IF	2.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	2.0
	434845	BE267057	Hs.325321	hypothetical protein R32184_1	2.0
	410422	AL042014	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	2.0
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.0
30	451656	BE327088	Hs.212752	ESTs	2.0
	442068	BE312873	Hs.314932	ESTs	2.0
	446846	AW197626	Hs.271901	ESTs, Moderately similar to S08686 finge	2.0
	442690	AJ014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.0
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.0
35	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.0
	402798				2.0
	404554				2.0
	TABLE 258:				
40	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
	Pkey	CAT Number	Accession		
45	407909	1025254_1	AW103986 BE156395 BE156391 BE156190 BE156184 BE156388 BE156394		
	408432	1058667_1	AW195262 R27868 AW811262		
	409193	110747_1	AA131483 AA065156 AA076448		
	409745	115237_1	AA077391 AJ347618 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450		
	410447	1203929_1	AW816134 BE063456 AW748795 BE150839		
50	410790	1221131_1	AW803357 AW803423 AW812233 R06814		
	411256	1236790_1	AW834039 AW834040 AW834047 AW845410 BE003128 AW852479		
	411380	1242343_1	AW841619 AW851958 AW851851 AW851985		
	411632	1252361_1	AW854829 AW854805 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826		
	411658	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605		
55	411829	1260309_1	AW865749 BE179419 BE179492		
	412225	1284108_1	AW902042 N77591		
	412370	1291952_1	AW946614 AW946622 AW946663 AW946667 AW946615 AW946619		
	412391	1292625_1	AW947710 AW947698 AW947697 AW947713		
	413257	1355963_1	BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037		
60	413604	1379715_1	R51767 BE152515 Z44834 H23397		
	414406	1443333_1	BE297904 BE294312		
	414550	1460990_1	BE379808		
	415346	1534581_1	Z43108 F06295 R13085		
	415406	1536026_1	T26510 F07926 R53367		
65	415586	1540116_1	Z45481 F12393 T74437		
	415635	1540853_1	F13168 R21289 T77628		
	416871	1626761_1	H98716 N90792 N24283		
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499		
	417980	1712954_1	R32235 R32247 R32219		
70	418333	173_2	W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353 AW088477		
	418856	179649_1	A1887846 AW502624 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 A1124782 AA889402		
	419217	182954_1	AA765804 AA765530 AA055698 AA594019 A1267368 AA456946 R93354 AF264624 AW668618 AA601493		
	419225	1830274_1	AA362858 AW863761 AA229428		
75	419311	183793_1	AA504571 AA235243 AA411737 AW969068 AA406543		
	420352	192979_1	U70073		
	422128	211994_1	AA689591 AW974261 AA236240 AJ077451 AA631399 AW974262		
	422156	212379_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280		
80	422176	212714_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991		
	423756	231725_1	N34524 AA305071 AW954803 AA502335 AJ433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512		
	423867	232732_1	AI334966 W32951 H62656 H53902 R88904 AW835732		
	425189	247825_1	H80977 BE147695 AA305496 AW962366 AA436754		
			AA828125 AA834883 AA330555		
			AA331886 AW962659 AW962655 T89841		
			H16622 R17322 AA351959		

5	425517	252729_1	AF121179 BE162736 AA358827
	426076	260504_1	AW962714 AA369277 AA369278
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426531	268760_1	AA381071 AA381084 AA380862
	429875	310034_1	AI091815 AA460162 AA460761
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
	432088	341195_1	AA525454 H74039 R89502 T77379
10	433532	368950_1	AW975367 AA598607 AA742735
	434559	38889_1	AF147315 AW173079 T53029
	435065	399329_1	BE064391 BE064395 AA663613 N99644
	436190	41555_1	AK001059 AA633055
	436395	41905_1	AJ227900 AI094933 AW051119 F00947
	436532	421802_1	AA721522 AW975443 T93070
15	436722	425758_1	AW975977 AA729469 AA747132
	436872	42851_1	X15624
	437034	431713_1	AA742643 AA808575 AW976668
	439086	46852_1	AF085947 H70981 H78989
20	439228	47001_1	N51700 AF086051 N51792
	439518	47334_1	W76326 AF086341 W72300
	439546	47360_1	AF088056 W76297 W72448
	439566	47387_1	AF086387 W77884 W72711
	439710	47550_1	AF086543 W96291 W96225
25	443657	576685_1	R14973 R14967 AI081006
	444168	593829_1	AW379879 AI126285 H12014
	444386	604004_1	BE065183 AI144398 BE065367
	451129	859870_1	BE072881 BE072946 AI762181
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
30	453446	967533_1	BE299996 BE297115 BE270415 BE295214 BE296526
	453638	975649_1	AW814996 AL047199 AW850979
	453746	979731_1	AL120611 BE006190 BE006189
	454377	114761_1	AA076811 AW814764
	454389	115682_1	AW752571 AW847602 AA077979
35	454606	1226149_2	AW809752 AW810271 AW809944 AW810319 AW810215 AW810368 AW810167
	454630	1227352_1	BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142074 BE142347 BE142000 BE142375
	454631	1227443_1	AW811189 BE142133
	454679	1228929_1	AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335
40	454967	1247021_1	AW813110 AW813113
	455023	1249188_1	AW848276 AW848416 AW848160 AW847945 AW847947 AW848063 AW848113
	455202	1276542_1	AW850907 AW850901 AW850877
	455470	1292849_1	AW997641 AW891777
	455514	1321649_1	AW947992 AW947967 AW947950 AW947957 AW947953 AW947973 AW947966 AW947971 AW947947 AW947970 AW947995 AW947979 AW947952
45	455530	1322298_1	AW947956
	455584	1334741_1	AW983871 BE090302 AW983867 AW983845 AW983860 AW983853 AW983852
	455778	1364506_1	AW984744 AW984759
	455908	1382301_1	BE007420 BE007419 BE007422
50	456072	1470256_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
	456094	1504780_1	BE156306 BE156188 BE156298 BE156377 BE156374
	457374	328758_1	H54381 H54463 BE393262
	457578	359618_1	H95091 C01228
55	457730	393905_1	AA493662 AW897396 BE154814
			AA578027
			AW753613 AW753857 BE150374 BE150693 BE150394 AA808851 AA650159 AA654653 BE150419
60	TABLE 25C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	NI_position:	Indicates nucleotide positions of predicted exons.	
65	Pkey	Ref	Strand
	400822	7465000	Plus
	400859	9757499	Minus
	400917	7283186	Minus
	400992	8096828	Plus
	401012	7230838	Minus
	401048	7232177	Plus
70	401125	8570296	Minus
	401324	9863791	Plus
	401384	6850939	Minus
	401558	7139678	Plus
	401626	8575943	Minus
75	401676	9965536	Plus
	401714	6715702	Plus
	401729	8134856	Minus
	401827	2262095	Plus
	401876	8099107	Plus
80	402028	7139781	Plus
	402064	8117294	Plus
	402239	7690131	Plus
	402408	9796239	Minus
	402424	9796344	Minus

	402516	9798099	Minus	195342-195511
	402604	9909420	Plus	20393-20767
	402627	9931216	Plus	12136-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-26895,29279-29469
5	402721	8969253	Minus	144428-144715
	402798	3355547	Plus	23596-23867
	402856	9801288	Minus	90119-90411
	403048	4210991	Plus	44275-44592,49656-49955
10	403108	8980955	Plus	93253-93667
	403142	9444521	Plus	89286-90131
	403166	9838127	Minus	67762-67940,68695-68856,70394-70507
	403478	9958258	Plus	116458-116564
	403680	7331517	Minus	157184-157415
15	403751	7229815	Minus	158794-160929
	403790	8084957	Minus	87826-87947,89835-90002
	403797	8099896	Minus	123065-125008
	403857	7708910	Minus	2524-3408
	403881	7710245	Minus	107250-107685,108924-109213
20	403961	7596976	Minus	110393-110603
	403969	8569909	Plus	31237-31375,32405-32506
	404020	8655966	Minus	174449-174663
	404054	3548785	Plus	66713-69175
	404084	9944055	Plus	2795-2969
25	404108	8247074	Minus	63603-64942
	404170	9930793	Plus	168836-169248
	404185	4572584	Minus	129171-129327
	404240	5002624	Minus	116132-116407,116653-116922
	404295	9856663	Minus	75747-75947
30	404299	5738652	Minus	3826-4025
	404366	9964977	Plus	96589-96801
	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69039-70100
	404584	9857511	Plus	138651-139153
35	404589	9931665	Minus	32824-32985
	404642	9796810	Plus	102999-103145
	404652	9796969	Minus	108172-108296
	404721	9856648	Minus	173763-174294
	404756	7706327	Plus	82849-83627
40	404802	4581357	Minus	30093-30600
	404984	6939882	Plus	87221-87505
	405159	9966252	Plus	79659-79804
	405258	7329310	Plus	129930-130076
	405288	6139075	Minus	126268-126436
45	405353	2811095	Plus	118525-118892
	405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
	405558	1621110	Plus	4502-4644,5983-6083
	405588	5002511	Plus	46180-46366
	405605	5836195	Minus	117070-117270
50	405701	4263751	Plus	93243-93364
	405741	9966947	Minus	156747-156875,156936-157208
	405747	8469069	Minus	153933-154060
	405771	7018349	Plus	91191-91254,91510-91589
	405808	9929207	Plus	109758-111166
55	405884	6758747	Plus	62383-62583
	405915	7712162	Minus	43717-43859
	406028	8312303	Minus	177469-177829
	406085	9123888	Plus	18665-18843
	406169	6684220	Minus	12620-14251
60	406267	7528342	Minus	2570-2731
	406326	9212385	Plus	84508-84655
	406347	9255981	Plus	90900-91091
	406474	9795567	Plus	52758-53211
	406577	7711730	Plus	11377-11509
65	406610	8312226	Plus	13096-13334

TABLE 26A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 26A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

80	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	453655	AW960427	Hs.79059	transforming growth factor, beta receptor	136.7
	417275	XG3578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polypeptide	22.6

	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	18.5
	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	15.2
5	417167	AW206437	Hs.4290	ESTs	14.8
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6
	408068	AW148652	Hs.167398	ESTs	12.6
10	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	12.5
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2
	412638	AA910199	Hs.203838	ESTs	12.2
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	12.1
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	11.9
15	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39804	Hs.31961	ESTs	10.8
	446353	AI290919	Hs.153661	ESTs	10.4
	420290	AW977318	Hs.194480	ESTs	10.3
	414220	BE298094		gb:601118231F1 NIH_MGC_17 Homo sapiens c	10.3
20	414290	AI568801	Hs.71721	ESTs	10.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0
	414937	R38698	Hs.12382	ESTs	10.0
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5
	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	9.5
25	412454	R55745	Hs.167330	ESTs	9.5
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4
	415315	F12240	Hs.250655	prothymosin, alpha (gene sequence 28)	9.3
	441790	AW294909	Hs.132208	ESTs	9.2
	448117	H49129	Hs.172982	ESTs	9.1
30	400661				9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
	409031	AA376836	Hs.76728	ESTs	8.7
35	428106	BE620016	Hs.182470	PTD010 protein	8.3
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapie	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.2
40	418036	Z37976	Hs.83337	latent transforming growth factor beta b	8.0
	456490	U83171	Hs.97203	small inducible cytokine subfamily A (Cy	8.0
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	8.0
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	7.9
45	437073	AI885608	Hs.94122	ESTs	7.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	7.8
50	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	7.8
	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	405800				7.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	7.7
55	426356	BE536836	Hs.98682	hypothetical protein FKSG32	7.7
	423440	R25234	Hs.143434	contactin 1	7.7
	445148	AI214510	Hs.146304	ESTs	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	424087	N69333	Hs.143434	contactin 1	7.6
60	437479	R61866	Hs.101277	ESTs	7.5
	405071				7.5
	421224	AW402154	Hs.125812	ESTs	7.4
	442025	AW887434	Hs.11810	CDA11 protein	7.4
	459476	BE185844		gb:ILS-HT0731-110500-087-c08 HT0731 Homo	7.2
65	430573	AA744550	Hs.136345	ESTs	7.1
	401836				7.1
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152	AB001325	Hs.234642	aquaporin 3	7.1
	419474	AW968619	Hs.155849	ESTs	7.1
	401780				7.1
70	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens c	7.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0
	433098	AW190593	Hs.151143	ESTs	7.0
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	6.9
75	451285	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-	6.8
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.8
	419273	BE271180	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	6.8
	443155	R54485	Hs.23772	ESTs	6.8
	450561	R49674	Hs.25909	ESTs	6.8
80	433068	NM_006456	Hs.288215	sialyltransferase	6.8
	440729	AA904739	Hs.128204	ESTs	6.8
	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting ankyrin-reta	6.7
	423589	AA328082	Hs.209569	ESTs	6.6
	415681	AI379882	Hs.72630	ESTs	6.5

	413510	F13044		gb:HSC3H101 normalized infant brain cDN	6.4
	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4
	453344	BE349075	Hs.44571	ESTs	6.4
5	450642	R39773	Hs.7130	copine IV	6.4
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4
10	400332	S66407	Hs.248032	FLT4	6.4
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (f	6.3
	446129	AW244073	Hs.145946	ESTs	6.3
	454076	AW204712	Hs.61957	ESTs	6.3
	425526	AA359933		gb:EST69040 Fetal lung II Homo sapiens c	6.3
15	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
	434273	AA913143	Hs.26303	ESTs	6.3
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	AI769514	Hs.209890	EST	6.2
	430754	AW862610	Hs.157068	ESTs	6.2
20	438356	AA805530	Hs.48527	ESTs	6.2
	422743	BE304678	Hs.119598	ribosomal protein L3	6.2
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	426388	AW081394	Hs.97103	ESTs	6.2
	452502	AI904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.2
	402546				6.1
25	457534	AI761307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958				6.1
	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs	6.1
	422262	AL022315	Hs.113987	lectin, galactoside-binding, soluble, 2	6.1
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sapiens c	6.0
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	6.0
35	401521				5.9
	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	R13727	Hs.21435	ESTs	5.9
	424806	AA382523	Hs.105689	MSTP031 protein	5.9
40	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9
	457483	AB034694	Hs.272558	endomucin-1	5.9
	417175	R44558	Hs.94002	ESTs	5.9
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
	436427	AI344378	Hs.143399	ESTs	5.8
45	411939	AI365585	Hs.146246	ESTs	5.8
	459053	AI807052	Hs.210361	ESTs	5.8
	411052	AW814950		gb:MR1-ST0206-130400-023-d06 ST0206 Homo	5.7
	431063	Z98949	Hs.326843	hypothetical protein bk125H2.1	5.7
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7
50	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7
	442676	AI733585	Hs.130897	ESTs	5.7
	446443	AV659082	Hs.134228	ESTs	5.7
	400865				5.7
	459080	AW192083	Hs.290855	ESTs	5.7
55	407952	AI215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	5.6
	425705	AF007833	Hs.159265	kruppel-related zinc finger protein hckr	5.6
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	5.6
	422994	AW891802	Hs.296276	ESTs	5.6
60	457148	AF091035	Hs.184627	KIAA0118 protein	5.6
	428356	AL046991	Hs.10338	ESTs	5.6
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	5.6
	402092				5.5
	440526	AI832243	Hs.211471	ESTs	5.5
65	444409	AI792140	Hs.49265	ESTs	5.5
	417877	AI025829	Hs.86320	ESTs	5.5
	458238	AW071521	Hs.333541	beta-amyloid binding protein precursor	5.4
	430702	U56979	Hs.250651	H factor 1 (complement)	5.4
	456189	H91010	Hs.44940	ESTs	5.4
70	427424	AA402453	Hs.113011	ESTs	5.4
	437354	AA749215	Hs.291886	ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-R02 BT0614 Homo	5.4
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.4
	427861	AA813185	Hs.98183	ESTs	5.3
75	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3
	444209	AI753134	Hs.146494	ESTs	5.3
	422831	R02504	Hs.332943	ESTs	5.3
	403180				5.3
80	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	5.3
	430339	W28608	Hs.239625	integral membrane protein 2B	5.3
	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.2
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.2
	437403	AI208149	Hs.121196	ESTs	5.2
	438285	AA782845	Hs.22790	ESTs	5.2

	439901	N73885	Hs.124169	ESTs	5.2
	438507	AA809052	Hs.211275	ESTs	5.2
	449222	AW293984	Hs.197621	ESTs	5.2
5	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	5.2
	419042	T81429	Hs.221065	ESTs	5.2
	436777	AA731199	Hs.293130	ESTs	5.2
	445071	AI280246	Hs.149504	ESTs	5.1
	408016	AW136827	Hs.256096	ESTs	5.1
10	412047	AA934589	Hs.49696	ESTs	5.1
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
15	459580	AA022888	Hs.176065	ESTs	5.1
	417616	R07728	Hs.268668	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate carrier-fi	5.1
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
20	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
	447135	TS8148		gb:yb98g06.s1 Stratagene lung (937210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0
	442240	AI791883	Hs.292719	ESTs	4.9
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
25	427972	AA864870	Hs.181304	putative gene product	4.9
	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093		gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	AI097452	Hs.135095	ESTs	4.9
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
30	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
	436670	AI690021	Hs.201536	ESTs	4.8
	448072	AI459306	Hs.24908	ESTs	4.8
	408936	AL138043	Hs.293549	ESTs	4.8
	412622	AW664708	Hs.171959	ESTs	4.8
35	414943	D80647	Hs.124193	ESTs	4.8
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
	453567	AI742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
40	405130				4.7
	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	4.7
	446218	AV657159		gb:AV657159 GLC Homo sapiens cDNA clone	4.7
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.7
	402176				4.7
45	416577	BE063207	Hs.79381	grancalcin	4.7
	436221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fis, clone OV	4.7
	420480	AL137361	Hs.98173	hypothetical protein	4.7
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	4.6
	435161	AF124150	Hs.272091	ESTs	4.6
50	404793				4.6
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6
	438571	AW020775	Hs.56022	ESTs	4.6
	445924	AI264671	Hs.164166	ESTs	4.6
	444585	AW170015	Hs.6594	ESTs	4.6
55	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
	418274	AI458587	Hs.128677	Human DNA sequence from clone RP1-50024	4.6
	425475	W56339	Hs.107057	ESTs	4.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	4.5
	414272	AI651603	Hs.46988	ESTs	4.5
60	446235	AI564022	Hs.138207	ESTs	4.5
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Homo sapiens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	4.5
	401024				4.5
65	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5
	423449	AI497900	Hs.33067	ESTs	4.5
	405138				4.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo	4.5
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	4.5
70	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4
	441184	AA922009	Hs.150269	ESTs	4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4
	445481	AW661846	Hs.148836	ESTs	4.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	4.4
75	404769				4.4
	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW628326	Hs.27151	ESTs	4.4
	449093	AB035356	Hs.22998	neurexin 1	4.4
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
80	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4
	417888	R23053		gb:yh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4
	435078	AW518888	Hs.40937	ESTs	4.4

	413493	BE144444		gb:MR0-HT0168-141199-002-f09 HT0168 Homo	4.3
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3
	459650	R25754	Hs.301185	ESTs	4.3
5	404828				4.3
	423782	AA472209	Hs.323117	ESTs	4.3
	426867	AA460967	Hs.22668	ESTs	4.3
	426802	AA385182	Hs.46699	ESTs	4.3
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	4.3
10	412112	BE180342		gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3
	401522	N47812	Hs.306198	CGI-35 protein	4.3
	419055	AI365384	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
	410171	H07892	Hs.12431	ESTs	4.3
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	4.3
15	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	4.3
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	4.3
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	4.3
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2
20	433389	AF038171		gb:Homo sapiens clone 23671 mRNA sequenc	4.2
	454356	AW390363	Hs.11522	hypothetical protein from Xq28	4.2
	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5'/3'	4.2
	443998	AI620661	Hs.296276	ESTs	4.2
25	452197	AW023595	Hs.232048	ESTs	4.2
	451117	AA015752	Hs.205173	ESTs	4.2
	404501	AW247252	Hs.75514	nucleoside phosphorylase	4.2
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2
30	440323	AA970614	Hs.127992	ESTs	4.2
	425767	AF054176	Hs.159483	chromosome 1 open reading frame 7	4.1
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin 1	4.1
	413121	T96090	Hs.142678	ESTs	4.1
35	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	4.1
	450235	AA007512	Hs.17538	ESTs	4.1
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypothe	4.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1
40	408496	AI683802	Hs.136182	ESTs	4.1
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
	434101	AA625205	Hs.259599	KIAA1622 protein	4.1
	451837	T92157	Hs.16970	ESTs	4.1
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1
	437630	AI252782	Hs.153026	SWAP-70 protein	4.1
45	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.1
	400216				4.0
	429830	AI537278	Hs.225841	DKFZP434D193 protein	4.0
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0
50	405354				4.0
	427931	AW206512	Hs.186996	ESTs	4.0
	428775	AA434579	Hs.143691	ESTs	4.0
	449422	AA001373	Hs.59821	ESTs	4.0
	453864	AW021407	Hs.21068	hypothetical protein	4.0
55	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0
	420784	T65158	Hs.102399	ESTs, Moderately similar to S65657 alpha	4.0
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	4.0
	429628	H09604	Hs.13268	ESTs	4.0
60	410087	F12079	Hs.332579	ESTs	4.0
	409840	AW502122		gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	4.0
	452854	AA437061	Hs.14060	prokineticin 1 precursor	4.0
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.0
	427443	AA402713	Hs.97872	ESTs	4.0
65	414990	C17758	Hs.221652	Homo sapiens cDNA FLJ14323 fis, clone PL	3.9
	412678	AA115575	Hs.114914	ESTs	3.9
	405629				3.9
	420299	AI056871	Hs.15276	ESTs	3.9
	453098	Z25935	Hs.86379	ESTs	3.9
70	435752	AF230801		gb:Homo sapiens growth hormone receptor	3.9
	441005	Z41305	Hs.303172	Homo sapiens mRNA: cDNA DKFZp547G133 (fr	3.9
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypothe	3.9
	442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	3.9
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.9
75	406697	M21388	Hs.123017	Human unproductively rearranged Ig mu-ch	3.9
	443850	AW014723	Hs.334612	ESTs	3.9
	412677	AW029608	Hs.17384	ESTs	3.9
	422788	AL117352	Hs.120828	Human DNA sequence from clone RPS-876B10	3.9
	405377				3.9
80	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [3.9
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9
	431960	AW241821	Hs.301927	c6.1A	3.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9
	427264	AA400117	Hs.125747	ESTs	3.9

	422746	NM_004484	Hs.119651	glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acut	3.9
	414666	NM_004466	Hs.76828	glypican 5	3.8
5	418217	AJ910647	Hs.13442	ESTs	3.8
	419118	AA234223	Hs.139204	ESTs	3.8
	445017	AJ205493	Hs.176860	ESTs	3.8
	405867				3.8
	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
10	453863	X02544	Hs.572	orosomucoid 1	3.8
	457821	H47166	Hs.124322	ESTs, Weakly similar to A47582 B-cell gr	3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
	456083	U46922	Hs.77252	fragile histidine triad gene	3.8
15	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	3.8
	449057	AB037784	Hs.22941	KIAA1363 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
	414764	AW013887	Hs.72047	ESTs	3.8
	404391				3.7
20	433629	R13140	Hs.13359	ESTs	3.7
	424738	AJ963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7
	440530	AA888646	Hs.174187	ESTs	3.7
25	433930	AA620338	Hs.273781	ESTs	3.7
	409662	AW452320	Hs.279726	ESTs	3.7
	437268	AJ754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	AJ248205	Hs.153244	ESTs	3.7
	408593	R19566	Hs.197617	ESTs	3.7
30	417091	AA193283	Hs.291990	ESTs	3.7
	448556	AW885606	Hs.5064	ESTs	3.7
	423135	N67655	Hs.26411	ESTs	3.7
	400135				3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	3.7
35	457221	AW383197	Hs.218260	ESTs	3.7
	451660	AJ807927	Hs.249601	ESTs	3.7
	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.7
	446818	AJ342668	Hs.279765	ESTs	3.7
	447795	AW295151	Hs.163612	ESTs	3.7
40	427562	R56424	Hs.26534	ESTs	3.6
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.6
	454339	AW381880		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	439274	AF086092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
45	422897	AA679784	Hs.4290	ESTs	3.6
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6
	421908	AW935200	Hs.285814	sprouty (Drosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	3.6
50	400685				3.6
	417154	AJ674701	Hs.21388	ESTs	3.6
	447176	Z42549	Hs.160893	ESTs	3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
	449231	BE410360	Hs.298573	KIAA1720 protein	3.6
55	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
	405977				3.6
	441470	BE503874	Hs.301986	ESTs	3.6
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6
60	441235	AJ884585	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6
	450236	AW162998	Hs.24684	KIAA1376 protein	3.6
	425364	AF052150	Hs.155959	Homo sapiens clone 24533 mRNA sequence	3.6
	426775	AA384564	Hs.108829	ESTs	3.6
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6
	416876	AW501916	Hs.117897	ESTs	3.6
65	400878				3.6
	425153	AW023193	Hs.27046	ESTs	3.6
	432222	AJ204995		gb:an03c03.x1 Stratagene schizo brain S1	3.5
	415047	F13142		gb:HSC3JD031 normalized infant brain cDN	3.5
	401532				3.5
70	446495	D60923	Hs.153460	ESTs	3.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901	BE155527		gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5
75	455697	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	3.5
	405678				3.5
	418207	C14685	Hs.34772	ESTs	3.5
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5
	417027	AA192306	Hs.23926	triadin	3.5
80	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
	417702	R09935	Hs.191146	ESTs	3.5
	445687	W80382	Hs.149297	ESTs	3.5
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypotheti	3.5
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5

	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo sapiens c	3.5
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5
	415621	AJ648602	Hs.55468	ESTs	3.5
5	454437	AJ248173	Hs.191460	hypothetical protein MGC12936	3.5
	446066	AJ343931	Hs.149383	ESTs	3.5
	423374	AB037770	Hs.127656	KIAA1349 protein	3.5
	419347	C15944	Hs.90005	superior cervical ganglia, neural specific	3.5
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, alpha	3.5
10	451776	W45679	Hs.169854	hypothetical protein SP192	3.5
	432305	M62402	Hs.274313	insulin-like growth factor binding protein	3.5
	456995	T89832	Hs.170278	ESTs	3.5
	403323				3.5
	425022	M95724	Hs.154207	centromere protein C 1	3.5
	439394	AA149250	Hs.56105	ESTs	3.5
15	433803	AI823593	Hs.27688	ESTs	3.4
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4
	411474	AW848427		gb:U3-CT0214-150200-075-H10 CT0214 Homo	3.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4
20	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	3.4
	427173	BE255017	Hs.97540	ESTs	3.4
	408112	AW451982	Hs.248613	ESTs	3.4
	446092	N33522	Hs.145894	ESTs	3.4
25	416868	AI656856	Hs.292597	ESTs	3.4
	458234	BE551408	Hs.127196	ESTs	3.4
	419555	AA244416		gb:nc07d11.s1 NC1_CGAP_Pr1 Homo sapiens	3.4
	414314	BE312991		gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	400425	AY004252	Hs.287385	PR domain containing 12	3.4
30	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	3.4
	434053	AW445136	Hs.134946	ESTs	3.4
	449997	AI683052	Hs.201577	KIAA1829 protein	3.4
	433461	AI636047	Hs.197623	ESTs	3.4
	428006	AA418743	Hs.98306	KIAA1862 protein	3.4
35	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-asso	3.4
	443294	AI733625	Hs.133053	ESTs	3.4
	428212	AW444451	Hs.134812	ESTs	3.4
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	3.4
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.4
40	428536	AI143139	Hs.2288	visinin-like 1	3.3
	426597	AA382250	Hs.145601	ESTs	3.3
	410366	AI267589	Hs.302689	hypothetical protein	3.3
	458258	AW406546	Hs.127971	ESTs	3.3
	401738				3.3
45	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.3
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.3
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3
	434998	AW975157	Hs.26037	ESTs	3.3
50	456359	AI967991	Hs.93574	homeo box D3	3.3
	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type I, b	3.3
	454267	AA437199	Hs.656	cell division cycle 25C	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	3.3
55	436602	AI793222	Hs.166817	ESTs	3.3
	449204	AB000099	Hs.23251	Down syndrome critical region gene 4	3.3
	417935	R53697	Hs.170044	ESTs	3.3
	423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	3.3
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	3.3
60	453406	AI192987	Hs.61784	hypothetical protein FLJ14451	3.3
	420164	AW339037	Hs.24908	ESTs	3.3
	447826	AW779317	Hs.258556	ESTs	3.3
	419875	AA853410	Hs.93557	proenkephalin	3.3
	444612	AW138111	Hs.22902	ESTs	3.3
65	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	3.2
	415242	R45986	Hs.295014	ESTs	3.2
	418188	AW139413	Hs.151880	ESTs	3.2
	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	3.2
	421640	AW966652		gb:EST378726 MAGE resequences, MAGI Homo	3.2
70	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.2
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forhead trans	3.2
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2
75	403092				3.2
	452971	AI873878	Hs.91789	ESTs	3.2
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2
	401485				3.2
	401949				3.2
80	457452	AW972675		gb:EST384766 MAGE resequences, MAGL Homo	3.2
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2
	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2
	421200	AA284811	Hs.264433	ESTs	3.2
	430142	NM_000437	Hs.234392	platelet-activating factor acetylhydrola	3.2

	433197	AB040889	Hs.281022	KIAA1456 protein	3.2
	443509	AV645470		gb:AV645470 GLC Homo sapiens cDNA clone	3.2
	440827	A1733110	Hs.128128	ESTs	3.2
5	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferase	3.2
	409257	AW370362		gb:RC1-BT0255-181099-012-007 BT0255 Homo	3.2
	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLJ00038 protein,	3.2
	416789	AA223439	Hs.79933	cyclin I	3.2
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2
10	420156	AW449258	Hs.6187	ESTs	3.2
	455577	BE008341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
	400617	AF151064	Hs.36069	hypothetical protein	3.2
	437129	AL049327	Hs.302057	Homo sapiens mRNA; cDNA DKFZp564E016 (fr	3.2
	451820	AW058357	Hs.337353	ESTs	3.2
15	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2
	419956	AL137939	Hs.40096	ESTs	3.1
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
20	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
	445886	A1793176	Hs.145596	ESTs	3.1
	414401	A1760159	Hs.124833	ESTs	3.1
	441573	BE563966	Hs.6529	ESTs, Weakly similar to I78885 serine/th	3.1
	450725	R71389	Hs.175951	ESTs	3.1
25	458805	A1282933	Hs.23294	hypothetical protein FLJ14393	3.1
	417868	A1078534	Hs.122592	ESTs	3.1
	458391	A1792628	Hs.133273	ESTs	3.1
	423346	A1267677	Hs.127416	synaptotagmin 1	3.1
	454486	AW857077		gb:RC1-CT0302-140300-016-004 CT0302 Homo	3.1
30	408341	AW182952	Hs.249957	ESTs	3.1
	410669	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	3.1
	404907				3.1
	434910	A1333863	Hs.215474	ESTs, Moderately similar to alternative	3.1
	436990	A1149729	Hs.120557	ESTs	3.1
35	441921	A1733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	454673	AW812807		gb:RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
	429470	A1878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1
	408217	A433201	Hs.279860	tumor protein, translationally-controlled	3.1
40	417313	AA195602		gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi	3.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	3.1
	425339	AA936330	Hs.198113	ESTs	3.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.1
45	449078	AK001256	Hs.22975	KIAA1576 protein	3.1
	429608	U49250	Hs.210862	T-box, brain, 1	3.1
	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1
	428465	AW970976	Hs.293653	ESTs	3.1
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1
50	447965	AW292577	Hs.94445	ESTs	3.1
	413918	AW015898	Hs.71245	ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.1
	425810	A1923627	Hs.31903	ESTs	3.1
	427865	AA416931	Hs.126065	ESTs	3.1
55	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	3.1
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1
	448084	A1467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.0
60	422963	M79141	Hs.13234	ESTs	3.0
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.0
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	3.0
	414686	BE409757	Hs.23189	ESTs, Moderately similar to TBB2_HUMAN T	3.0
	458360	A1027207	Hs.132253	ESTs	3.0
65	451829	AW964081	Hs.247377	ESTs	3.0
	445179	A1949743	Hs.224768	ESTs	3.0
	433090	A1720050	Hs.145362	immortalization-upregulated protein	3.0
	432018	AA524447	Hs.152377	ESTs	3.0
	407988	N47760	Hs.285107	hypothetical protein FLJ13397	3.0
70	405911				3.0
	418808	A1821836	Hs.10359	ESTs	3.0
	431900	AW972048	Hs.192534	ESTs	3.0
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
	423952	AW877787	Hs.136102	KIAA0853 protein	3.0
75	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	405793				3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
80	427071	AA397958	Hs.192719	ESTs	3.0
	434961	AW974956		gb:EST387061 MAGE resequences, MAGN Homo	3.0

TABLE 26B:

Pkey: Unique Eos probeset identifier number

CAT number: Accession:		Gene cluster number Genbank accession numbers	
Pkey	CAT Number	Accession	
5	409257	1112994_1	AW370362 AW809101
	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	411052	1230374_1	AW814950 R98513 H69459 BE176242 H54583
	411279	1237516_1	AW884776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258
10	411474	1247047_2	AW848427 AW848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162
	411607	1251251_1	AW853498 AW853442 AW853590 AW853433 AW853592
	411772	1257386_1	BE170301 AW861539 AW904851 BE154336 BE154090 BE154275
	412112	1277883_1	BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898
15	413164	1351422_1	BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345
			AW893614 AW893615 H85799 H83501 BE180220
			BE068494 BE068414 BE068332 BE068347 BE068706 BE068623 BE068450 BE068480 BE068350 BE068295 BE068498 BE068765 BE068328
			BE068778 BE068671 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068580 BE068445 BE068567 BE068521 BE068549
			BE068392 BE068307 BE068692 BE068473 BE068754 BE068476 BE068685 BE068626 BE068591 BE068745 BE068434 BE068759 BE068628
20			BE068723 BE068529 BE068689 BE068383 BE068422 BE068470 BE068522 BE068618 BE068354 BE068748 BE068683 BE068303 BE068602
			BE068739 BE068374 BE068302 BE068625 BE068596 BE068663 BE068429 BE068605 BE068693 BE068672 BE068401 BE068579 BE068329
			BE068390 BE068419 BE068393 BE068447 BE068675 BE068311 BE068540 BE068301 BE068543 BE068719 BE068369 BE068324 BE068588
			BE068568 BE068317 BE068384 BE068547 BE068674 BE068436 BE068321 BE068361 BE068676 BE068499 BE068299 BE068352 BE068410
			BE068293 BE068418 BE068552 BE068598 BE068327 BE068550 BE068712 BE068661 BE068733 BE068525 BE068752 BE068357 BE068330
			BE068565 BE068538 BE068340 BE068537 BE068761 BE068632 BE068758
25	413493	1373555_1	BE144444 BE144430
	413510	1374377_1	F13044 T77009 BE145525 BE145493
	413544	1375671_1	BE147225 BE147205 BE147234
	414220	1426940_1	BE298094 BE267860
	414314	1435028_1	BE312991 BE272945
30	414366	1438636_1	BE549143 BE390613 BE277344
	414456	1447655_1	H74314 BE299593
	414593	1464909_1	BE386764 BE387560
	414630	1468083_1	BE410857 BE390605
	415047	1517450_1	F13142 Z42926 F06135 F06147 H08517 D51360 T75341
35	417313	166644_1	AA195602 W01148 N40632
	417888	1706092_1	R23053 R79884 R76271
	419555	185884_1	AA244416 AA244401
	421249	200649_1	AA285362 AW752386 AW847156 AA285373 AW879575 AW879558
	421640	204833_1	AW966652 AW966653 AA294989 AA385977
40	421813	207654_1	BE048255 AA313083 AA298419
	422760	221034_1	BE409561 BE162756 AW732798
	425526	252776_1	AA359933 AA358889 AW955306 AW962995 AW837746 AW837755 AW837697
	430212	314437_1	AA469153 AI718503 AA469225
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
45	433389	36497_1	AF038171 Z43209 F07347
	434961	396357_1	AW974956 AA781075 AA654944
	435752	41050_1	AF230801 AF230800 AA401795 AA398260
	437483	43756_1	AL390174 AW898817
	440198	48824_2	BE560093
50	443509	57199_1	AV645470 T84636 T82805
	446052	65988_1	AA358760 AA158850 AW062737 AW062738 AV656291
	446218	66686_1	AV657159 BE145509 BE145512 BE145505 BE145507
	447135	70963_1	T58148 AW516579 AW059603
	452346	912205_1	BE243534 BE243752 AI880228 L44326
55	452502	919733_1	AI904296 BE007223 R30687
	454065	998401_1	BE394588 AW024754 BE183166 BE183167
	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
			BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
60	454339	1122972_1	AW381980 BE152244 BE152235 BE152238 BE152232
	454486	1215703_1	AW857077 AW861268 AW847383 AW795787
	454506	1219857_1	AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787
	454673	1228669_1	AW812807 AW812815 AW812802
	455040	1250028_1	AW852286 AW851934 AW852096 AW852274
65	455225	1252318_1	AW996689 AW996380 AW996453 BE085650 AW868687 BE085595
	455577	1333898_1	BE006341 BE006307 BE006311
	455617	1346117_1	BE078070 BE061030 BE077927
	455697	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	455901	1381569_1	BE155527 BE155503 BE155188 BE155126
70	456235	168686_1	AA203637 AA832266 H67452
	456407	184986_1	AW968614 AA243209 AA281411
	457452	339381_1	AW972675 AA541366 AA523039
	459150	919196_1	BE155356 BE153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492
75	TABLE 26C:		
	Pkey:	Unique number corresponding to an Eos probe set	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA	
	Strand:	sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	NI_position:	Indicates DNA strand from which exons were predicted.	
80		Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand
	400661	8118474	Plus
	400685	8118768	Minus
			NI_position
			84912-85187
			72969-73050, 73713-73800

5	400865	1945037	Minus	44482-45526
	400878	9864757	Plus	31493-32842
	401024	8117489	Plus	60551-60802
	401315	9212516	Minus	198960-199619
	401485	7341723	Plus	68009-68209,68841-69077
	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124950,125050-125418
	401738	2982169	Minus	41547-41757
10	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401836	7534063	Plus	71981-72084
	401949	3492889	Plus	160728-161660
	402092	7249154	Minus	107533-108094
	402176	7543687	Minus	10-750
15	402546	7637348	Plus	24673-25170
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403180	7523976	Minus	63603-63759
	403323	8348082	Minus	120366-120845
	403796	8099896	Minus	75073-77664
20	404391	3135305	Minus	26030-26173,27852-27997
	404769	8099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
	404907	7331453	Minus	102880-103828
25	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150449
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
30	405377	5649375	Plus	216656-216848
	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
35	405867	6758731	Minus	74553-75173
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 27A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 27A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor
 R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polypeptide	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth)	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca ⁺⁺ transporting, plasma membrane	15.5	16.8
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
65	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEIN	12.6	16.5
	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
70	446353	AI290919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	R55745	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypothet	9.0	14.7
	412453	R20205	Hs.167330	ESTs	9.0	13.7
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
	409031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.2	8.3
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0	8.9

	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	7.9	9.6
	437073	AI885608	Hs.94122	ESTs	7.9	11.3
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9	16.4
5	440209	H05049	Hs.22269	neurexin 3	7.8	34.3
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypothe	7.8	9.0
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7	5.0
	423440	R25234	Hs.143434	contactin 1	7.7	9.9
	445148	AI214510	Hs.146304	ESTs	7.6	9.1
10	416294	D86980	Hs.79170	KIAA0227 protein	7.6	7.6
	424087	N69333	Hs.143434	contactin 1	7.6	10.3
	437479	R61866	Hs.101277	ESTs	7.5	9.3
	430573	AA744550	Hs.136345	ESTs	7.1	2.8
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1	10.4
15	419474	AW968619	Hs.155849	ESTs	7.1	3.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0	6.9
	433098	AW190593	Hs.151143	ESTs	7.0	9.2
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	6.9	3.1
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.8	5.0
20	443155	R54485	Hs.23772	ESTs	6.8	3.5
	450561	R49674	Hs.25909	ESTs	6.8	8.1
	433068	NM_006456	Hs.288215	sialyltransferase	6.8	2.0
	423589	AA328082	Hs.209569	ESTs	6.6	10.5
	415681	AI379882	Hs.72630	ESTs	6.5	9.0
25	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.4	7.1
	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	9.5
	450642	R39773	Hs.7130	copine IV	6.4	5.7
	429322	D86984	Hs.199243	KIAA0231 protein	6.4	8.2
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4	2.3
30	446129	AW244073	Hs.145946	ESTs	6.3	8.3
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3	2.1
	434273	AA913143	Hs.26303	ESTs	6.2	10.3
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2	3.5
	451301	AI769514	Hs.209890	EST	6.2	12.4
35	438356	AA805530	Hs.48527	ESTs	6.2	8.1
	426388	AW081394	Hs.97103	ESTs	6.2	8.6
	452502	AI904296		gb:PM-BT046-Z20199-286_1 BT046 Homo sapi	6.1	2.8
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1	6.3
	442979	AW440782	Hs.174743	ESTs	6.1	6.3
40	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0	3.8
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9	21.4
	425087	R62424	Hs.126059	ESTs	5.9	8.1
	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9	3.1
	417175	R44558	Hs.94002	ESTs	5.8	12.5
45	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8	2.2
	436427	AI344378	Hs.143399	ESTs	5.8	13.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7	4.4
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7	12.5
	442676	AI733585	Hs.130897	ESTs	5.7	6.8
50	446443	AV659082	Hs.134228	ESTs	5.7	6.4
	459080	AW192083	Hs.290855	ESTs	5.6	15.6
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	5.6	8.2
	428356	AL046991	Hs.10338	ESTs	5.6	6.2
	417877	AI025829	Hs.86320	ESTs	5.4	4.9
55	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3	13.1
	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3	6.6
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.2	6.0
	438285	AA782845	Hs.22790	ESTs	5.2	7.3
	439901	N73885	Hs.124169	ESTs	5.2	2.7
60	449222	AW293984	Hs.197621	ESTs	5.2	8.1
	408016	AW136827	Hs.256096	ESTs	5.1	2.5
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1	3.0
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1	7.3
	409263	AA089573	Hs.50319	ESTs	5.1	12.9
65	453830	AA534296	Hs.20953	ESTs	5.1	3.4
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0	4.8
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0	20.1
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0	3.9
	448505	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0	6.1
70	442240	AI791883	Hs.292719	ESTs	4.9	6.7
	427972	AA864870	Hs.181304	putative gene product	4.9	5.2
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9	2.8
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8	3.7
	408936	AL138043	Hs.293549	ESTs	4.8	6.6
75	414943	D80647	Hs.124193	ESTs	4.8	3.1
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8	2.3
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8	9.1
	416577	BE063207	Hs.79381	granulatin	4.7	2.2
	420480	AL137361	Hs.98173	hypothetical protein	4.7	2.8
80	404793				4.6	2.2
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6	7.4
	438571	AW020775	Hs.56022	ESTs	4.6	5.4
	444585	AW170015	Hs.6594	ESTs	4.6	6.0
	414272	AI651603	Hs.46988	ESTs	4.5	2.2

5	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5	30.9
	423449	AI497900	Hs.33067	ESTs	4.5	20.8
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0
	429876	AB028977	Hs.225974	KIAA1054 protein	4.4	19.2
	429726	AW626326	Hs.27151	ESTs	4.4	10.2
10	449093	AB035356	Hs.22998	neurexin 1	4.4	9.4
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4	15.1
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4	8.2
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4	2.4
	435078	AW518888	Hs.40937	ESTs	4.4	5.7
15	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3	5.9
	426867	AA460967	Hs.22668	ESTs	4.3	6.0
	412112	BE180342		gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3	3.2
	410171	H07892	Hs.12431	ESTs	4.3	5.3
	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2	5.0
20	421249	AA285362		gb:HTH277 HTC0L1 Homo sapiens cDNA 5'3'	4.2	3.5
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2	3.9
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin 1	4.1	7.0
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypothe	4.1	3.9
25	408496	AI683802	Hs.136182	ESTs	4.1	4.7
	434101	AA625205	Hs.259599	KIAA1622 protein	4.1	6.3
	430212	AA469153		gb:nc67104.s1 NCI_CGAP_Prl Homo sapiens	4.0	2.5
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	4.0	7.4
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0	5.1
30	441869	NM_003947	Hs.8004	huntinglin-associated protein interactin	4.0	32.3
	429628	H09604	Hs.13268	ESTs	4.0	4.5
	410087	F12079	Hs.332579	ESTs	4.0	6.9
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.0	2.6
	441005	Z41305	Hs.303172	Homo sapiens mRNA: cDNA DKFZp547G133 (fr	3.9	21.7
35	412677	AW029608	Hs.17384	ESTs	3.9	2.2
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9	7.2
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9	2.2
	414666	NM_004466	Hs.76828	glypican 5	3.8	6.2
	418217	AI910647	Hs.13442	ESTs	3.8	3.2
40	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	ESTs	3.8	10.7
	433629	R13140	Hs.13359	ESTs	3.7	2.7
	424738	AI963740	Hs.46826	ESTs	3.7	2.1
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7	5.3
45	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.7	53.7
	423135	N67655	Hs.26411	ESTs	3.7	21.7
	446818	AI342668	Hs.279765	ESTs	3.7	2.6
	427562	R56424	Hs.26534	ESTs	3.6	3.6
	439274	AF086092	Hs.48372	ESTs	3.6	34.5
50	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6	6.0
	422897	AA679784	Hs.4290	ESTs	3.6	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6	24.6
	417154	AI674701	Hs.21388	ESTs	3.6	5.8
	447176	Z42549	Hs.160893	ESTs	3.6	6.4
55	405977				3.6	3.9
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 lis, clone C	3.6	5.4
	426775	AA384564	Hs.108829	ESTs	3.6	3.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6	2.8
60	425153	AW023193	Hs.27046	ESTs	3.6	4.9
	446495	D60923	Hs.153460	ESTs	3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
	418421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
	418207	C14685	Hs.34772	ESTs	3.5	16.0
65	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5	6.2
	417027	AA192306	Hs.23926	triadin	3.5	2.5
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothe	3.5	5.5
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5	23.6
70	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5	42.3
	433803	AI823593	Hs.27688	ESTs	3.4	3.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4	9.8
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4	4.7
75	427173	BE255017	Hs.97540	ESTs	3.4	2.4
	446092	N33522	Hs.145894	ESTs	3.4	3.5
	416868	AI656856	Hs.292597	ESTs	3.4	4.5
	458234	BE551408	Hs.127196	ESTs	3.4	4.5
	434053	AW445136	Hs.134946	ESTs	3.4	3.9
80	428536	AI143139	Hs.2288	visinin-like 1	3.3	42.3
	410366	AI267589	Hs.302689	hypothetical protein	3.3	14.4
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3	4.6
	434998	AW975157	Hs.26037	ESTs	3.3	4.7
	456359	AI967991	Hs.93574	homeo box D3	3.3	4.4
	426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type I, b	3.3	5.2
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3	9.0
	419875	AA853410	Hs.93557	proenkephalin	3.3	3.6

5	444612	AW138111	Hs.22902	ESTs	3.3	3.0
	415242	R45986	Hs.295014	ESTs	3.2	2.2
	421640	AW966652		gb:EST378726 MAGC resequences, MAGI Homo	3.2	3.8
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fs, clone C	3.2	2.4
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2	3.2
10	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2	2.2
	403092				3.2	2.9
	452971	AI873878	Hs.91789	ESTs	3.2	4.5
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2	2.7
	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2	2.8
15	421200	AA284811	Hs.264433	ESTs	3.2	2.7
	440827	AI733110	Hs.128128	ESTs	3.2	2.1
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2	4.3
	420156	AW449258	Hs.6187	ESTs	3.2	19.0
	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2	2.0
20	419956	AL137939	Hs.40096	ESTs	3.1	8.7
	423930	AA332697	Hs.42721	ESTs	3.1	2.7
	417868	AI078534	Hs.122592	ESTs	3.1	12.6
	423346	AI267677	Hs.127416	synaptotagmin 1	3.1	12.0
	441921	AI733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1	4.3
25	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1	5.3
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1	7.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	6.3
	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	30.1
	429608	U49250	Hs.210662	T-box, brain, 1	3.1	2.2
30	442308	AA899402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1	3.0
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1	10.9
	427865	AA416931	Hs.126065	ESTs	3.1	7.5
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1	3.4
	451829	AW964081	Hs.247377	ESTs	3.0	6.2
35	405911				3.0	2.4
	418808	AI821836	Hs.10359	ESTs	3.0	6.2
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0	5.1
	423952	AW877787	Hs.136102	KIAA0853 protein	3.0	2.1
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0	2.1
40	405793				3.0	2.7
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	14.3
	427071	AA397958	Hs.192719	ESTs	3.0	2.1
	453534	NM_014796	Hs.33187	KIAA0748 gene product	3.0	14.5
	413903	AA496493	Hs.23136	ESTs	3.0	2.2
45	426866	U02330	Hs.172816	neuregulin 1	3.0	11.3
	434945	AB033065	Hs.4280	KIAA1239 protein	3.0	3.5
	412639	AW961284	Hs.296235	ESTs	2.9	4.9
	453590	AF150278	Hs.33578	KIAA0820 protein	2.9	33.1
	414502	AL133721	Hs.224680	ESTs	2.9	2.3
50	434367	AB020700	Hs.3830	KIAA0893 protein	2.9	23.1
	425121	AI797511	Hs.154679	synaptotagmin I	2.9	8.1
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.9	20.8
	401213				2.9	3.2
	401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9	3.4
55	415191	AA190381	Hs.120810	ESTs	2.9	3.0
	449275	AW450848	Hs.205457	perlecan	2.9	5.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.9	35.0
	411421	BE272110	Hs.21177	ESTs	2.9	2.0
	430865	AI073424	Hs.5232	HSPC125 protein	2.9	11.4
60	437486	AW952089	Hs.5636	RAB6A, member RAS oncogene family	2.9	2.2
	442357	AI458586	Hs.135706	ESTs	2.9	6.0
	408274	R17315		gb:yg12g11.1 Soares infant brain 1N18 H	2.9	2.2
	444185	AW298350	Hs.66020	ESTs	2.8	5.0
	420173	AA256151	Hs.22999	ESTs	2.8	5.1
65	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.8	7.0
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	2.8	4.4
	440260	AI972867	Hs.7130	copine IV	2.8	10.6
	417084	H08370	Hs.33067	ESTs	2.8	8.4
	438257	AW474419	Hs.224794	ESTs	2.8	2.8
70	441934	T23939	Hs.7344	ESTs	2.8	6.2
	447885	F11528	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	2.8	3.5
	423552	AF107028	Hs.129783	sodium channel, voltage-gated, type II,	2.8	3.4
	450940	AI744943	Hs.143209	ESTs, Weakly similar to I38022 hypotheti	2.8	14.4
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.8	21.7
75	445887	AI263105	Hs.145597	ESTs	2.8	5.1
	425494	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr	2.8	2.4
	438202	AW169287	Hs.22588	ESTs	2.8	11.9
	436199	R38946	Hs.127951	hypothetical protein FLJ14503	2.8	6.0
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.8	2.4
80	415462	R52692	Hs.12698	ESTs	2.8	3.4
	418070	NM_000844	Hs.83407	glutamate receptor, metabotropic 7	2.8	4.5
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.8	9.5
	430371	D87466	Hs.240112	KIAA0276 protein	2.8	7.0
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp76202215 (f	2.7	2.5
	415838	R44336	Hs.7093	ESTs	2.7	3.6
	438675	AA813725	Hs.213568	ESTs	2.7	2.5
	419558	AW953679		gb:EST365749 MAGC resequences, MAGC Homo	2.7	3.1

	446318	AI949389	Hs.18067	ESTs	2.7	4.1
	445183	AB007877	Hs.12385	KIAA0417 gene product	2.7	5.3
	457012	R41480	Hs.127630	ESTs	2.7	19.0
5	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	7.2
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.7	2.8
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.7	3.8
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	2.7	6.9
	434731	AA648049	Hs.121518	ESTs	2.7	5.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
	407709	AA456135	Hs.23023	ESTs	2.7	2.5
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	2.7	3.3
	443305	AI050693	Hs.133318	ESTs	2.7	5.9
	435648	H24347	Hs.27524	ESTs	2.7	15.0
15	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.7	2.7
	436771	AW975687	Hs.292979	ESTs	2.7	6.0
	428689	NM_014351	Hs.189810	sulfotransferase family 4A, member 1	2.7	4.8
	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	2.7	4.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.7	3.1
20	410330	AW023630	Hs.46786	ESTs	2.6	29.5
	434398	AA121098	Hs.3838	serum-inducible kinase	2.6	2.6
	438831	BE263273	Hs.6439	synapsin II	2.6	7.8
	419066	Z98492	Hs.6975	PRO1073 protein	2.6	3.4
	412643	AW971239	Hs.293982	ESTs	2.6	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	2.6	17.9
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6	2.9
	401421				2.6	2.0
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	2.6	3.8
30	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583	AW994403	Hs.100861	hypothetical protein FLJ14500	2.6	3.7
	417919	AI928203	Hs.86379	ESTs	2.6	3.0
	434293	NM_004445	Hs.3796	EphB6	2.6	3.2
35	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6	6.4
	443037	AW500305	Hs.299166	syntaxin 7	2.6	2.2
	440736	D56919	Hs.265848	myomegalin	2.6	7.1
	404648				2.6	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
40	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.6	3.9
	441190	H09073	Hs.25046	ESTs	2.6	3.1
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.6	2.9
	442731	AI868167	Hs.131044	ESTs	2.6	4.1
	416836	D54745	Hs.80247	cholecystokinin	2.6	14.9
45	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
	436321	AA709133	Hs.180144	ESTs	2.5	2.8
	439693	AI741816	Hs.125897	ESTs	2.5	3.6
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664	Homo sapiens mRNA; cDNA DKFZp434A1627 (f	2.5	3.8
50	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	2.5	3.1
	443992	AW022228	Hs.322922	ESTs	2.5	27.9
	444124	R43097	Hs.6818	ESTs	2.5	5.3
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.5	38.0
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	2.5	3.8
55	446277	AI284218	Hs.159204	ESTs	2.5	2.2
	410111	AI620206	Hs.189647	ESTs	2.5	3.5
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	2.5	4.8
	410718	AI920783	Hs.191435	ESTs	2.5	4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
60	426274	AW968000	Hs.143389	ESTs, Weakly similar to T14318 ubiquitin	2.5	2.8
	433496	AF064254	Hs.49765	VLCS-H1 protein	2.5	4.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	2.5	3.3
	437368	AI471969	Hs.182606	ESTs	2.5	3.0
	441985	BE047625	Hs.169815	ESTs	2.5	3.6
65	410025	BE220489	Hs.113592	ESTs, Moderately similar to I54374 gene	2.5	9.2
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.5	3.6
	429956	AI374651	Hs.22542	ESTs	2.5	23.9
	429028	AA443439	Hs.48797	ESTs	2.5	2.8
	438109	AI076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.5	2.3
	440888	N45600	Hs.326880	ESTs	2.5	3.9
	445246	AI217713	Hs.147586	ESTs	2.5	2.6
	440152	AB002376	Hs.7006	KIAA0378 protein	2.4	23.6
	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	2.4	2.1
75	415122	D60708	Hs.22245	ESTs	2.4	3.9
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	2.4	9.8
	437948	AA772920	Hs.303527	ESTs	2.4	9.8
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-6	2.4	2.8
	427115	AW972853	Hs.112237	ESTs	2.4	2.2
80	452074	BE299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4	10.0
	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-activat	2.4	3.5
	434520	AA205273	Hs.177011	hypothetical protein	2.4	3.1
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.4	3.0
	442272	AA988302	Hs.129172	ESTs	2.4	2.1

	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.4	2.7
	444647	H14718	Hs.11506	Human clone Z3589 mRNA sequence	2.4	2.8
	415827	H17462	Hs.23079	ESTs	2.4	15.0
5	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.4	3.9
	445200	AA084460	Hs.12409	somatostatin	2.4	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA: cDNA DKFZp564C1416 (f	2.4	2.4
	420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein	2.4	4.3
	432122	AA526514		gb:nif0102.s1 NCI_CGAP_Ov2 Homo sapiens	2.4	4.3
10	444125	AI124882	Hs.118121	ESTs	2.4	3.5
	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.4	10.8
	457519	X69438	Hs.3052	early growth response 4	2.4	2.4
	409371	R51736	Hs.12381	ESTs	2.4	2.1
	456303	AA224872	Hs.115088	ESTs	2.4	3.2
15	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.4	23.4
	400979				2.4	4.1
	435296	R49685	Hs.24980	ESTs	2.4	6.5
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4	18.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	2.2
20	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.4	2.7
	408974	AW015458	Hs.297017	ESTs	2.4	2.5
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	2.4	2.8
	413153	N94205		gb:za27a08.r1 Soares fetal liver spleen	2.4	2.5
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
	424940	AA985308	Hs.194327	ESTs	2.3	6.3
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	2.3	4.1
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	2.3	2.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.3	8.7
30	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.3	3.2
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.3	5.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.3	54.7
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	2.3	9.1
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
35	414828	AA156651		gb:z105h05.r1 Soares_pregnant_uterus_NbH	2.3	2.4
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3	8.5
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	2.3	26.3
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	2.3	2.5
	423420	AI571364	Hs.128382	Homo sapiens mRNA: cDNA DKFZp7111224 (f	2.3	7.6
40	439450	R51613	Hs.125304	ESTs	2.3	26.3
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	2.3	2.2
	447179	AW015633	Hs.157299	ESTs	2.3	3.8
	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	2.3	2.3
	433449	AW772282		gb:hn71b05.x1 NCI_CGAP_Kd11 Homo sapien	2.3	3.8
45	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	2.5
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.3	7.8
	425130	AA448208	Hs.99163	ESTs	2.3	4.1
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	2.5
	438283	AI458931	Hs.37282	ESTs	2.3	4.2
50	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.3	3.0
	412100	AW892731		gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.7
	448981	AI968719	Hs.195387	ESTs	2.3	3.2
	416101	R24854	Hs.268806	ESTs	2.3	6.5
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.3	40.1
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	2.3	2.9
	420230	AL034344	Hs.284186	forkhead box C1	2.3	2.4
	451559	AL119980	Hs.20935	hypothetical protein DKFZp761D221	2.3	5.7
	404835				2.3	2.1
60	456765	AI497900	Hs.33067	ESTs	2.3	4.1
	455517	AW984068		gb:RCO-HN0006-160300-011-e06 HN0006 Homo	2.3	2.4
	408206	AF041853	Hs.43670	kinesin family member 3A	2.2	18.5
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.2	3.9
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	2.2	2.6
65	458694	F12832	Hs.13298	ESTs	2.2	4.9
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	439642	W81441	Hs.153967	ESTs	2.2	2.4
	450138	AW152104	Hs.200879	ESTs	2.2	4.9
	454222	BE144344	Hs.7589	ESTs, Weakly similar to A45010 X-linked	2.2	3.7
70	405326				2.2	2.7
	431342	AW971018	Hs.21659	ESTs	2.2	5.2
	453101	AW952776	Hs.94943	ESTs	2.2	3.3
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	2.2	2.8
	451398	AI793124	Hs.144479	ESTs	2.2	4.6
75	438208	AL041224	Hs.65379	ESTs	2.2	10.4
	408449	NM_004408	Hs.166161	dynamitin 1	2.2	6.1
	414130	AI670831	Hs.71592	Homo sapiens cDNA: FLJ21893 fis, clone H	2.2	3.1
	445016	U79716	Hs.12246	refin	2.2	3.9
	424375	AF070547	Hs.146312	Homo sapiens clone 24820 mRNA sequence	2.2	2.3
80	424645	NM_014682	Hs.151449	KIAA0535 gene product	2.2	11.7
	409729	D51315	Hs.106289	ESTs	2.2	4.9
	432809	AA565509	Hs.131703	ESTs	2.2	19.9
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4
	428532	AF157326	Hs.184786	TBP-interacting protein	2.2	6.5

5	413074	AI871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
	452768	AW069459	Hs.61539	ESTs	2.2	2.0
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.2	3.2
	426281	AK000987	Hs.169111	oxidation resistance 1	2.2	2.3
10	428411	AW291464	Hs.10338	ESTs	2.2	2.3
	413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	2.2	3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	7.9
	405385				2.2	2.4
15	447285	AI371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	452667	T87219	Hs.13219	ESTs	2.2	3.1
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	2.1	8.3
	410339	AI916499	Hs.298258	ESTs	2.1	3.2
	413231	D87461	Hs.75244	BCL2-like 2	2.1	4.5
20	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	2.1	2.2
	451952	AL120173	Hs.301663	ESTs	2.1	36.5
	415841	Z45637	Hs.7093	ESTs	2.1	2.4
	441086	AI928489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1	2.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
25	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.1	5.3
	449712	R56545	Hs.6100	ESTs	2.1	4.5
	409660	AW452065	Hs.258905	ESTs	2.1	2.1
	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1	5.4
	434138	AA625804		gb:zu88h01.s1 Soares_testis_NHT Homo sap	2.1	3.0
30	448610	NM_006157	Hs.21602	nel (chicken)-like 1	2.1	4.8
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.1	2.9
	414876	AW950925	Hs.924	crystallin, mu	2.1	3.4
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.7
	451249	AA016227	Hs.27280	ESTs	2.1	4.1
35	451475	T19093	Hs.26450	KIAA0725 protein	2.1	2.1
	448743	AB032962	Hs.21896	KIAA1136 protein	2.1	29.7
	430814	U89336	Hs.247993	NGS protein	2.1	2.7
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.1	2.3
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
40	427335	AA448542	Hs.251677	G antigen 7B	2.1	2.2
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	2.1	2.3
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	2.1	5.9
	446383	T05816	Hs.92511	ESTs	2.1	2.9
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	2.1	2.1
45	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111	R39039	Hs.328455	EST	2.1	3.3
	452238	F01811	Hs.187931	ESTs	2.1	4.9
	445279	R41900	Hs.22245	ESTs	2.1	9.8
	448799	AI937094	Hs.179080	ESTs	2.1	3.1
50	418338	NM_002522	Hs.84154	neuronal pentraxin I	2.1	8.3
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	4.1
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
	429954	AI918130	Hs.21374	ESTs	2.1	7.2
55	415292	H29016	Hs.200576	ESTs	2.1	3.9
	423563	R34734	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.1	3.1
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	2.1	4.7
	459309	AA040620	Hs.5672	hypothetical protein AF140225	2.1	2.2
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
60	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	2.1	5.4
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin	2.1	6.6
	448792	R42550	Hs.12826	ESTs	2.1	4.1
	449500	AW956345	Hs.12926	ESTs	2.1	2.4
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	2.1	5.8
65	433361	AW469373	Hs.300141	ribosomal protein L39	2.1	2.7
	452946	X95425	Hs.31092	EphA5	2.1	5.0
	426167	AF039023	Hs.167496	RAN binding protein 6	2.0	2.2
	453666	AW015681	Hs.135229	ESTs, Weakly similar to A2BP_HUMAN ATAXI	2.0	3.1
	424632	AB014523	Hs.151406	KIAA0623 gene product	2.0	3.5
70	448589	AF017090	Hs.21554	KIAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
	445627	AW818475	Hs.7363	ESTs	2.0	2.1
	417092	H97508	Hs.181165	eukaryotic translation elongation factor	2.0	2.5
	453653	AW505554	Hs.144559	ESTs	2.0	4.7
75	435850	AF250847	Hs.283514	mitochondrial ceramidase	2.0	3.7
	435086	AW975243	Hs.122596	ESTs	2.0	2.1
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.0	2.8
	431645	AF078849	Hs.266483	dynein light chain-A	2.0	2.5
80	429834	AI929645	Hs.225936	synapsin I	2.0	3.6
	439607	BE540565	Hs.159460	ESTs	2.0	17.5
	408033	AW138045	Hs.242256	ESTs	2.0	4.0
	430317	AB020645	Hs.239189	glutaminase	2.0	2.7
	419631	AW188117	Hs.303154	pepoye protein 3	2.0	2.6
	432660	AI288430	Hs.64004	ESTs	2.0	2.3
	454048	H05626	Hs.6921	ESTs	2.0	15.9
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0	3.1

5	423246	AL119114	Hs.77196	spectrin, alpha, non-erythrocytic 1 (atp)	2.0	2.9
	415898	AI267700	Hs.317584	ESTs	2.0	4.8
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORT1	2.0	5.1
	424983	AI742434	Hs.169911	ESTs	2.0	15.9
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.0	2.7
	450006	AI241555	Hs.60171	ESTs	2.0	3.5

TABLE 27B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

15	Pkey	CAT Number	Accession
	408274	104999_1	R17315 Z43964 AA053547
	412100	1277224_1	AW892731 H08502 Z45826
	412112	1277883_1	BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 AW893614 AW893615 H85799 H83501 BE180220
20	413153	1350849_1	N94205 BE067565 BE067556
	413510	1374377_1	F13044 T77009 BE145525 BE145493
	414828	149563_1	AA156651 AA156622 R14472
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
25	419558	185904_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
	421249	200649_1	AA285362 AW752386 AW847156 AA285373 AW879575 AW879558
	421640	204833_1	AW966652 AW966653 AA294989 AA385977
	429995	311738_1	AA463571 AI277645 AL118763
30	430212	314437_1	AA469153 AI718503 AA469225
	432122	341756_1	AA526514 AW973343 AA554293
	433449	366532_1	AW772282 AA592974
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
35	437483	43756_1	AL390174 AW898817
	439780	47673_1	AL109688 R23665 R26578
	452502	919733_1	AI904296 BE007223 R30687
	455517	1321782_1	AW984068 AW984072 AW984077
	456407	184986_1	AW968614 AA243209 AA281411

TABLE 27C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NT_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	NT_position
	400979	8072554	Plus	160842-161028
	401213	9858408	Plus	98243-98380,98489-98619
	401421	7452889	Minus	142291-142461
50	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	404648	9796894	Minus	115334-116020
	404793	7232206	Minus	61087-61590
	404835	6970743	Plus	85462-85684,88139-88287,90338-91018,94827-94990
55	405326	4375975	Plus	10633-10709,30805-30893,38078-38253,55112-55327,57718-57818,66696-66841
	405385	6552772	Plus	48332-48454
	405793	1405887	Minus	89197-89453
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 28A: About 139 genes up-regulated in glioma compared to normal adult tissues
 Table 28A lists about 139 genes up-regulated in glioma compared to normal adult tissues. In order to identify new genes that are associated with glioma, a non-redundant set of 6614 genes that have been previously identified were removed from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. Genes associated with glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes). The "average" glioma level was set to the 94th percentile value amongst various glioblastoma, astrocytoma, and oligodendroglioma specimens; the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant organs and tissues and other non-malignant brain tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. Predicted protein domains are noted.

Pkey:	Unique Eos probeset identifier number
ExAccon:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
Prot. Doms:	Predicted Protein Domains
R1:	glioma vs normal adult tissues

75	Pkey	ExAccon	UniGene ID	Unigene Title	Protein Domains	R1
	443902	W28470	Hs.12600	N-ethylmaleimide-sensitive factor a		4.0
	441476	R44566	Hs.173134	ESTs		4.0
	446048	AI272364	Hs.182081	KIAA1811 protein		3.8
80	407061	X97748		gb:H.sapiens PTX3 gene promotor reg		3.7
	414323	NM_014759	Hs.334688	KIAA0273 gene product	fn3;TM;	3.6
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length inser	lactamase_B,Rhomboid,TPR	3.6
	429319	AL023754	Hs.199068	similar to calcium/calmodulin depen	pklnase;TM;SS	3.6
	443412	W84893	Hs.9305	angiotensin receptor-like 1		3.5
	425533	T47802	Hs.9305	angiotensin receptor-like 1		3.5

5	408610	AW026692	Hs.285050	ESTs	ion_trans_K_tetra,Kv2chan	3.4
	450678	AL109703	Hs.25314	Homo sapiens mRNA full length inser		3.4
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, recep	Y_phosphatase,ART;TM;SS	3.4
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA seque		3.4
	412581	AA224244	Hs.182704	ESTs, Moderately similar to alterna		3.3
	424911	AA984364	Hs.7913	ESTs		3.3
	452753	AA028049	Hs.277728	SEC14 (S. cerevisiae)-like 2	CRAL_TRIO	3.3
	436648	R18656	Hs.352385	ESTs	pkinase,pkinase_C,PMP22_C	3.2
10	452130	AW248349	Hs.28088	SGC32445 protein	TB2_DP1_HVA22;TM;SS	3.2
	448848	AF131851	Hs.22241	hypothetical protein		3.2
	426470	AA528794	Hs.128644	ESTs		3.2
	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (104kd)	ank,DAGKa,DAGKc,DAG_PE-bi	3.2
	439783	AI125760	Hs.24835	hypothetical protein FLJ14594	ig_LRR,LRRNT,LRRCT;TM;S	3.2
15	411358	R47479	Hs.94761	KIAA1691 protein	TM;SS	3.2
	409433	AA074382	Hs.135255	ADAMTS14		3.2
	456940	H46986	Hs.31861	ESTs		3.1
	423744	D26158	Hs.1701	ELAV (embryonic lethal, abnormal vi	rm, Gene66;	3.1
	432227	U28389	Hs.274122	erythrocyte membrane protein band 4	VHP;TM;	3.1
20	449181	X96783	Hs.23179	synaptotagmin V	C2;TM;SS	3.1
	422274	NM_015564	Hs.114169	KIAA0416 protein	LRR,LRRNT,LRRCT;TM;SS	3.1
	424607	NM_016848	Hs.151123	neuronal Shc	PID,SH2;	3.1
	416898	BE219510	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02	EGF,Rhabd_glycop;TM;SS=	3.1
	438162	NM_014618	Hs.6090	deleted in bladder cancer chromosom	TM;SS	3.1
25	439892	AL043463	Hs.6755	RaP2 interacting protein 8	RUN;SS	3.1
	445330	R52656	Hs.21691	ESTs	7tm_1	3.0
	451766	NM_001406	Hs.26988	ephrin-B3	Ephrin;TM;SS	3.0
	444457	AI204146	Hs.92556	ESTs	Fork_head	3.0
	458247	R14439	Hs.209194	ESTs		3.0
30	424616	U72671	Hs.151250	intercellular adhesion molecule 5,	ig_ICAM_N;TM;SS	3.0
	408971	R38990	Hs.13485	ESTs		3.0
	423940	NM_012429	Hs.277728	SEC14 (S. cerevisiae)-like 2	CRAL_TRIO;TM;	3.0
	458124	AW005548	Hs.124590	ESTs		3.0
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA seque		3.0
35	444808	H20019	Hs.286084	ESTs	ank,ras,PH,ArfGap,HCO3_co	3.0
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase;TM;	2.9
	424016	AW163729	Hs.6140	hypothetical protein MGC15730	ig;SS	2.9
	421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen;TM;SS	2.9
	418055	R18516	Hs.351299	ESTs, Weakly similar to 138022 hypo	ZZ_ZZ	2.9
40	444819	AI697836	Hs.148433	ESTs		2.9
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel	ASC;TM;	2.9
	416237	H30684	Hs.159863	ESTs		2.9
	432270	AK001008	Hs.274233	Homo sapiens cDNA FLJ10146 fis, clo		2.9
45	405569			NM_031481*:Homo sapiens soluble car	mito_carr;TM;SS	2.9
	428950	BE311879	Hs.194673	phosphoprotein enriched in astrocyt	DED;TM;	2.9
	426128	NM_001471	Hs.160717	gamma-aminobutyric acid (GABA) B re	7tm_3,sushi,ANF_receptor;	2.9
	447758	H17302	Hs.93967	ESTs, Weakly similar to NBHUC8 deco	LRR,LRRNT,LRRCT;TM;SS	2.9
	445331	H04489	Hs.12520	Homo sapiens clone 23568, 23621, 23	PC_rep	2.9
50	431010	BE251246	Hs.248214	complexin 1	TM;	2.9
	433065	N62902	Hs.343660	Homo sapiens PAC clone RP4-651K2 fr	:SS	2.9
	426845	AB025186	Hs.172740	microtubule-associated protein, RP1	EB1,CH;TM;	2.9
	454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane,PRK	2.9
	438859	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 prot	bZIP,K-box,7tm_2,EGF_cadh	2.9
	410515	F12086	Hs.4257	ESTs	PID,SH2,PID,SH2	2.8
55	434022	R18374	Hs.117956	ESTs	hormone_rec,zf-C4	2.8
	428960	AF052224	Hs.194684	bassoon (presynaptic cytomatrix pro	Carla_C4,RPH3A_effector;T	2.8
	426290	AB007918	Hs.169182	KIAA0449 protein	WD40;TM;	2.8
	417287	AI831678	Hs.285714	KIAA1599 protein	C2;TM;	2.8
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	PT2;TM;SS	2.8
60	417941	AI056049	Hs.96297	ESTs	Band_41,ERM	2.8
	452707	AI093823	Hs.45070	ESTs		2.8
	424873	AB018294	Hs.153610	KIAA0751 gene product	C2,PDZ;TM;	2.8
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related mol	Ets;TM;	2.8
65	415935	H09663	Hs.106490	ESTs	PID	2.8
	437999	AW905038	Hs.90242	ESTs	ion_trans	2.8
	428248	AI126772	Hs.40479	ESTs		2.8
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HU	Gelsolin,VHP,p450	2.8
	406634	AA386235	Hs.74576	GDP dissociation inhibitor 1	GDI;TM;	2.8
	453439	AI572438	Hs.32976	guanine nucleotide binding protein	G-gamma;TM;	2.8
70	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CO	rm	2.8
	420888	AB006713	Hs.100058	dihydropyrimidinase-like 4	Dihydroorotase;TM;	2.7
	440001	AI740721	Hs.128292	ESTs		2.7
	417622	AW298163	Hs.82318	WAS protein family, member 3	WH2;TM;	2.7
	438626	AI198059	Hs.26370	ESTs		2.7
75	404439			ENSP00000067222*:Mitochondrial 28S	OLF;SS	2.7
	448375	NM_004644	Hs.21022	adaptor-related protein complex 3,	Adaptin_N;TM;	2.7
	420989	AB002372	Hs.323833	synaphilin	TM;	2.7
	419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide e	cNMP_binding,DEP,RasGEF,R	2.7
	414562	AW955734	Hs.112195	ESTs, Weakly similar to 2108402A ca		2.7
80	410865	T16342	Hs.66727	ESTs, Weakly similar to T31613 hypo	IRK	2.7
	421146	AI082215	Hs.97993	ESTs, Moderately similar to SERP1		2.7
	419087	AI671245	Hs.24835	hypothetical protein FLJ14594	ig_LRR,LRRNT,LRRCT;TM;S	2.7
	421499	AI271438	Hs.236131	homeodomain-interacting protein kin	pkinase,Peptidase_M1;TM	2.7
	425014	AI251449	Hs.171939	ESTs	PID,PDZ	2.7

5	448655	AL035289	Hs.21708	hypothetical protein from clone 248	TM;SS	2.7
	424410	W79027	Hs.271762	ESTs		2.7
	447117	AI362798	Hs.40183	ESTs		2.7
	447478	BE618843	Hs.28144	fibronectin type 3 and SPRY domain-	fn3,SPRY;TM;	2.7
	437645	R20728	Hs.21164	ESTs		2.7
	433698	H24201	Hs.247423	adducin 2 (beta)	Aldolase-II;TM;	2.7
	419701	AA248999	Hs.7913	ESTs		2.7
10	410510	AW294625	Hs.64064	potassium voltage-gated channel, su	cNMP_binding,ion_trans,PA	2.7
	452869	AB014534	Hs.30898	KIAA0634 protein	fn3;SS	2.7
	428045	T15465	Hs.182231	thyrotropin-releasing hormone	;SS	2.7
	425218	NM_014909	Hs.155182	KIAA1036 protein	TM;	2.7
	425558	AF040723	Hs.158300	huntingtin-associated protein 1 (ne	TM;	2.6
	440789	AB007857	Hs.7416	KIAA0397 gene product	TBC,RUN;TM;	2.6
15	418423	NM_014732	Hs.301658	KIAA0513 gene product	TM;	2.6
	450400	AI694722	Hs.279744	ESTs	lectin_c	2.6
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	SH2,SH3;TM;SS	2.6
	443759	BE390832	Hs.134729	FXD domain-containing ion transpor	ATP1G1,PLM_MAT8;TM;SS	2.6
	425069	AA687465	Hs.298184	potassium voltage-gated channel, sh	aldo_ket_red	2.6
20	429291	AI933057	Hs.349189	mannosyl (alpha-1,3-)-glycoprotein		2.6
	424798	AW016523	Hs.182850	ESTs		2.6
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 prot	TM;SS	2.6
	417212	AW952823	Hs.351547	NS1-binding protein	E2_N,E2_C,DNA_mis_repair,	2.6
	432265	BE382679	Hs.285753	SCG10-like-protein	Stathmin;TM;SS	2.6
25	417005	C21115	Hs.26612	ESTs, Moderately similar to S23650		2.6
	421091	W22821	Hs.351612	ribosomal protein L26	TM;	2.6
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene	homeobox,CUT;TM;	2.6
	431967	AJ243653	Hs.373498	organic cation transporter	sugar_tr;TM;SS	2.6
	439151	AW135066	Hs.283110	carbonic anhydrase X	carb_anhydrase;TM;SS	2.6
30	424134	AF070637	Hs.140950	hypothetical protein	DUF176;SS	2.6
	430213	AW993446	Hs.235445	hypothetical protein FLJ21313	GRAM;TM;	2.6
	445954	AA148926	Hs.27836	hypothetical protein FLJ22362	fn3;TM;	2.6
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM;SS	2.6
35	446236	NM_006293	Hs.301	TYRO3 protein tyrosine kinase	fn3,ig,ptkinase;TM;	2.6
	433706	AW947250	Hs.283645	ESTs	PH,RhoGAP	2.6
	423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7;TM;	2.5
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome	Opioids_neuropep;SS	2.5
	448923	AL034562	Hs.22584	prodynorphin		2.5
	408115	AB033107	Hs.42796	KIAA1281 protein		2.5
40	446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clo		2.5
	427989	H85525	Hs.40479	gb:yv88h06.r1 Soares melanocyte 2Nb	TM;SS	2.5
	435833	BE259178	Hs.41641	Bruno (Drosophila)-like 4, RNA bin	nm;TM;	2.5
	423797	BE259384	Hs.132898	fatty acid desaturase 1	heme_1,FA_desaturase;TM	2.5
	448277	BE622827	Hs.99486	hypothetical protein FLJ13044	mito_carr;TM;SS	2.5
45	417298	AW665639	Hs.37958	ESTs		2.5
	415577	AF257770	Hs.20530	poly(rC)-binding protein 4	KH-domain;TM;	2.5
	420742	U79251	Hs.99902	opioid-binding protein/cell adhesio	ig;TM;SS	2.5
	419109	BE169157	Hs.172717	ESTs	ptkinase,LRRCT,ig,LRR,LRRN	2.5

50	TABLE 28C:	
	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
55	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405569	6006906	Plus	99719-99873
404439	7139680	Plus	55316-55585

60	TABLE 29A: ABOUT 362 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE	
	Table 29A lists about 362 genes up-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 28A, except that the ratio of "average" glioma to "average" normal brain was greater than or equal to 3.0, the "average" glioma level was set to the 99th percentile value amongst various glioma specimens, the "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant adult brain specimens, the "average" glioma value was greater than or equal to 50 units.	
	Predicted protein domains are noted.	

65	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
70	Protein Domains:	Predicted Protein Domains
	R1:	glioma vs non-malignant adult brain tissue

75	Pkey	ExAccn	Unigene ID	Unigene Title	Protein Domains	R1
	414477	U41635	Hs.76228	amplified in osteosarcoma	ptkinase,LRR;TM;SS	11.2
	407241	M34516		gb:Human omega light chain protein	TM;	10.9
	408972	AL050100	Hs.49378	DKFZP585D0919 protein	TM;	7.0
	417512	X76534	Hs.82226	glycoprotein (transmembrane) numb	PKD;TM;SS	6.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HU	Gelsolin,VHP,p450	6.3
	428847	AI954833	Hs.98881	ESTs		6.2
80	407061	X97748		gb:H.sapiens PTX3 gene promotor reg		5.4
	440020	AI480204	Hs.177131	ESTs		5.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN		5.3
	406837	R70292	Hs.156110	immunoglobulin kappa constant		5.2
	407607	NM_001887	Hs.37135	crystallin, beta B1	crystallin;TM;	5.1

5	435013	H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquin	5.1
	424916	AW867440	Hs.23096	ESTs	5.1
	409659	AW970843	Hs.55682	eukaryotic translation initiation f	5.1
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypo	5.1
	406621	X57809	Hs.181125	immunoglobulin lambda locus	5.1
	430418	R98852	Hs.36029	heart and neural crest derivatives	5.1
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific	5.0
	429707	W76631	Hs.211819	matrix metalloproteinase 23B	5.0
10	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome	5.0
	441321	H17182	Hs.7771	B-cell associated protein	5.0
	406848	AJ264844	Hs.275865	ribosomal protein S18	4.9
	423505	AF064090	Hs.129708	tumor necrosis factor (ligand) supe	4.8
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.8
15	431882	NM_001426	Hs.271977	engrailed homolog 1	4.8
	446295	AJ355029	Hs.101660	ESTs, Weakly similar to T14171 atax	4.8
	409170	W91994	Hs.16145	ESTs	4.8
	421155	H87879	Hs.102267	lysyl oxidase	4.7
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	4.7
20	412115	AK001763	Hs.73239	hypothetical protein FLJ110901	4.7
	450463	AW952018	Hs.201398	G protein coupled receptor interact	4.7
	445980	AJ268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN	4.7
	406807	AA057605	Hs.180920	ribosomal protein S9	4.6
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.6
25	401699			Target Exon	4.6
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	4.6
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clo	4.6
	406858	AA505445	Hs.300697	immunoglobulin heavy constant gamma	4.6
	406699	L06505	Hs.182979	ribosomal protein L12	4.6
30	406663	U24683		immunoglobulin heavy constant mu	4.6
	427714	AJ119850	Hs.2186	eukaryotic translation elongation f	4.6
	407260	L09095		gb:Homo sapiens mRNA fragment	4.5
	406803	H42321	Hs.163593	ribosomal protein L18a	4.5
	430397	A924533	Hs.105607	bicarbonate transporter related pro	4.5
35	414044	BE614194	Hs.75721	profilin 1	4.5
	424238	AA337401	Hs.137635	ESTs	4.5
	421532	AW138207	Hs.146170	hypothetical protein FLJ22969	4.4
	421241	X91817	Hs.102866	transketolase-like 1	4.4
	436398	H87136	Hs.5174	ribosomal protein S17	4.4
40	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and	4.4
	446921	AB012113	Hs.16530	small inducible cytokine subfamily	4.3
	433271	BE621697	Hs.14317	nucleolar protein family A, member	4.3
	408964	M21305		FGENES predicted novel secreted pro	4.3
	432191	AA043193	Hs.273186	hypothetical protein, clone Teletho	4.3
45	420890	AA434058	Hs.100071	6-phosphogluconolactonase	4.3
	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA139	4.2
	406687	M31126	Hs.352054	matrix metalloproteinase 11 (stroma	4.2
	425157	NM_006227	Hs.283007	phospholipid transfer protein	4.2
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei	4.2
50	446490	AK000706	Hs.15125	hypothetical protein FLJ20699	4.2
	431750	AA514986	Hs.283705	ESTs	4.2
	428327	AW206236	Hs.28773	ESTs	4.2
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	4.1
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clo	4.1
55	433170	AB037816	Hs.8982	KIAA1395	4.1
	423084	AU076474	Hs.123178	translocase of inner mitochondrial	4.1
	407926	AW956382	Hs.59771	ESTs	4.1
	445636	AW105401	Hs.350068	ribosomal protein L29	4.1
	418689	AJ360883	Hs.375584	hypothetical protein FLJ11029	4.1
60	450690	AA296696	Hs.333418	FXRD domain-containing ion transpor	4.1
	419092	J05581	Hs.89603	mucin 1, transmembrane	4.0
	447813	AJ394345	Hs.238513	hypothetical protein MGCS442	4.0
	436419	AJ948626	Hs.171356	ESTs	4.0
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214	4.0
65	443402	U77846	Hs.356316	elastin (supraaortic aortic steno	4.0
	433435	BE545277	Hs.340959	Ts translation elongation factor, m	4.0
	413595	AW235215	Hs.16145	ESTs	4.0
	412607	Z33642	Hs.74115	immunoglobulin superfamily, member	4.0
	419913	AW270040	Hs.34455	ESTs	4.0
70	415209	F00183	Hs.172004	titin	4.0
	439310	AF086120	Hs.102793	ESTs	3.9
	421777	BE562088	Hs.108196	HSPC037 protein	3.9
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain	3.9
	402241			Target Exon	3.9
75	432716	AJ762964	Hs.205180	ESTs	3.9
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	3.9
	434214	AF119871	Hs.155860	hypothetical protein PRO2268	3.9
	406855	AA902829		gb:ok72e06.s1 NCI_CGAP_GCA Homo sap	3.9
	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	3.9
80	403364			Target Exon	3.9
	412339	BE151267	Hs.314466	ESTs	3.8
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot	3.8
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) act	3.8
	405201			Target Exon	3.8
				nm	5.1
				;SS	5.1
				nm	5.1
				ig,HSP70,Ppx-GppA;TM;SS	5.1
				HLH	5.1
				TM;SS	5.0
				ig,Peptidase_M10;TM;SS=	5.0
				Band_7;TM;	5.0
				Ribosomal_S13;	4.9
				TNF;TM;SS	4.8
				Zn_carbOpept,Propep_M14;T	4.8
				homeobox;TM;	4.8
				LJM	4.8
				nm	4.8
				Lysyl_oxidase,Aldose_epim	4.7
				Glyco_hydro_20,Glyco_hydr	4.7
				;SS	4.7
				C1q,Collagen;TM;SS	4.7
				zf-C2H2,bZIP	4.7
				Ribosomal_S4,S4,tRNA_inL	4.6
				transmembrane4;TM;SS	4.6
				TM;	4.6
				TM;	4.6
				ig;TM;	4.6
				Ribosomal_L11;TM;	4.6
				;SS	4.6
				COX8,SHMT,MIF,GST_C,EF1G_	4.6
				Ribosomal_L18ae;TM;	4.5
				HCO3_cotransp;TM;	4.5
				profilin;TM;	4.5
				TM;SS	4.5
				Armadillo_seq,HEAT;TM;S	4.4
				transketolase,transket_py	4.4
				Ribosomal_S17e,PolyA_pol;	4.4
				pkinase,ICE_p10,ICE_p20;T	4.4
				IL8;SS	4.3
				;	4.3
				ABC1;TM;	4.3
				Glucosamine_iso;TM;	4.3
				TM;	4.3
				hemopexin,Peptidase_M10;T	4.2
				LBP_BPI_CETP,LBP_BPI_CETP	4.2
				TM;	4.2
				cpn60_TCP1	4.2
				cystatin,Coprogen_oxidase,	4.2
				TM;	4.1
				TM;	4.1
				nm	4.1
				TYA;SS	4.1
				filament,GTP_EFTU,EF6_C,G	4.1
				ATP1G1_PLM_MAT8;TM;SS	4.1
				SEA;TM;SS	4.0
				ubiquitin;TM;SS	4.0
				AT_hook,ATHILA	4.0
				PMM	4.0
				PDZ_LIM,pkinase	4.0
				EF_TS,UBA;	4.0
				nm	4.0
				ig;TM;SS	4.0
				EPH_lbd,ln3,pkinase,	4.0
					4.0
				casein_kappa,pkinase,ig,n	3.9
				TM;	3.9
				Collagen,fibrinogen_C;TM=	3.9
				p450;TM;SS	3.9
				LRR,UPAR_LY6;TM;	3.9
				TM;SS	3.9
				;SS	3.9
				hemopexin,Peptidase_M10;T	3.9
				SH2,Y_phosphatase	3.9
				tubulin	3.8
				TIMP	3.8
				PA28_alpha,PA28_beta;	3.8
				mito_carr,SH2,SH3,Alpha_a	3.8

5	436906	H95990	Hs.181244	major histocompatibility complex, c	ig,MHC_I;TM;SS	3.8
	407319	A1743332	Hs.257729	ESTs, Moderately similar to ALU7_HU	nm,Lipoprotein_2	3.8
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	Cys_knot	3.8
	430240	BE303038	Hs.236547	Homo sapiens, clone IMAGE:2905978,	HEAT_PBS;TM;	3.8
	442487	AF191019	Hs.8361	hypothetical protein, estradiol-ind	LRR,LRRNT;TM;SS	3.8
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4;TM;	3.8
	419942	U25138	Hs.93841	potassium large conductance calcium	CaKb;TM;SS	3.8
	410584	AB011112	Hs.64742	KIAA0540 protein		3.8
10	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like	LIM;SS	3.8
	406874	AW161706	Hs.180842	ribosomal protein L13	Ribosomal_L13e;SS	3.7
	429249	X81479	Hs.2375	egf-like module containing, mucin-1	7tm_2EGF_GPS,S_locus_gly	3.7
	430799	C19035	Hs.164259	ESTs	FKBP,TPR	3.7
	453099	H62087	Hs.31659	thyroid hormone receptor-associated	WD40;TM;	3.7
15	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1	WD40;TM;	3.7
	444795	AJ193356	Hs.160316	ESTs	E2F_TDP,KOW,Ribosomal_L14	3.7
	443834	AJ741510	Hs.173548	ESTs	Tropomyosin,ACOX	3.7
	429731	AK001592	Hs.212172	beta-carotene 15,15'-dioxygenase	CUB,MAM,F5_8_type_C	3.7
	426433	L38969	Hs.169875	thrombospondin 3	RPE65;SS	3.7
20	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	TSPN,tsp_3,EGF,toxin;TM	3.7
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardia	pkinese	3.7
	447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	myosin_head,IQ,Myosin_tai	3.7
	430281	AJ878842	Hs.237924	CGI-69 protein	Ammonium_transp,FacCD;TM=	3.7
	448360	AL117560	Hs.306352	Homo sapiens mRNA: cDNA DKFZp566P23	mito_carr/homeobox;TM;S	3.7
25	446057	AJ402277	Hs.366053	Trp-p8 transient receptor potential		3.7
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM;SS	3.7
	406854	AA613705	Hs.252259	ribosomal protein S3	KH-domain,Ribosomal_S3_C;	3.7
	422532	AL008726	Hs.118126	protective protein for beta-galacto	serine_carbpept,GalP_UDP_	3.7
30	428171	AA489323	Hs.182825	ribosomal protein L35	Ribosomal_L29;	3.6
	442285	W28729	Hs.356072	uncharacterized hypothalamus protei		3.6
	411281	BE392792	Hs.4786	Homo sapiens cDNA: FLJ22849 fis, cl	cadherin	3.6
	457657	AW411509	Hs.352567	hypothetical protein PRO2121	UQ_con;TM;	3.6
	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid		3.6
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation;TM=	3.6
35	445411	ALJ37255	Hs.12646	hypothetical protein FLJ22693	hormone_rec,zf-CCCH;TM;	3.6
	400785			C11000861:gil9938016[ref]NP_064687.	TM;SS	3.6
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	TM;	3.6
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interf	fn3;TM;SS	3.6
	427818	AW511222	Hs.193765	ESTs		3.6
40	449957	D31365	Hs.24220	hypothetical protein	TM;	3.6
	451529	AJ917901	Hs.208641	ESTs	actin	3.6
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	Nol1_Nop2_Sun;TM;	3.6
	431659	AA031875	Hs.266940	I-complex-associated-testis-express	Tclx-1;TM;	3.6
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, cl	zf-C3HC4,SPRY	3.6
45	412896	AW804157	Hs.375570	major histocompatibility complex, c	ig,MHC_II_beta;TM;SS	3.6
	441748	R14439	Hs.209194	ESTs		3.6
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	KH-domain,Ribosomal_S3_C;	3.5
	457464	AW972234	Hs.126680	ESTs		3.5
	429619	AL120751	Hs.211568	eukaryotic translation initiation f	sushi,HYR;SS	3.5
50	423309	BE006775	Hs.126782	sushi-repeat protein		3.5
	438682	AA354489	Hs.375594	EBP50-PDZ interactor of 64 kD	Amino_oxidase	3.5
	453022	AA031499	Hs.118489	ESTs	TM;SS	3.5
	434042	AJ589941	Hs.8254	Homo sapiens, Similar to tumor diff		3.5
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protei		3.5
55	417298	AW665639	Hs.37958	ESTs		3.5
	403943			C5000355:gil4503225[ref]NP_000765.1		3.5
	429497	AB028953	Hs.204121	KIAA1030 protein	fn3;TM;	3.5
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenas	adh_short;TM;SS	3.5
60	428343	AL043021	Hs.12705	ESTs	WD40;SS	3.5
	456376	AA663904	Hs.89862	TNFRSF1A-associated via death domai	death;TM;	3.5
	400348	AJ251708	Hs.352588	Target		3.5
	404854			Target Exon	:SS	3.5
	427930	AA417696	Hs.372121	ESTs		3.5
65	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep	serpin;SS	3.5
	406806	AW088535	Hs.350108	ribosomal protein, large, P0	TM;	3.5
	406793	AW264291	Hs.5662	guanine nucleotide binding protein	WD40;TM;	3.5
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clo		3.5
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	Glyco_hydro_47;TM;SS	3.5
70	404243			NM_006778:Homo sapiens ring finger	zf-C3HC4,zf-B_box;TM;SS	3.4
	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain trans	Ets;SS	3.4
	432831	AJ821702	Hs.115959	ESTs, Weakly similar to I38022 hypo		3.4
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clo	TM;	3.4
	418558	AW082266	Hs.85131	Fas (TNFRSF6)-associated via death	death,DED;SS	3.4
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	CUE;TM;	3.4
75	403246			Target Exon	HMG_box;SS	3.4
	416330	AU077101	Hs.79222	galactosidase, beta 1	Glyco_hydro_35;TM;SS	3.4
	404864			NM_025204:Homo sapiens hypothetica		3.4
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, cl	7tm_3	3.4
	430284	AJ693534	Hs.293196	ESTs		3.4
80	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN	RNA_pol_LRNA_pol_L,RasGA	3.4
	456050	R79445	Hs.76230	ribosomal protein S10	S10_plectin;TM;	3.4
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	fn3;TM;	3.4
	408909	AW502034	Hs.287379	ESTs, Weakly similar to T26022 hypo	death,pkinese;TM;	3.4
	428028	US2112	Hs.182018	interleukin-1 receptor-associated k		3.4

	424213	BE390125	Hs.143187	hypothetical protein	DEAD, helicase_C; TM;	3.4
	416432	BE391767	Hs.79322	glutamyl-IRNA synthetase		3.4
	400233			Eos Control	Ribosomal_S9;	3.4
	403252			Target Exon	TM; SS	3.4
5	409433	AA074382	Hs.135255	ADAMTS14		3.4
	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic	rm, PABP; TM;	3.4
	448222	A1648587	Hs.20725	Mov10 (Moloney leukemia virus 10, m	TM;	3.4
	432982	AA531058	Hs.182248	truncated calcium binding protein	OPR_ZZ; TM;	3.4
10	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	FBPase; TM;	3.4
	444626	AA320893	Hs.117062	hypothetical protein FLJ14497	pyr_redox; TM; SS	3.4
	427751	AF000152	Hs.355816	conserved gene amplified in osteosarcoma	NIF; TM;	3.4
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial	mito_carr; TM;	3.4
	428046	AW812795	Hs.337534	ESTs. Moderately similar to I38022	ank	3.4
15	456575	AW063659	Hs.191649	ESTs	Myosin_tail	3.4
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	IBR	3.4
	414738	L24038	Hs.77183	v-rat murine sarcoma 3611 viral onc	pk kinase, DAG, PE-bind, RBD; T	3.4
	456356	M74715	Hs.89560	iduronidase, alpha-L-	Glyco_hydro_39; SS	3.3
	429668	AA626142	Hs.179991	ESTs. Weakly similar to S28942 prot		3.3
20	404913			NM_024408: Homo sapiens Notch (Dros	EGF, ank, notch, metalthio, E	3.3
	426059	BE292842	Hs.166120	interferon regulatory factor 7	IRF; SS	3.3
	451619	AA018854	Hs.353196	glutathione peroxidase 3 (plasma)	Ph; SS	3.3
	410225	AW608964	Hs.12030	ESTs		3.3
	402534			Target Exon		3.3
25	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	GLFV_dehydrog, GLFV_dehydr	3.3
	421712	AK000140	Hs.107139	hypothetical protein	TM; SS	3.3
	433333	A016521	Hs.71816	v-akt murine thymoma viral oncogene	pk kinase, PH, pk kinase_C	3.3
	424915	R42755	Hs.23096	ESTs	rm	3.3
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, cdo		3.3
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM; SS	3.3
	446478	A1950021	Hs.370306	ESTs	TM;	3.3
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM; TM;	3.3
	456655	AJ376736	Hs.111779	secreted protein, acidic, cysteine-	kazal; SS	3.3
	438912	AF085843		gb:Homo sapiens full length insert		3.3
35	428396	U70539	Hs.184161	exostoses (multiple) 1	Exostosis; TM; SS	3.3
	437546	AW074836	Hs.173984	T-box 1	T-box, WD40; TM;	3.3
	410693	BE044206		gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H	C1q, Collagen, cystati	3.3
	414961	U27266	Hs.927	myosin-binding protein H	tn3, ig; TM;	3.3
	422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-O-s		3.3
40	426120	AA325243	Hs.166887	copine 1	C2, rm; TM;	3.3
	452383	T70900	Hs.27189	ESTs	zf-C2H2, PRK	3.3
	456799	AC004923	Hs.135187	unc93 (C.elegans) homolog B	TM;	3.3
	409227	AA808165	Hs.130323	Homo sapiens, clone IMAGE:3960432,	NA; NA	3.3
	432659	AA281633	Hs.278586	KIAA1108 protein	TBC; TM;	3.3
	448997	AA130390	Hs.25549	hypothetical protein FLJ20898	TM; SS	3.3
45	446990	AJ354717	Hs.223908	ESTs	transmembrane4	3.3
	437259	AJ377755	Hs.120695	ESTs	MHC_II_alpha, ig	3.3
	423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_tr; TM;	3.3
	421563	NM_006433	Hs.105806	granulysin	:SS	3.3
50	453804	AA300204	Hs.35276	KIAA0852 protein	TM;	3.3
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible	NAD_binding, flavodoxin, FA	3.3
	453933	A1452933	Hs.65377	ESTs	EF_TS, UBA, transmembr	3.3
	449267	A1638640	Hs.220624	ESTs		3.3
	418165	R45959	Hs.6637	ESTs	mito_carr	3.3
55	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phos	acid_phosphat; TM; SS	3.3
	402475			ubiquitin specific protease 18	:	3.2
	404233			Target Exon	HIT	3.2
	406655	M21533	Hs.277477	major histocompatibility complex, c	ig, MHC_I; TM; SS	3.2
60	414556	AW975063	Hs.343443	ribosomal protein L36	Ribosomal_L36e;	3.2
	450191	AW137243	Hs.248074	ESTs	homeobox; TM;	3.2
	435906	A1686379	Hs.110796	SAR1 protein	arf, ras; TM;	3.2
	412540	C18341	Hs.73999	thyroid hormone receptor interactor	SH3, FCH; SS	3.2
	422562	A1962060	Hs.118397	AE-binding protein 1	Zn_carbOpept, F5_F8_type_C	3.2
	431051	AA491143	Hs.283374	ESTs. Weakly similar to CA15_HUMAN	TM;	3.2
65	407984	AW134708	Hs.243569	ESTs		3.2
	441494	AW452344	Hs.129977	ESTs		3.2
	423114	AU076497	Hs.1614	cholinergic receptor, nicotinic, al	Neur_chan_LBD, Neur_chan_m	3.2
	419833	AA251131	Hs.220697	ESTs	WHEP-TRS, tRNA-synt_1b, non	3.2
	419036	T80967	Hs.372603	gb:yd23112.s1 Soares fetal liver sp		3.2
70	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_pellucida; TM; SS	3.2
	453094	AA740928	Hs.27356	ESTs		3.2
	426989	A1815206	Hs.367644	ESTs	BAG, ubiquitin	3.2
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2	ank;	3.2
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn sub	SH3, HS1_rep; TM;	3.2
75	438930	AW843633	Hs.343261	hypothetical protein AL110115	HLH	3.2
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	thioredox; TM;	3.2
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	PHD	3.2
	409293	R02673	Hs.110156	ESTs		3.2
	407115	AA084921	Hs.76230	ribosomal protein S10	S10_plectin; TM;	3.2
80	401174			Target Exon	transmembrane4, EF_TS, UBA	3.2
	400217			Eos Control	ras; SS	3.2
	408676	A1815189	Hs.57475	sex comb on midleg homolog 1		3.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen in	TM; SS	3.2
	403694			Target Exon	UDPGT	3.2

414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein		
451118	A1862096	Hs.60640	ESTs	EGF,vwc,TIL;SS	3.2
422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic	ER_lumen_recept	3.2
437388	AL339586	Hs.14478	Homo sapiens mRNA; cDNA DKFZp762H18		3.2
429150	AF120103	Hs.197366	smoothed (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G,	3.2
430379	AF134149	Hs.240395	potassium channel, subfamily K, mem	ion_trans;TM;SS	3.2
434956	BE266566	Hs.4268	hypothetical protein DKFZp434K046	Cullin;TM;	3.2
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (ca	efhand,S_100;TM;	3.2
452493	A1904031	Hs.106826	KIAA1696 protein	PHD,Myc-LZ,DC1,AT_hook;TM	3.2
413100	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314		3.2
420764	BE250676	Hs.19928	hypothetical protein SP329	F-box;TM;	3.2
421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen;TM;SS	3.2
406738	AA587983		gb:rij30b09.s1 NCI_CGAP_AA1 Homo sap	TM,Ribosomal_S5;TM;SS=	3.1
434288	AW189075	Hs.116265	fibrillin3	EGF,granulin,TB,EB,TIL;TM	3.1
438264	T86773	Hs.6133	calpain 5	Calpain_III,Peptidase_C2,	3.1
436819	AA731746	Hs.120232	ESTs	mm	3.1
459298	R86701		gb:ym86d09.r1 Soares adult brain N2	TM;	3.1
452127	BE562126	Hs.28081	eukaryotic translation initiation f	mm,7tm_1,SNF;TM;	3.1
422305	A1928242	Hs.293438	ESTs, Highly similar to AF198488 1		3.1
414393	AA146855		gb:zo41h10.r1 Stratagene endothelia		3.1
423369	BE219099	Hs.279513	ESTs		3.1
429457	BE243065	Hs.202955	hypothetical protein FLJ20507	Cys-protease-3C;TM;	3.1
409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sa	TM;SS	3.1
429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A	ABC_tran;TM;SS	3.1
445519	A1635202	Hs.170132	hypothetical protein FLJ22494	TM;	3.1
410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TFIIIS;TM;	3.1
407228	M25079	Hs.155376	hemoglobin, beta	globin;TM;	3.1
411573	AB029000	Hs.70823	KIAA1077 protein	Sulfatase;TM;	3.1
406654	M90686	Hs.73885	HLA-G histocompatibility antigen, c	ig,MHC_I;TM;SS	3.1
435072	AW592176	Hs.116932	ESTs	zf-RanBP,MDM2	3.1
456642	AW451623	Hs.109752	putative c-Myc-responsive	:SS	3.1
445457	AF168793	Hs.12743	camitine O-octanoyltransferase	Carn_acyltransf;TM;	3.1
448389	AW188950	Hs.345838	ESTs	ZOG-Fel1_Oxy,mm,SH3,ras	3.1
458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	C1q,Collagen;TM;SS	3.1
451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-4	TM;	3.1
414688	A1750246	Hs.76901	for protein disulfide isomerase-rel	thiorel;SS	3.1
428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I03	UM,Ran_BP1,GRIP,TPR,pro_	3.1
425067	BE223071	Hs.169142	ESTs		3.1
410639	BE269047	Hs.65234	hypothetical protein FLJ20596	DEAD,helicase_C,PRK,ALP3;	3.1
413011	AW068115	Hs.821	biglycan	LRR,LRRNT;SS	3.1
421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	Ribosomal_L20,Na_Pi_cotra	3.1
447164	AF026941	Hs.17518	viprin; similar to inflammatory r	MoaA_NiB_PqqE;TM;	3.1
414907	X90725	Hs.77597	polo (Drosophila)-like kinase	Ribosomal_L37ae,kinase,P	3.1
418613	AA744529	Hs.86575	mitogen-activated protein kinase ki	kinase,CNH;TM;	3.1
406734	A1565616		gb:to16h12.x1 NCI_CGAP_U12 Homo sap		3.1
410188	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	Ricin_B_lectin,Glycos_tra	3.1
437959	AA72068	Hs.375604	KIAA1856 protein	elf5_elf2B,W2;TM;	3.1
406764	AA429825	Hs.343443	ribosomal protein L36	Ribosomal_L36e;	3.1
406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p;	3.1
451080	H41082	Hs.271783	ESTs		3.1
414875	H42679	Hs.77522	major histocompatibility complex, c	ig,MHC_II_alpha;TM;SS	3.1
416365	U15131	Hs.79265	suppression of tumorigenicity 5	DENN,dDENN,uDENN;TM;SS=	3.1
400261			Eos Control	ig,MHC_II_beta;TM;SS	3.1
412270	AC005262	Hs.73797	guanine nucleotide binding protein	G-alpha_arf;TM;	3.1
456843	BE301883	Hs.152707	glioblastoma amplified sequence		3.1
443071	AL080021	Hs.8986	complement component 1, q subcompon	C1q,Collagen;SS	3.1
426196	BE272095	Hs.167791	reticulocalbin 1, EF-hand calcium b	efhand;SS	3.1
424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A13	cadherin;TM;SS	3.1
439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside	Ham1p_like;TM;	3.1
450761	R75930	Hs.174838	Homo sapiens cDNA FLJ14192 fs, clo		3.1
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3	Y_phosphatase,DSPP;TM;S	3.1
432396	AW295956	Hs.11900	hypothetical protein FLJ14972	Xlink,zf-CCCH,G-patch,non	3.1
407904	W44735	Hs.107260	Homo sapiens cDNA: FLJ21278 fs, d		3.1
452500	AW373011	Hs.54558	hypothetical protein FLJ22222		3.1
432171	A1202503	Hs.343661	ESTs, Weakly similar to ALUB_HUMAN	WD40	3.1
416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha	lectin_c;TM;SS	3.1
442492	AA528489	Hs.234518	ribosomal protein L23	Ribosomal_L14;	3.0
421210	U80016	Hs.102598	mucosal vascular addressin cell adh	TM;SS	3.0
439429	AF150286		gb:AF150286 Human mRNA from cd34 st	RA,Band_7,MBOAT	3.0
447463	AW378685	Hs.18625	Mitochondrial Acyl-CoA Thioesterase	Acyl-CoA_hydro;TM;	3.0
448352	AA337951	Hs.20991	SET domain, bifurcated 1	AtpC-TSA,SET,MBD;TM;SS=	3.0
428291	AA534009	Hs.183487	interferon stimulated gene (20kD)		3.0
445669	A1570830	Hs.174870	ESTs		3.0
452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep,isp_1,Rep	3.0
430069	A1219293	Hs.293660	Homo sapiens, clone IMAGE:3535476,	SPRY,zf-box,zf-C3HC4;TM	3.0
451028	AA021258	Hs.123073	ESTs		3.0
446021	BE389213	Hs.286	ribosomal protein L4	Ribosomal_L4;TM;	3.0
434652	AF148713	Hs.125830	bladder cancer overexpressed protei	WD40,DUF6;	3.0
425829	AL133079	Hs.134126	crystallin, gamma S	crystal;TM;	3.0
424909	S78187	Hs.153752	cell division cycle 25B	Rhodanese;SS	3.0
423579	NM_004121	Hs.1675	gamma-glutamyltransferase-like acti	G_glu_transpept;TM;SS	3.0
444652	BE513613	Hs.11538	actin related protein 2/3 complex,	WD40;TM;	3.0
441283	AA927670	Hs.131704	ESTs	CUB,MAM,F5_F8_type_C	3.0

5	437415	AL137400	Hs.306456	pre-mRNA processing factor 18	Band_41,hormone2,Prp18;TM	3.0
	444542	AI161293	Hs.280380	aminopeptidase	NAD_binding,flavodoxin,FA	3.0
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	zf-RanBP,MDM2	3.0
	447910	AL137679	Hs.20000	Homo sapiens mRNA; cDNA DKFZp434D24	Exonuclease,SS	3.0
	426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	DUF232,SS	3.0
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease	tsp_1,Reprolysin,Pep_M12B	3.0
	430482	AF131810	Hs.241545	hypothetical protein	TM;SS	3.0
	427661	AA410292	Hs.104761	ESTs	wnt1	3.0
	451876	T63141		gb:yb99a12.s1 Stratagene lung (9372	SH3	3.0
10	453862	AL137493	Hs.35945	Homo sapiens mRNA; cDNA DKFZp434B12	ig;TM;	3.0
	452965	AI904779	Hs.247525	Human DNA sequence from clone RP11-	C2,PHD,RPH3A_effector,zf-	3.0
	441455	AJ271671	Hs.7854	zinc/ferritin regulated transporter-like	Zip;TM;SS	3.0
	452600	AI910842	Hs.103381	ESTs	Exo_endo_phos	3.0
	450775	AA902384	Hs.73853	bone morphogenetic protein 2	TGFb_propeptide,TGF-beta,	3.0
15	417634	W27202	Hs.82327	glutathione synthetase	GSH_synthase;TM;	3.0
	415152	W22644	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clo		3.0
	410093	AW589558	Hs.295883	ESTs, Weakly similar to KIAA0970 pr		3.0
	412404	AW075995	Hs.86228	TRIAD3 protein		3.0
20	443466	BE243123	Hs.321045	IKK-related kinase epsilon; inducib	pkinese,RIO1;TM;	3.0

TABLE 29B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

25	Pkey	CAT Number	Accession
	458147	1030220_1	AW848781 AW848490 AW849062 AW752597 AW752699
	406855	0_0	AA902829
30	400233	11259_1	BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334
			BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828257 AW958606 BG831252
			BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488 AI133550
			BM011511 BI227282 BG489212 BG478388 BE727789 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114 BG420536
			BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178 BI194428 BI117210
35			BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145 BM017978 BI193934
			BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459 BG764737 BG761808
			BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762 BG480900 BG419627
			BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729 BG110091 BG106500
			BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405 BE395269 BG832027
40			BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301 BI160946 BG105893
			BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145 BG831227 BG774290
			BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336 AW328236 BG339458 BF972634
			BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI182822 BI457127 BG831491 BG759864 AI830010 BF568381 BE907238
			BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564 BM045000 BG339617 BG282794 BG335767
45			BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919 BG480626 AW196817 BG336261 BE906157
			BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344 AI433577 BE894416 BE886992 BE409223
			BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AJ871751 BE744523 BI192663 BG831669 AI000225 BE743836 BE272515 AA628078
			BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297 BE391448 BE390780 BE388821 BE258477 BE905970
50			BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542 BE744156 BE394125 BE742207 BE395265 BE392942
			BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753 BE272370 BE907458 BE612801 BE392484 BE907635
			BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180 BF037570 BE908312 BE615015 BE256977 BE746875
			BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825 BE906472 BE906509 BE906017 BE910442 BE514657
			BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298 AW327827 BE394422 BF569178 BE263240 AI700512
55			BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866
			AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280
			AA379888 F29022 BF089981 F10103 F24305
	438912	4071_1	AF085843 R70623 R70523
	410693	1054267_1	BE044206 AW797320 BE161676 AW797356 AW797352
	413100	1490226_1	BE065224 BE065168 BE065313 BE065208
60	406738	0_0	AA587983
	459298	90831_2	AL157655 BF802216 R86701 BF802224 R84600 BF356151 BG982935
	414393	15833_3	AL532972 BI092731 AI765546 AA393801 AI129669 AI393538 AW519008 AI432598 AW295856 AI650941 AI470541 AI550388 AI146856 AI074762
			BE895187 AA393867 BI052082
	406734	0_0	AI565616 AI190141
65	400261	23110_1	BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472
			AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606
	439429	452694_1	AF150286 AV739062 AA835857
	451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998

TABLE 29C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	Nt_position
	401699	3176654	Minus	33285-34084
	402241	7690131	Minus	125073-125206, 130996-131125
	403364	8571785	Plus	120351-120465
	405201	7230116	Plus	36934-37314
	400785	8131682	Plus	43113-43967
	403943	7711864	Plus	100742-100904, 101322-101503
80	404854	7143420	Plus	14260-14537

404243	5672609	Plus	74695-75123
403246	7637831	Minus	143547-143654,143741-143900
404864	5263010	Plus	94495-94661,95055-95195,97396-97506,9760
403252	7677983	Plus	102214-102692
404913	7341740	Plus	97717-97976
402534	9801061	Plus	58989-59457
402475	7547191	Plus	65363-65725
404233	8218045	Minus	84791-85123
401174	9438414	Minus	132847-133917
403694	7107765	Plus	142925-143080,165505-166186,167486-16763

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 30A lists about 282 genes up-regulated in glioma compared to non-malignant adult brain tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 28A, except that the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 4.0, the "average" glioma level was set to the 99th percentile value amongst various glioma specimens, the "average" normal adult brain tissue level was set to the 75th percentile value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: glioma vs. non-malignant adult brain tissues likely to encode extracellular or cell-surface proteins

Pkey	Accession	UniGene ID	Unigene Title	Protein Domains	R1
406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma	ig;TM;	37.6
407241	M34516		gb:Human omega light chain protein	TM;	22.7
414477	U41635	Hs.76228	amplified in osteosarcoma	kinase,LRR;TM;SS	22.7
417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	PKD;TM;SS	15.4
406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18a;TM;	14.2
429707	W76631	Hs.211819	matrix metalloproteinase 23B	ig,Peptidase_M10;TM;SS=	12.8
419092	J05581	Hs.89603	mucin 1, transmembrane	SEA;TM;SS	12.8
414738	L24038	Hs.77183	v-raf murine sarcoma 3611 viral onc	kinase,DAG_PE-bind,RBD;T	12.4
441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 ts, cl	7tm_3:none	11.6
406621	X57809	Hs.181125	immunoglobulin lambda locus	ig,HSP70,Ppx-GppA;TM;SS	11.0
410584	AB011112	Hs.64742	KIAA0540 protein	none	11.0
426395	BE151985	Hs.355669	hypothetical protein FLJ23316	kinase,none	10.7
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b an	ig;TM;SS	10.7
430379	AF134149	Hs.240395	potassium channel, subfamily K, mem	ion_trans;TM;SS	10.3
408972	AL050100	Hs.49378	DKFZP586D0919 protein	TM;	9.9
446921	AB012113	Hs.16530	small inducible cytokine subfamily	IL8;SS	9.9
452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep,isp_1,Rep	9.7
418101	AL047476	Hs.296310	gap junction protein, alpha 4, 37kD	connexin;TM;SS	8.5
400290	H18836	Hs.31608	hypothetical protein FLJ20041	Cys_knot	8.4
401699			Target Exon	TM;	8.1
423309	BE006775	Hs.126782	sushi-repeat protein	sushi,HYR;SS	8.1
427600	AW630918	Hs.179774	proteasome (prosome, macropain) act	PA28_alpha,PA28_beta;	7.9
436906	H95990	Hs.181244	major histocompatibility complex, c	ig,MHC_1;TM;SS	7.8
425335	BE394327	Hs.296267	folistatin-like 1	efhand,kazal,arf,ras,7tm_	7.7
413011	AW068115	Hs.821	biglycan	LRR,LRRNT;SS	7.7
446295	AI355029	Hs.101660	ESTs, Weakly similar to T14171 atax	LIM	7.7
436398	H87136	Hs.5174	ribosomal protein S17	Ribosomal_S17e,PolyA_pol;	7.6
435013	H91923	Hs.110024	NM_020142:Homo sapiens NAOH:tubiquin	none	7.4
431809	AI623488	Hs.333488	Homo sapiens, clone IMAGE:3603998,	TM;SS	7.4
424608	X80695	Hs.151134	oxidase (cytochrome c) assembly 1-1	60KD_IMP;TM;	7.3
438560	AA481690	Hs.300697	immunoglobulin heavy constant gamma	ig	7.3
429297	X82494	Hs.198862	fibulin 2	EGF_ANATO,TIL,spidertoxin	7.3
450463	AW952018	Hs.201398	G protein coupled receptor interact	C1q,Collagen;TM;SS	7.2
417342	W40277	Hs.81994	glycophorin C (Gerbig blood group)	TM;	7.2
414688	AI750246	Hs.76901	for protein disulfide isomerase-rel	thiorel;SS	7.2
414044	BE614194	Hs.75721	profilin 1	profilin;TM;	7.1
404864			NM_025204:Homo sapiens hypothetica	;	7.1
452127	BE562126	Hs.28081	eukaryotic translation initiation f	rm,7tm_1,SNF;TM;	7.0
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	SS	7.0
409826	AW501112	Hs.353013	hypothetical protein FLJ23412	none	6.9
434343	AW956705	Hs.3804	DKFZP564C1940 protein	Idl_recept_a;TM;	6.9
427714	AF119850	Hs.2186	eukaryotic translation elongation f	COX8,SHMT,MIF,GST_C,EF1G_	6.9
437259	AI377755	Hs.120695	ESTs	MHC_II_alpha,ig,none	6.9
429212	NM_001504	Hs.198252	G protein-coupled receptor 9	7tm_1;TM;	6.8
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A re	Neur_chan_LBD,Neur_chan_m	6.8
423505	AF064090	Hs.129708	tumor necrosis factor (ligand) supe	TNF;TM;SS	6.8
413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA139	TM;	6.7
430542	AI557486	Hs.119122	ribosomal protein L13a	Ribosomal_L13,LACT,arf,ra	6.7
435906	AI686379	Hs.110796	SAR1 protein	arf,ras;TM;	6.6
429307	AU076592	Hs.198951	jun B proto-oncogene	bZIP;TM;	6.4
437388	AL359586	Hs.14478	Homo sapiens mRNA: cDNA DKFZp762H18	none	6.4
415714	NM_002290	Hs.78672	laminin, alpha 4	laminin_EGF,laminin_G,Tro	6.3
406733	AA976565	Hs.297753	vimentin	filamentbZIP,Apoipoprot	6.3
411296	BE207307	Hs.10114	growth suppressor 1	ZOG-Fell_Oxy;TM;SS	6.3
441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	6.3
444637	T19101	Hs.11494	fibulin 5	EGF,TIL,SS	6.3

5	413731	BE243845	Hs.75511	connective tissue growth factor
	422901	R81936	Hs.374568	ribosomal protein L44
	430397	AJ924533	Hs.105607	bicarbonate transporter related pro
	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (per
	434867	AF159442	Hs.103382	phospholipid scramblase 3
	431449	M55994	Hs.256278	tumor necrosis factor receptor supe
	440676	NM_004987	Hs.112378	LM and senescent cell antigen-like
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3)-glycoprotein
10	439310	AF086120	Hs.102793	ESTs
	410169	AI373741	Hs.59384	hypothetical protein MGC3047
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot
	414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein
	427715	BE245274	Hs.180428	KIAA1181 protein
15	409220	BE243323	Hs.51233	tumor necrosis factor receptor supe
	450690	AA296696	Hs.333418	FXD domain-containing ion transpor
	433848	AF095719	Hs.93764	carboxypeptidase A4
	446404	AA019961	Hs.26216	LOC50627
	441641	AIG50417	Hs.247068	ESTs, Moderately similar to ALU8_HU
20	418875	W19971	Hs.233459	ESTs
	424748	AA346257	Hs.134933	ESTs
	439737	AJ751438	Hs.41271	Homo sapiens collagen, type VIII, a
	448950	AF288687	Hs.9275	CGI-152 protein
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, c
25	423084	ALU076474	Hs.123178	translocase of inner mitochondrial
	402241			Target Exon
	425157	NM_006227	Hs.283007	phospholipid transfer protein
	428343	AL043021	Hs.12705	ESTs
	447990	BE048821	Hs.20144	small inducible cytokine subfamily
30	412607	Z33642	Hs.74115	immunoglobulin superfamily, member
	447625	AW505364	Hs.19074	LATS (large tumor suppressor, Dros
	408056	AA312329	Hs.42331	ephrin-A4
	445960	AZ68399	Hs.140489	ESTs, Weakly similar to LINC1_HUMAN
	406874	AW161706	Hs.180842	ribosomal protein L13
35	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death
	414638	W03516	Hs.76698	stress-associated endoplasmic retic
	409190	AU076536	Hs.50984	sarcoma amplified sequence
	429150	AF120103	Hs.197366	smoothed (Drosophila) homolog
	453099	H62087	Hs.31659	thyroid hormone receptor-associated
40	414443	ALU077268	Hs.76144	platelet-derived growth factor rece
	441283	AA927670	Hs.131704	ESTs
	414249	AI797994	Hs.279929	gp25L2 protein
	451154	AA015879	Hs.33536	ESTs
	406655	M21533	Hs.277477	major histocompatibility complex, c
45	406656	M16714	Hs.89643	major histocompatibility complex, c
	449224	AW995911	Hs.295883	hypothetical protein FLJ23399
	422562	AI962060	Hs.118397	AE-binding protein 1
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene
50	428327	AW206236	Hs.28773	ESTs
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin subs
	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid
	430281	AI878842	Hs.237924	CGI-69 protein
	426433	L38969	Hs.169875	thrombospondin 3
	432716	AI762964	Hs.205180	ESTs
55	451564	AU076698	Hs.132760	hypothetical protein MGC15729
	409340	BE174629	Hs.321130	hypothetical protein MGC2771
	432680	T47364	Hs.278613	interferon, alpha-inducible protein
	404913			NM_024408: Homo sapiens Notch (Dros
60	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil
	406687	M31126	Hs.352054	matrix metalloproteinase 11 (stroma
	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mi
	441595	AW206035	Hs.356457	ESTs
	450435	AI695975	Hs.201805	ESTs
65	443177	BE268461	Hs.202	benzodiazepine receptor (peripheral
	433435	BE545277	Hs.340959	Ts translation elongation factor, m
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei
	419913	AW270040	Hs.34455	ESTs
	446696	AF279265	Hs.298476	solute carrier family 26, member 6
70	448997	AA130390	Hs.25549	hypothetical protein FLJ20898
	413891	BE271020	Hs.355753	tumor suppressor deleted in oral ca
	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep
	448249	AW855331	Hs.337124	ESTs
	412819	T25829	Hs.24048	FK506 binding protein precursor
75	426059	BE292842	Hs.166120	interferon regulatory factor 7
	432295	BE091049	Hs.343655	ribosomal protein S15a
	412540	C18341	Hs.73999	thyroid hormone receptor interactor
	414455	AW270645	Hs.76194	ribosomal protein S5
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-
80	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1
	444824	AA843575	Hs.12056	asialoglycoprotein receptor 1
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 simil
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2
	429457	BE243065	Hs.202955	hypothetical protein FLJ20507

Cys_knot, tsp_1, vwc, IGFBP;	6.2
sushi, none	6.2
HCO3_cotransp, TM;	6.1
EGF, ig, laminin_B, laminin_	6.1
SAPA, Scramblase, TM; SS	6.1
TNFR_c6, TM; SS	6.1
UIM; SS	6.0
GNT-1, Glycos_transf_2, TM=	5.9
casein_kappa, kinase, ig, n	5.9
ig; TM;	5.8
TIMP, none	5.8
none	5.8
TM;	5.8
TNFR_c6, death, Lipoprotein	5.8
ATP1G1_PLM_MAT8, TM; SS	5.8
Zn_carbOpept, Propep_M14; T	5.7
none	5.7
Pterin_4a, fibrinogen_C, Co	5.7
Xlink, none	5.7
none	5.7
C1q, Collagen, none	5.7
E1-E2_ATPase, Hydrolase, TM	5.6
ig, MHC_1; TM; SS	5.6
rm	5.6
p450; TM; SS	5.6
LBP_BPI_CETP, LBP_BPI_CETP	5.6
WD40; SS	5.6
IL8; SS	5.6
ig; TM; SS	5.5
kinase, kinase_C, UBA, Pol	5.5
Ephrin; TM; SS	5.5
zf-C2H2, bZIP, none	5.5
Ribosomal_L13e; SS	5.4
death, DED; SS	5.4
TM; SS	5.4
transmembrane4, TM; SS	5.4
COX8, SHMT, MIF, GST_C, EF1G_	5.3
WD40; TM;	5.3
ig, kinase; TM;	5.3
CUB, MAM, F5_F8_type_C, none	5.3
Sulfotransfer, EMP24_GP25L	5.3
TIMP, none	5.2
ig, MHC_1; TM; SS	5.2
transketolase, transket_py	5.2
fn3; TM;	5.2
Zn_carbOpept, F5_F8_type_C	5.2
TM; SS	5.2
cystatin, Coprogen_oxidase,	5.2
ras; TM;	5.2
none	5.2
mito_carr, homeobox; TM; S	5.2
TSPN, tsp_3, EGF, toxin; TM	5.1
LRR_UPAR_LY6; TM;	5.1
sugar_tr, Condensation; TM=	5.1
aa_permeases, pyridoxal_de	5.1
TM; SS	5.1
EGF, ank, notch, metalthio, E	5.1
Collagen, fibrinogen_C; TM=	5.1
TM; SS	5.1
hemopexin, Peptidase_M10; T	5.1
PID, MACPF, Jdl_recept_a, ts	5.0
sugar_tr, none	5.0
EGF, laminin_B, laminin_EGF	5.0
TspO_MBR; TM; SS	5.0
EF_TS, UBA;	5.0
none	5.0
EPH_Ibd, fn3, kinase,	5.0
Sulfate_transp, STAS, xan_u	5.0
TM; SS	5.0
none	5.0
serpin; SS	5.0
carb_anhydase, UCH-1, UCH-	5.0
FKBP; TM; SS	5.0
IRF; SS	5.0
Ribosomal_S8, RNase_PH, KH-	5.0
SH3, FCH; SS	5.0
Ribosomal_S7;	5.0
kazal; SS	5.0
E2F_TDP, KOW, Ribosomal_L14	4.9
lectin_c, Tropomyosin; TM	4.9
TFIS, RNA_POL_M_15KD, UPF0	4.9
TM; SS	4.9
Cys-protease-3C; TM;	4.9

5	449475	A1348027	Hs.108557	hypothetical protein PP1057	transmembrane4;TM;SS	4.9
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM;TM;	4.9
	442110	AF113008	Hs.8102	ribosomal protein S20	Ribosomal_S10;TM;	4.9
	415209	F00183	Hs.172004	titin	none	4.9
	451849	A199261	Hs.27191	hypothetical protein from clone 247	TM;	4.9
	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	hemopexin;Peptidase_M10;T	4.9
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interf	fn3;TM;SS	4.9
	431303	AW241605	Hs.253928	ESTs	none	4.9
10	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	Xlnk,zf-CCCH,G-patch,non	4.9
	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994,	none	4.8
	430498	X02910	Hs.241570	tumor necrosis factor (TNF superfam	TNF;TM;SS	4.8
	449957	D31365	Hs.24220	hypothetical protein	TM;	4.8
	419603	BE262579	Hs.91566	PL6 protein	OMPdecase;TM;SS	4.8
15	427588	L25081	Hs.179735	ras homolog gene family, member C	ras,none	4.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	Ribosomal_L20,Na_Pi_cotra	4.8
	404854			Target Exon	:SS	4.7
	411281	BE392792	Hs.4786	Homo sapiens cDNA: FLJ22849 fis, cl	cadherin	4.7
	414045	NM_002951	Hs.75722	ribophorin II	gpdh,gpdh_C,piii_assembly	4.7
20	431830	Y15645	Hs.271387	small inducible cytokine subfamily	IL8;SS	4.7
	412896	AW804157	Hs.375570	major histocompatibility complex, c	ig,MHC_II_beta;TM;SS	4.7
	429305	AF095727	Hs.287832	myelin protein zero-like 1	ig,transmembrane4;TM;SS	4.7
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	4.7
	422687	AW068823	Hs.119206	insulin-like growth factor binding	zf-C2H2,ig,none	4.7
25	444542	AJ161293	Hs.280380	aminopeptidase	NAD_binding,flavodoxin,FA	4.7
	429833	NM_012079	Hs.288627	diacylglycerol O-acyltransferase (m	ACAT;TM;	4.7
	456376	AA663904	Hs.89862	TNFRSF1A-associated via death domai	death;TM;	4.7
	438568	R98865	Hs.11135	major histocompatibility complex, c	MHC_II_alpha,ig,none	4.7
	456356	M74715	Hs.89560	iduronidase, alpha-L-	Glyco_hydro_39;SS	4.7
30	420486	AF036365	Hs.98303	caveolin 3	Caveolin;TM;	4.6
	425123	AW205274	Hs.154695	phosphomannomutase 2	PMM;SS	4.6
	439512	AA418287	Hs.58093	Homo sapiens, clone IMAGE:3163559,	laminin_EGF;TM;	4.6
	418424	Y13622	Hs.85087	latent transforming growth factor b	EGF,TB,spideroxin,granul	4.6
35	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, cl	zf-C3HC4,SPRY,none	4.6
	432659	AA281633	Hs.278586	KIAA1108 protein	TBC;TM;	4.6
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprote	tsp_1,Reprolysin,Pep_M12B	4.6
	437408	AL359598	Hs.36606	Homo sapiens mRNA; cDNA DKFZp547B08	none	4.6
	427349	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma	ubiquitin;TM;	4.6
40	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood	ig;TM;SS	4.6
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	PHD	4.6
	427969	NM_001963	Hs.2230	epidermal growth factor (beta-uroga	EGF,ldl_recept_b,EB;TM;	4.6
	447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	Ammonium_transp,FecCD;TM=	4.6
	418916	BE392781	Hs.89474	ADP-ribosylation factor 6	arf,ras;TM;	4.6
	425720	AA362394	Hs.293984	hypothetical protein MGC13102	TM;SS	4.6
45	419942	U25138	Hs.93841	potassium large conductance calcium	CaKB;TM;SS	4.6
	403105			Target Exon	ISK_Channel;TM;SS	4.6
	418067	AI127958	Hs.83393	cystatin E/M	cystatin;SS	4.6
	427863	AF189712	Hs.181002	MLL septin-like fusion	GTP_CDC;TM;	4.5
50	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214	PMM,none	4.5
	456799	AC004923	Hs.135187	unc93 (C.elegans) homolog B	TM;	4.5
	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase	ig	4.5
	458766	AW183618	Hs.55610	solute carrier family 30 (zinc tran	Cation_efflux;TM;SS	4.5
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2	ank;	4.5
	441281	BE501247	Hs.144084	ESTs	Collagen,C4,none	4.5
55	439720	AI935202	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, cl	SDF,sugar_tr	4.5
	410184	AW503667	Hs.59545	ring finger protein 15	SPRY,zf-B_box,zf-C3HC4;TM	4.5
	431760	NM_005317	Hs.268531	granzyme M (lymphocyte met-ase 1)	trypsin;TM;SS	4.5
	446990	AJ354717	Hs.223908	ESTs	transmembrane4	4.5
60	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	IBR	4.5
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guan	ANF_receptor,guanylate_cy	4.5
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer,	Cys_knot,tsp_1,vwc,IGFBP;	4.5
	451118	AI862096	Hs.60640	ESTs	EGF,vwc,TIL;SS	4.5
	457657	AW411509	Hs.352567	hypothetical protein PRO2121	UQ_con;TM;	4.4
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	PHD,SET,zf-CXXC,EGF,ank,n	4.4
65	429497	AB028953	Hs.204121	KIAA1030 protein	fn3;TM;	4.4
	444090	S69115	Hs.10306	natural killer cell group 7 sequenc	PMP22_Claudin;TM;SS	4.4
	454005	AF039237	Hs.288600	hypothetical protein MGC3123	TM;SS	4.4
	412270	AC005262	Hs.73797	guanine nucleotide binding protein	G-alpha,arf;TM;	4.4
70	406729	AA069711		gb:zm52b11.s1 Stratagene fibroblast	filamentbZIP,Apolipoprot	4.4
	404610			Homo sapiens cDNA FLJ11027 fis, cl	EGF,laminin_B,laminin_EGF	4.4
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	fn3;TM;	4.4
	406973	M34996	Hs.198253	major histocompatibility complex, c	ig,MHC_II_alpha;TM;SS	4.4
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma	ERGA_ERG24,none	4.4
	404243			NM_006778:Homo sapiens ring finger	zf-C3HC4,zf-B_box;TM;SS	4.4
75	443834	AI741510	Hs.173548	ESTs	CUB,MAM,F5_FB_type_C,none	4.4
	446057	AI420227	Hs.366053	Trp-p8 transient receptor potential	none	4.4
	413661	AA071146	Hs.343354	ribosomal protein L18	Ribosomal_L18e,L15;TM;S	4.4
	414875	H42679	Hs.77522	major histocompatibility complex, c	ig,MHC_II_alpha;TM;SS	4.4
	439730	AF035292	Hs.6654	KIAA0657 protein	fn3;ig;	4.3
80	406257			Target Exon	7tm_1,none	4.3
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mR	ig;TM;	4.3
	414961	U27266	Hs.927	myosin-binding protein H	fn3;ig;TM;	4.3
	430265	L36033	Hs.237356	stromal cell-derived factor 1	IL8;SS	4.3
	429249	X81479	Hs.2375	egl-like module containing, mucin-I	7tm_2,EGF,GPS,S_locus_gly	4.3

433541	AW081538	Hs.220324	hypothetical protein FLJ13052	NAD_kinase;TM;	4.3
400575			NM_022146:Homo sapiens neuropeptide	7tm_1;TM;SS	4.3
427661	AA410292	Hs.104761	ESTs	wnt:none	4.3
452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156,	TM;	4.3
433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN	RNA_pol_L,RNA_pol_L,RasGA	4.3
422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic	ER_lumen_recept:none	4.3
421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen;TM;SS	4.3
422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-O-s	none	4.3
437596	AA761490	Hs.351250	ESTs, Moderately similar to S65657	kinase,WD40	4.3
419285	D31887	Hs.89868	KIAA0062 protein	Zip;TM;SS	4.3
453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans;TM;SS	4.2
410693	BE044206		gb:hp040c08.x1 Soares_NFL_T_GBC_S1 H	C1q,Collagen,cystati	4.2
413100	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314	none	4.2
432497	AA551104		ESTs, Moderately similar to ALUC_HU	none	4.2
423041	BE170842	Hs.123059	chloride channel Kb	CBS,voltage_CLC;TM;SS	4.2
449799	AI143466	Hs.125060	ESTs	none	4.2
438472	AW974907	Hs.86228	TRIAD3 protein	none	4.2
432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,kinase,SAM;T	4.2
424488	AK000413	Hs.149227	hypothetical protein FLJ20406	Xlink_xf-CCCH,G_patch;TM=	4.2
406809	AF000574	Hs.22405	leukocyte immunoglobulin-like recep	ig,Gemini_mov;TM;SS	4.2
407586	Z37544	Hs.37121	phospholipase C, beta 3 (phosphatid	C2,Pi-PLC-Y,Pi-PLC-X;TM	4.2
407228	M25079	Hs.155376	hemoglobin, beta	globin;TM;	4.2
450900	H61005	Hs.37902	ESTs	none	4.2
410188	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	Rcin_B_lectin,Glycos_tra	4.2
458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	C1q,Collagen;TM;SS	4.2
403138			NM_006056:Homo sapiens G protein-co	7tm_1,HECT;TM;SS	4.2
432074	AA525248	Hs.149723	ESTs	Y_phosphatase:none	4.2
438682	AA354489	Hs.375594	EBP50-PDZ interactor of 64 kD	none	4.2
401908			C17000154:gil12003980 gb AAG43830.1	TM;SS	4.2
451287	AK002158	Hs.26194	likely homolog of mouse immunity-as	TM;	4.2
407904	W44735	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl	none	4.1
403694			Target Exon	UDPGT-	4.1
423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_tr;TM;	4.1
425603	U52219	Hs.158329	G protein-coupled receptor 50	7tm_1;TM;SS	4.1
421485	AA243499	Hs.104800	hypothetical protein FLJ10134	TM;SS	4.1
414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	transmembrane4;TM;SS	4.1
423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase	disintegrin,Reprolysin,Pe	4.1
432171	AI202503	Hs.343661	ESTs, Weakly similar to ALUB_HUMAN	WD40	4.1
434552	AF148713	Hs.125830	bladder cancer overexpressed protei	WD40,DUF6;	4.1
429592	AB029041	Hs.209646	KIAA1118 protein	Troponin,Exo_endo_phos,IQ	4.1
432982	AA531058	Hs.182248	truncated calcium binding protein	OPR,ZZ;TM;	4.1
424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protei	TM;SS	4.1
441455	AJ271671	Hs.7854	zincron regulated transporter-lik	Zip;TM;SS	4.1
400785			C11000861:gil9938016 ref NP_064687.	TM;SS	4.1
447232	AW499834	Hs.327	interleukin 10 receptor, alpha	TM;SS	4.1
450785	AA852713	Hs.108885	Homo sapiens, alpha-1 (VI) collagen	vwa,Collagen;TM;SS	4.1
424027	AW337575	Hs.201591	ESTs	7tm_2,HRM:none	4.1
435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	EGF,DSLEB;TM;SS	4.1
437118	AB037857	Hs.300591	CD9 partner 1	none	4.1
411410	R20693	Hs.69954	laminin, gamma 3	laminin_B,laminin_EGF,lam	4.1
413902	AU076743	Hs.75613	CD36 antigen (collagen type I recep	E2F_TDP,CD36;SS	4.1
428938	AC002425	Hs.194660	ceroid-lipofuscinosis, neuronal 3,	CLN3;TM;SS	4.1
453094	AA740928	Hs.27356	ESTs	none	4.1
440811	BE384713	Hs.74655	ESTs, Weakly similar to T34482 hypo	hormone_rec,zf-C4:none	4.0
407287	AI678812	Hs.345139	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sa	ras,cadherin	4.0
428028	U52112	Hs.182018	interleukin-1 receptor-associated k	death,kinase;TM;	4.0
428469	BE549205	Hs.184488	flotillin 2	none	4.0
423114	AU076497	Hs.1614	cholinergic receptor, nicotinic, al	Neur_chan_LBD,Neur_chan_m	4.0
426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	DUF232;SS	4.0
444626	AA320893	Hs.117062	hypothetical protein FLJ14497	pyr_redox;TM;SS	4.0

TABLE 30B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT Number	Accession
456147	1030220_1	AW848781 AW848490 AW849062 AW752597 AW752699
406729	0_0	AA069711
410693	1054267_1	BE044206 AW797320 BE161676 AW797356 AW797352
413100	1490226_1	BE065224 BE065168 BE065313 BE065208
432497	852_71	AW874688 R94134 AA551104 AA777322 A1033094 BE247143

TABLE 30C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401699	3176654	Minus	33285-34084
404864	5263010	Plus	94495-94661,95055-95195,97396-97506,9760

5	402241	7690131	Minus	125073-125206,130996-131125
	404913	7341740	Plus	97717-97976
	404854	7143420	Plus	14260-14537
	403105	8980016	Minus	145287-145744
	404610	9588566	Minus	89583-89725,90402-90555,91428-91673
10	404243	5672609	Plus	74695-75123
	406257	7417784	Plus	55821-56037
	400575	9886575	Plus	131603-132095
	403138	9211494	Minus	164684-165066,167757-168651
	401908	8698760	Minus	126888-127024
15	403694	7107765	Plus	142925-143080,165505-166186,167486-16763
	400785	8131682	Plus	43113-43967

TABLE 31A: ABOUT 189 GENES DOWN-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE
 Table 31A lists about 189 genes down-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 30A, except that the numerator was set to the 90th percentile amongst various non-malignant brain specimens, the denominator was set to the 90th percentile value amongst various gliomas, the numerator was greater than or equal to 50 units, and the ratio was greater than or equal to 2.5 (i.e. 2½-fold downregulation in brain tumor vs. normal brain).

Key:
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: non-malignant adult brain tissue vs. glioma

Key	ExAccn	UniGene ID	Unigene Title	Protein Domains	R1
30	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	
	432874	W94322	Hs.279651	F420_oxidored;TM;SS	14.5
	452669	AA216363	Hs.262958	SH3;TM;SS	8.3
	426300	U15979	Hs.168228	hypothetical protein DKFZp434B044	
	447990	BE048821	Hs.20144	delta-like homolog (Drosophila)	8.2
35	439477	W69813	Hs.58042	small inducible cytokine subfamily	8.2
	411602	L01406	Hs.767	ESTs, Moderately similar to GFR3_HU	7.3
	417067	AJ001417	Hs.81086	growth hormone releasing hormone re	7.1
	426488	X03350	Hs.4	solute carrier family 22 (extraneur	6.1
	447656	NM_003726	Hs.19126	alcohol dehydrogenase 1B (class I),	6.0
40	436950	L05779	Hs.113	src kinase-associated phosphoprotei	5.9
	406837	R70292	Hs.156110	epoxide hydrolase 2, cytoplasmic	5.3
	410387	A127367	Hs.47094	immunoglobulin kappa constant	5.2
	432855	AF017988	Hs.279565	ESTs	4.9
	441499	AW298235	Hs.101689	secreted frizzled-related protein 5	4.8
45	421481	AW391972	Hs.104696	ESTs	4.7
	420255	NM_007289	Hs.1298	KIAA1324 protein	4.6
	407230	AA157857	Hs.182265	membrane metallo-endopeptidase (neu	4.5
	412445	X51362	Hs.73893	keratin 19	4.5
	413966	AA133935	Hs.173704	dopamine receptor D2	4.4
50	415165	AW887604	Hs.78065	ESTs, Moderately similar to A53959	4.3
	420103	AA382259	Hs.95197	complement component 7	4.2
	426723	AW003069	Hs.183860	aldehyde dehydrogenase 1 family, me	4.2
	409081	AJ010277	Hs.50403	ESTs	4.1
	407142	AA412535	Hs.76152	T-box 19	4.0
55	414449	AA557660	Hs.76152	gb:zt99b10.s1 Soares_testis_NHT Hom	4.0
	444784	D12485	Hs.11951	decorin	4.0
	420321	D78761	Hs.96657	ectonucleotide pyrophosphatase/phos	4.0
	401700			hypothetical protein	3.9
	418807	NM_004944	Hs.88646	Target Exon	3.8
60	406746	AA580395	Hs.279860	deoxyribonuclease I-like 3	3.8
	449077	AW262836	Hs.252844	tumor protein, translationally-cont	3.8
	415718	F30631	Hs.200237	ESTs	3.7
	402449			Target Exon	3.7
	457489	AI693815	Hs.127179	cryptic gene	3.7
65	406743	AA911568	Hs.279860	tumor protein, translationally-cont	3.6
	416950	AL049798	Hs.80552	dermatopontin	3.6
	451554	AI474866	Hs.193237	ESTs	3.6
	440708	AF038962	Hs.7381	voltage-dependent anion channel 3	3.6
	426095	AI278023	Hs.89986	ESTs	3.5
70	406742	AI468091	Hs.279860	tumor protein, translationally-cont	3.5
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, c	3.5
	439457	AF086274		gb:Homo sapiens full length insert	3.4
	408796	AA688292	Hs.170345	ESTs	3.4
	440659	AF134160	Hs.7327	claudin 1	3.4
75	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	3.4
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group	3.4
	445234	AW137636	Hs.146059	ESTs	3.3
	430511	BE018156	Hs.2575	calpain 1, (mu/f) large subunit	3.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effec	3.3
80	413687	AI522318	Hs.103819	ESTs	3.3
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epi	3.3
	409738	BE222975	Hs.56205	insulin induced gene 1	3.3
	442046	AA974575	Hs.287385	ESTs	3.3
	413127	BE066529		gb:RC3-BT0333-300300-017-a12 BT0333	3.2
85	429350	AI754634	Hs.131987	ESTs	3.2
	427980	AA418305	Hs.303205	EST	3.2
				MAM;TM;	3.2
				LRR:none	3.2

	424498	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	AIP3;TM;SS	3.2
	435684	NM_001290	Hs.4980	LIM domain binding 2	LIM_bind;TM;	3.2
	402632			Target Exon	ig;TM;SS	3.1
5	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acid	wap;TM;SS	3.1
	410636	AA088177	Hs.172870	ESTs	TM;SS	3.1
	452658	N88604	Hs.30212	thyroid receptor interacting protei	PC1;TM;	3.1
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secr	laminin_G,LRRCCT,none	3.1
	430319	AI480214	Hs.356075	ninjurin 2	TM;SS	3.1
10	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	C2;TM;	3.1
	456063	NM_006744	Hs.76461	retinol-binding protein 4, intersti	lipocalin,TGF-beta,TGFb_p	3.1
	429798	AL117578	Hs.222909	DKFZP434C128 protein	TM;	3.1
	417677	NM_016055	Hs.82389	CGI-118 protein		3.1
	443792	AI763073	Hs.204873	ESTs		3.1
15	445861	BE293423	Hs.11809	single Ig IL-1R-related molecule	TIR;TM;	3.1
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	LRR,none	3.1
	456689	NM_002251	Hs.117780	potassium voltage-gated channel, de	ion_trans,K_tetra;TM;SS	3.1
	446492	AW205115	Hs.161287	ESTs	SPRY_zf-B_box,PAAD_D	3.1
	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN		3.0
20	458008	AA809314	Hs.123295	ESTs	SCAN_zf-C2H2,none	3.0
	449708	AI694598	Hs.202126	ESTs		3.0
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein	TM;SS	3.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	FMO-like,pyr_redox;TM;S	3.0
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1	PEPCK;TM;	3.0
25	453177	AW389509	Hs.223747	ESTs	zf-C2H2,none	3.0
	416781	AF072928	Hs.79877	myotubularin related protein 6		3.0
	447582	BE293520	Hs.18910	prostate cancer overexpressed gene	sugar_tr;TM;SS	3.0
	417365	D50683	Hs.82028	transforming growth factor, beta re	pkinase,WD40;TM;	3.0
	452540	AW161048	Hs.150549	ESTs, Weakly similar to T33997 hypo		2.9
30	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N10	PH,Ets,CH,spectrin,Ca_cha	2.9
	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, tr	sushi;TM;SS	2.9
	404445			Target Exon		2.9
	423323	AI951628	Hs.127007	potassium channel, subfamily K, mem	ion_trans;TM;SS	2.9
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M07	7tm_1,none	2.9
35	427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase	tRNA-synt_2,tRNA_anti,tRN	2.9
	452242	R50956	Hs.159993	glycosyltransferase		2.9
	440232	AI766925	Hs.112554	ESTs		2.9
	444634	AW611988	Hs.197813	ESTs	CKS	2.9
	445889	BE465186	Hs.266958	ESTs	TM;	2.9
40	414483	R25513	Hs.10683	ESTs		2.9
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 pr	TM;SS	2.9
	419768	T72104	Hs.93194	apolipoprotein A-I	Apolipoprotein;SS	2.9
	427804	AL049654	Hs.180871	protein kinase C, alpha binding pro	PDZ;SS	2.9
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2,	C2,PI3_P14_kinase,PI3Ka,P	2.9
45	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN	lipocalin;SS	2.9
	427842	AW936961		gb:RC1-DT0029-160200-013-a12 DT0029	efhand,mito_carr,none	2.8
	432834	F06459	Hs.289113	cytochrome b5 reductase 1 (BSR.1)	NAD_binding,FAD_binding_6	2.8
	421435	AW972072	Hs.372167	ESTs		2.8
	402458			C1002064:gij11993050jgb AAG42574.1	TM;SS	2.8
50	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	Calsequestrin;SS	2.8
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, bet	ETF_beta;SS	2.8
	459439	AW402931	Hs.352411	gb:U1-HF-BK0-abd-a-01-0-U1r1 NIH_M		2.8
	438622	L03151		gb:Homo sapiens cell-type T-cell im		2.8
	417023	AA192278	Hs.301596	ESTs, Moderately similar to S65657		2.8
55	453281	W46280	Hs.55940	ESTs, Weakly similar to A25704 syna		2.8
	403028			Target Exon	trypsin,trefol	2.8
	449029	N28989	Hs.22891	solute carrier family 7 (cationic a	aa_permeases;TM;SS	2.8
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) h	EGF,cadherin,laminin_G;TM	2.8
60	406918	M88357		gb:Homo sapiens DNA-binding protein	zf-C2H2,KRAB,zf-BED;TM;	2.7
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector protein S	TM;	2.7
	443990	AW205085	Hs.39557	ESTs		2.7
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM;	2.7
	431713	AK000388	Hs.267997	EHM2 gene	Band_41;TM;	2.7
	431469	N49424	Hs.124159	ESTs	SH3	2.7
65	400386	AF075290		gap junction protein, alpha 3, 46kD	connexin;TM;SS	2.7
	406684	X16354	Hs.50964	carcinoembryonic antigen-related ce	ig;TM;SS	2.7
	449874	AA135688	Hs.10083	Homo sapiens, clone IMAGE:4139786,	TM;	2.7
	403213			NM_019595:Homo sapiens intersecin	SH3,efhand,C2,PH,RhoGEF;T	2.7
	459665	BE159784	Hs.47647	gb:MRO-HT0408-220300-001-h06 HT0408		2.7
70	421823	N40850	Hs.28625	ESTs		2.7
	422693	BE300073	Hs.279860	tumor protein, translationally-cont	TCTP,none	2.7
	454906	AI219323	Hs.101077	ESTs, Weakly similar to T22363 hypo		2.7
	447075	AV662037	Hs.124740	ESTs, Weakly similar to I38022 hypo	TM;	2.7
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	tm,none	2.7
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypo		2.7
75	436972	AA284679	Hs.25640	claudin 3	PMP22_Claudin;TM;SS	2.7
	441379	AW175787	Hs.334841	selenium binding protein 1	TM;	2.7
	421143	AB024536	Hs.102171	immunoglobulin superfamily containi	ig_LRR,LRRNT,LRRCCT;TM;S	2.7
	422558	NM_006420	Hs.118249	brefeldin A-inhibited guanine nucle	Sec7,none	2.7
80	428900	AA437189	Hs.352324	Human DNA sequence from clone RP1-6	SS	2.7
	421153	AF009267	Hs.102238	Homo sapiens clone FBA1 Cri-du-chat		2.7
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen ge	efhand;TM;	2.6
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,MIP;TM;SS	2.6
	419158	AF031475	Hs.89648	arginine vasopressin (neurophysin I	hormone5,hormone4;SS	2.6

448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564807		2.6
437176	AW176909	Hs.42346	calcineurin-binding protein calsarc	Galactosyl_T;TM;SS	2.6
435075	R51094	Hs.12400	ESTs		2.6
403153			Target Exon		2.6
400387	AF133131		double homeobox, 5		2.6
425940	AB023184	Hs.163990	KIAA0967 protein	PDZ;SS	2.6
416157	NM_003243	Hs.342874	transforming growth factor, beta re	zona_pellucida;TM;SS	2.6
452554	AW452434	Hs.58006	ESTs, Weakly similar to ALUS_HUMAN	HLH,PAC,PAS,none	2.6
453247	T80198	Hs.111806	ESTs	wra,Cache,none	2.6
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A	ABC_tran,PRK;TM;SS	2.6
432877	AW974111	Hs.292477	ESTs	Ets,SAM_PNT,none	2.6
450115	AU591038	Hs.38132	ESTs		2.6
406337			C14000021:gi7242973 dbj BAA92547.1	Peptidase_M22	2.6
430877	NM_005269	Hs.2693	glioma-associated oncogene homolog	zf-C2H2;SS	2.6
453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (unduli		2.6
450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelia	NAD_binding,flavodoxin,FA	2.6
427620	NM_003705	Hs.179866	solute carrier family 25 (mitochond	ethand_mito_carr;TM;SS=	2.6
446585	AV659397	Hs.299668	ESTs, Weakly similar to I38022 hypo		2.6
427223	BE208189	Hs.174031	cytochrome c oxidase subunit Vlb	tubulin,FKBP,COX6B,7m_1,	2.6
428111	S76617	Hs.2243	B lymphoid tyrosine kinase	SH2,SH3,kinase;SS	2.6
440133	AI056255	Hs.133349	ESTs		2.6
419693	AA133749	Hs.301350	FXD domain-containing ion transpor	ATP1G1_PLM_MAT8;TM;SS	2.6
417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR,zf-C3HC4,PHD;TM;SS=	2.6
419100	AA464362	Hs.6748	hypothetical protein PP1665	squash,GOPD;TM;	2.6
449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clo		2.6
430937	X53463	Hs.2704	glutathione peroxidase 2 (gastroint	GSHPx;SS	2.6
425640	U34051	Hs.158460	cyclin-dependent kinase 5, regulato	CDK5_activator;TM;	2.6
409021	AA156640	Hs.49881	fatty acid binding protein 3, muscl	lipocalin,none	2.6
400538			ENSP00000239776*.BA425A6.2 (similar	TM;SS	2.6
446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell sur	TM;SS	2.6
408310	AW179023	Hs.191705	gb:PM3-ST0036-170899-001-e08 ST0036		2.6
433032	AI084066	Hs.20072	myosin regulatory light chain inter	Band_41;	2.6
419389	AI074951	Hs.319095	ESTs	DPPIV_N_term,none	2.6
453145	R63438	Hs.183454	Homo sapiens cDNA FLJ14883 fis, clo	STT3;TM;SS	2.6
443460	AL050275	Hs.9383	DKFZP566D213 protein	EGF,laminin_EGF,EB;TM;S	2.6
421903	AW079940	Hs.15951	ESTs, Weakly similar to S32436 coll	SS	2.5
421757	Z20897	Hs.296259	paraoxonase 3	Arylesterase;SS	2.5
428475	AF172940	Hs.184542	CGI-127 protein		2.5
424657	AA344719		gb:EST50901 Gall bladder II Homo sa		2.5
432862	AW004958	Hs.236720	amniotless protein	TM;SS	2.5
427195	W27230	Hs.173912	eukaryotic translation initiation f	DEAD,helicase_C;	2.5
447770	AB032417	Hs.19545	frizzled (Drosophila) homolog 4	Fz,Frizzled,7m_2;TM;SS	2.5
456523	AI083668	Hs.50601	hypothetical protein MGC10986	kinase,none	2.5
451846	T65840	Hs.11762	ESTs		2.5
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) ho	WD40;TM;	2.5
453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypo		2.5
441488	AW450935	Hs.7862	hypothetical protein FLJ20312	TM;	2.5
444669	F18939	Hs.153827	ESTs		2.5
452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, cl		2.5

TABLE 31B:			
Pkey:	Unique Eos probeset identifier number		
CAT number:	Gene cluster number		
Accession:	Genbank accession numbers		
Pkey	CAT Number	Accession	
439457	23338_1	AF086274 W69434 W69517	
413127	151610_1	BG007296 BF330853 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603	
		BE066274 BF334312	
427842	1164138_1	AW936960 AW936961 AA416706 R29415	
438622	46171_1	L03151 L03155 L03161	
424657	896375_1	AW963487 AA365077 AA344719	

TABLE 31C:			
Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NL_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	NL_position
401700	3176654	Minus	35416-35534
402449	9796674	Plus	59867-60039,62588-62828,63465-63623,6492
402632	9931268	Plus	101166-101419
404445	7596866	Minus	31112-31423
402458	9796782	Plus	170479-171134
403028	7670577	Minus	114150-114272
403213	7630897	Minus	162572-162739,164442-164540
403153	9799871	Minus	42232-43389
406337	9213455	Plus	90117-90337
400538	9797838	Plus	8752-9822

TABLE 32A: ABOUT 68 GENES UP-REGULATED IN GLIOMA COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT BRAIN TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Table 32A lists about 68 genes up-regulated in glioma compared to normal adult tissues and to non-malignant brain tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 2.5, the ratio of "average" glioma to "average" non-malignant brain tissues was greater than or equal to 2.0, the "average" glioma level was set to the 98th percentile value amongst various glioma specimens, the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant tissues, the "average" non-malignant brain tissues level was set to the 90th percentile value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: glioma vs. normal adult tissues and non-malignant brain tissues that are likely to encode proteins

Pkey	ExAccn	UniGene ID	Unigene Title	Protein Domains	R1
424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	7tm_2,HRM	8.8
418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (form		7.8
456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	7tm_2,HRM	7.5
430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypo		7.1
436480	AJ271643	Hs.87469	putative acid-sensing ion channel	ASC,TM;	6.3
407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322,	TM;	6.0
414825	X06370	Hs.77432	epidermal growth factor receptor (a	Furin-like, pkinase, Recep_	6.0
423779	AW071837	Hs.57971	ESTs	TNFR_c6	5.5
409638	AW450420	Hs.21335	ESTs	7tm_2,HRM	5.3
442613	AJ004002	Hs.130522	Kv channel-interacting protein 1	Neur_chan_LBD,Neur_c	5.2
436456	AW292677	Hs.248122	G protein-coupled receptor 24		5.1
424340	AA339036	Hs.7033	ESTs	lig_chan,ANF_receptor,non	5.0
425115	R44664	Hs.123956	ESTs	7tm_1	4.7
446809	AW590171	Hs.101413	ESTs	CaMBD,SK_channel,CaMBD,SK	4.4
413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	ubiquitin;SS	4.4
454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane,PRK	4.2
414821	M63835	Hs.77424	Fc fragment of IgG, high affinity I	ig;TM;SS	4.2
428141	D50402	Hs.182611	solute carrier family 11 (proton-co	Nramp;TM;	4.1
435472	AW972330	Hs.283022	triggering receptor expressed on my	ig;TM;SS	4.1
435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	ion_trans,KCNQ1_channel;T	3.8
448204	AJ475124	Hs.170561	ESTs	lig_chan,SBP_bac_3	3.7
433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA seque	lig_chan,SBP_bac_3,ANF_re	3.6
408243	Y00787	Hs.624	interleukin 8	HLH,PAS,IL8;TM;	3.6
415849	R20529	Hs.6806	ESTs	7tm_2,GPS,Gal_Lectin,HRM,	3.5
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	fn3;TM;SS	3.4
445070	NM_000677	Hs.258	adenosine A3 receptor	7tm_1;TM;SS	3.4
428037	NA7474	Hs.89230	potassium intermediate/small conduc	CaMBD,SK_channel	3.2
444006	BE395085	Hs.10086	type I transmembrane protein Fn14	kd_recept_a,PKD,MHC_I;TM	3.1
447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vaso		3.0
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR,Lysyl_oxidase;TM;S	3.0
424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF;TM=	3.0
446057	AJ420227	Hs.366053	Trp-p8 transient receptor potential		2.9
438204	AJ589645	Hs.128690	ESTs	7tm_1	2.9
431674	AA098901	Hs.301642	G-protein coupled receptor	GCV_H	2.9
424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clo		2.9
415209	F00183	Hs.172004	titin		2.8
438537	AK000511	Hs.6294	hypothetical protein DKFZp434L1435	IRNA-synt_1;TM;	2.8
431053	S40369	Hs.249141	Glutamate receptor subunit	lig_chan,ANF_receptor;TM=	2.8
408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1;TM;SS	2.8
414774	X02419	Hs.77274	plasminogen activator, urokinase	kringle,trypsin,plant_thi	2.8
426865	D63476	Hs.172813	PAK-interacting exchange factor bet	SH3,PH,RhoGEF,Terpene_syn	2.8
430897	U71092	Hs.248122	G protein-coupled receptor 24	7tm_1;TM;	2.7
438993	AA828995	Hs.54929	phosphorylase kinase, gamma 1 (musc	EGF,metalthio,integrin_B,	2.7
409552	AL119675	Hs.74619	proteasome (prosome, macropain) 26S	pkinase,Bac_DNA_binding;T	2.7
412817	AL037159	Hs.197366	smoothed (Drosophila) homolog	PC_rep;TM;	2.7
429150	AF120103	Hs.90786	ATP-binding cassette, sub-family C	COX8,SHMT,MIF,GST_C,EF1G_	2.7
419508	AW997938	Hs.82848	selectin L (lymphocyte adhesion mol	ABC_tran,ABC_membrane;TM=	2.7
417880	BE241595	Hs.149723	ESTs	EGF,lectin_c,sushi;TM;S	2.7
432074	AA525248	Hs.149723	ESTs	Y_phosphatase	2.6
402154			NM_031896: Homo sapiens calcium cha	PMP22_Claudin;TM;SS	2.6
431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_pellucida;TM;SS	2.6
419913	AW270040	Hs.34455	ESTs	EPH_lbd,fn3,pkinase,	2.6
412802	U41518	Hs.74602	aquaporin 1 (channel-forming integr	MIP;TM;SS	2.6
412070	AW893260	Hs.1570	histamine receptor H1	7tm_2,HRM	2.6
422676	D28481	Hs.114948	cytokine receptor-like factor 1	7tm_1;TM;SS	2.6
422311	AF073515	Hs.283713	hypothetical protein BC014245	fn3;TM;	2.6
444381	BE387335	Hs.182982	golgin-67	Collagen;TM;SS	2.6
419972	AL041465	Hs.85838	solute carrier family 16 (monocarbo	TM;SS	2.6
418526	BE019020	Hs.110613	KIA0220 protein	aa_permeases,pyridoxal_de	2.5
421997	R66740	Hs.234785	cyclic nucleotide gated channel alp	cNMP_binding,ion_trans;TM	2.5
430181	AF065314	Hs.147112	Homo sapiens cDNA: FLJ22322 fis, cl	EPH_lbd,pkinase,fn3,SAM,n	2.5
426318	AA375125	Hs.256150	NY-REN-41 antigen	TM;	2.5
434808	AF155108	Hs.89230	potassium intermediate/small conduc	CaMBD,SK_channel;TM;SS=	2.5
418843	AJ251016	Hs.322844	hypothetical protein DKFZp564A176	Sema,PSI,TIG,integrin_B;T	2.5
410290	AA402307				2.5

424909	S78187	Hs.153752	cell division cycle 25B	Rhodanese;SS	2.5
408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H	PTR2;TM;	2.5
414561	A1064813	Hs.195155	Homo sapiens amino acid transport s	Aa_trans;TM;	2.5

5

TABLE 32B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

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Pkey	CAT Number	Accession
438993	2580163_1	AJ926361 AA834879 AA828995
412070	287551_1	BG820657 AW890808 BF904755 AW893260 BI034684 BF963423 BF961550 M85689

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TABLE 32C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NT_position:	Indicates nucleotide positions of predicted exons.

20

Pkey	Ref	Strand	NT_position
402154	8516165	Minus	125299-125494

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TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER

Table 33A lists about 798 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of tumor to normal tissue

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Pkey	ExAccn	UnigeneID	Unigene Title	R1
421471	U90545	Hs.104635	solute carrier family 17 (sodium phospho	1007.4
445178	A1792241	Hs.129614	kidney-specific membrane protein	438.0
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	336.4
421727	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	323.6
440304	BE159984	Hs.125395	ESTs	295.0
436878	BE465204	Hs.47448	ESTs	258.8
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	258.6
421155	H87879	Hs.102267	lysyl oxidase	251.8
426471	M22440	Hs.170009	transforming growth factor, alpha	224.6
421478	A1683243	Hs.97258	ESTs	212.6
424086	A1351010	Hs.102267	lysyl oxidase	199.2
428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	186.4
426890	AA393167	Hs.41294	ESTs	183.4
441031	A1110684	Hs.7645	fibrinogen, B beta polypeptide	174.0
411642	NM_014932	Hs.71132	neuroigin 1	172.4
452838	U65011	Hs.30743	preferentially expressed antigen in mela	161.4
425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	151.0
438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	135.0
453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	134.8
453160	AJ263307	Hs.146228	ESTs	132.6
452431	U88879	Hs.29499	toll-like receptor 3	130.6
423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	120.4
420642	AK001520	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT	112.6
407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	111.8
431708	A1698136	Hs.108873	ESTs	109.8
446460	AW013999	Hs.150164	ESTs	103.6
443450	N66045	Hs.133529	ESTs	103.0
432865	AJ753709	Hs.152484	ESTs	101.4
442438	AA995998		gb:ros26b03.s1 NCI_CGAP_Kid5 Homo sapiens	98.8
433447	U29195	Hs.3281	neuronal pentraxin II	98.5
440311	AJ733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN !	98.2
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	97.0
437157	BE048860	Hs.120655	ESTs	94.4
453319	A1985369	Hs.20117	ESTs	91.4
447046	AA326187	Hs.17170	G protein-coupled receptor 4	90.2
439169	A1912122	Hs.41095	ESTs	86.6
431870	AW449902	Hs.105500	ESTs	84.4
438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	83.8
445279	R41900	Hs.22245	ESTs	82.4
451592	A1805416	Hs.213897	ESTs	79.4
422966	A1648419	Hs.122613	dimethylglycine dehydrogenase precursor	78.8
423109	M59305	Hs.123655	natriuretic peptide receptor C/guanylate	78.0
415989	A1267700	Hs.111128	ESTs	77.0
422544	AB018259	Hs.118140	KIAA0716 gene product	74.8
425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	74.8
429352	AK001512	Hs.200097	hypothetical protein FLJ10650	73.0

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	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	72.2
	441665	AI301355	Hs.151285	ESTs	71.6
	435094	AI560129	Hs.277523	EST	71.2
	403345				69.6
5	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	69.0
	440482	AA886658	Hs.50873	ESTs	67.6
	457100	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	67.0
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	65.2
10	407905	AW103655	Hs.252905	ESTs	63.2
	422998	AK000588	Hs.122939	hypothetical protein FLJ20581	61.8
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	61.2
	449448	D60730	Hs.57471	ESTs	60.6
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	59.8
15	419752	AA249573	Hs.152618	ESTs	58.4
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	58.2
	408609	AA330431	Hs.640	calcitonin receptor	57.4
	451009	AA013140	Hs.115707	ESTs	57.2
	435610	AI862767	Hs.114157	ESTs, Weakly similar to putative p150 [H	56.4
20	411893	R82845	Hs.273789	ESTs	56.2
	415227	AW821113	Hs.72402	ESTs	55.2
	433859	AW896758	Hs.163925	ESTs	55.0
	450459	AI697193	Hs.299254	ESTs	54.4
	400302	N48056	Hs.1915	isolate hydrolase (prostate-specific memb	53.4
25	421831	AA298836	Hs.22026	ESTs	52.8
	438817	AI023799	Hs.163242	ESTs	52.1
	449101	AA205847	Hs.23016	G protein-coupled receptor	52.0
	410025	BE220489	Hs.113592	ESTs	51.8
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein,	48.0
30	436751	AA732217	Hs.294054	ESTs	46.6
	445424	AB028945	Hs.12696	coractin SH3 domain-binding protein	45.4
	444059	R69743	Hs.75442	albumin	44.8
	442671	AI005668	Hs.134779	EST	44.4
	445657	AW612141	Hs.279575	ESTs	44.3
35	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapi	44.0
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	43.8
	422553	AI697720	Hs.171455	ESTs	43.6
	452461	N78223	Hs.108106	transcription factor	42.8
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	42.6
40	452240	AI591147	Hs.61232	ESTs	41.7
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	41.4
	452788	AW294571	Hs.136040	ESTs	41.4
	419287	X91906	Hs.89872	chloride channel 5 (nephrolithiasis 2, X	40.6
	428822	W28418	Hs.301148	potassium voltage-gated channel, Isk-rel	40.2
45	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	40.0
	434208	T92641	Hs.127648	hypothetical protein PRO2176	39.2
	442168	AI253165	Hs.146022	ESTs	38.8
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	38.6
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	38.4
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	38.4
50	428795	R45503	Hs.97469	ESTs, Weakly similar to I49698 alpha-1,3	37.6
	406411				37.6
	423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	37.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	37.2
55	448788	AI570286	Hs.107070	ESTs	37.2
	441826	AW503603	Hs.129915	phosphotriesterase related	37.0
	409263	AA069573	Hs.50319	ESTs	36.8
	425577	BE464496	Hs.280977	ESTs	36.2
	452249	BE394412	Hs.61252	ESTs	34.8
60	435986	AA703158	Hs.187848	ESTs	34.4
	417236	AI908497	Hs.170737	Homo sapiens cDNA: FLJ23251 fis, clone C	33.8
	440234	AW117264	Hs.126252	ESTs	33.8
	435334	R94223	Hs.117747	ESTs	33.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	33.1
65	424871	NM_004525	Hs.153595	low density lipoprotein-related protein	32.8
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	32.4
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (f	32.4
	451050	AW937420	Hs.69662	ESTs	32.0
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_U11 Homo sapiens	31.6
70	434539	AW748078	Hs.214410	ESTs	31.0
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	30.6
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	30.5
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	30.4
	413573	AI733859	Hs.149089	ESTs	30.2
75	421037	AI684808	Hs.197653	ESTs	30.2
	449353	AA001220	Hs.271369	ESTs	30.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	29.6
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	29.6
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	29.6
80	459508	R83265	Hs.205956	ESTs	29.2
	414245	BE148072	Hs.75850	WAS protein family, member 1	28.8
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	28.6
	445925	AI733820	Hs.145664	ESTs	28.4
	412616	AW970584	Hs.291033	ESTs	28.0

	424638	AJ472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	27.6
	445885	AJ734009	Hs.127699	KIAA1603 protein	27.6
	410247	AF181721	Hs.61345	RU2S	27.4
5	406414				27.2
	435951	AF269162	Hs.41267	c21orf7 form A-D	27.2
	458680	N73773	Hs.282950	ESTs	27.0
	419948	AB041035	Hs.93847	NADPH oxidase 4	26.4
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	26.3
10	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	26.0
	446346	AI290205		gb:q179g06.x1 Soares_NhHMPu_S1 Homo sapi	26.0
	448595	AB014544	Hs.21572	KIAA0644 gene product	25.8
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	25.6
	433242	AB040938	Hs.113940	KIAA1505 protein	25.6
15	453118	AW195849	Hs.252757	ESTs	25.6
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	25.2
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	25.2
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	24.6
	436788	AA766908	Hs.259047	ESTs	24.4
20	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	24.4
	419172	AW338625	Hs.22120	ESTs	24.3
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	24.2
	413623	AA825721	Hs.246973	ESTs	24.0
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247 Homo	23.8
25	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	23.8
	432809	AA565509	Hs.131703	ESTs	23.7
	440102	AI672443	Hs.131190	ESTs	23.6
	451559	AL119980	Hs.128857	ESTs	23.2
	410811	AW805687	Hs.300648	ESTs	23.0
30	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	23.0
	453628	AW243307	Hs.170187	ESTs	22.8
	401352				22.6
	451561	N52812	Hs.177403	ESTs	22.6
	401976				22.4
35	410658	AW105231	Hs.192035	ESTs	22.4
	416220	N49776	Hs.121773	ESTs	22.2
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	22.0
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	22.0
	444144	BE159397	Hs.7736	hypothetical protein	21.8
40	438504	AW665281	Hs.224625	ESTs	21.2
	439157	AA912737	Hs.20160	ESTs	20.8
	429006	AA443143	Hs.50929	Homo sapiens cDNA FLJ13842 fis, clone TH	20.5
	442006	AW975183	Hs.292663	ESTs	20.2
	409569	AW573153	Hs.256216	ESTs	19.8
45	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	19.8
	404200				19.6
	446591	H44186	Hs.15456	PDZ domain containing 1	19.2
	420218	AW958037	Hs.22437	Homo sapiens cDNA: FLJ23366 fis, clone H	18.9
	408390	AA054222	Hs.40400	ESTs	18.8
50	444038	AW134509	Hs.135077	ESTs	18.8
	446443	AV659082	Hs.134228	ESTs	18.8
	442204	AI635450	Hs.21914	ESTs	18.4
	451177	AI969716	Hs.13034	ESTs	18.2
	453931	AL121278	Hs.25144	ESTs	18.1
55	437212	AI765021	Hs.210775	ESTs	18.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	18.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU S	17.8
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	17.6
	441082	AW444804	Hs.202655	ESTs	17.6
60	446259	AA425204	Hs.42278	Homo sapiens cDNA FLJ13391 fis, clone PL	17.6
	423609	AA328348	Hs.218289	ESTs	17.4
	428301	AW628666	Hs.98440	ESTs	17.4
	446364	AB006624	Hs.14912	KIAA0286 protein	17.4
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	17.0
65	424929	AI640761	Hs.224988	ESTs	17.0
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	17.0
	449122	AI631310	Hs.196955	ESTs	17.0
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	16.8
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	16.8
70	418053	AA211493		gb:zn55d06.s1 Stratagene muscle 937209 H	16.8
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	16.8
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	16.6
	421002	AF116030	Hs.100932	transcription factor 17	16.5
	419296	AA236115	Hs.120785	ESTs	16.2
75	421659	NM_014459	Hs.106511	protocadherin 17	16.0
	417589	T82075	Hs.13911	ESTs	16.0
	446057	AI420227	Hs.149358	ESTs	15.8
	434636	AA083764	Hs.241334	ESTs	15.6
80	446797	AI682536	Hs.163495	Homo sapiens cDNA FLJ13608 fis, clone PL	15.6
	443718	AI083580	Hs.221373	ESTs	15.4
	409748	AI670776	Hs.20961	ESTs	15.2
	443211	AI128388	Hs.143655	ESTs	15.0
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	14.9
	444692	AW779922	Hs.145047	ESTs	14.8

	445436	AI224105	Hs.151408	ESTs	14.6
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	14.5
	405943				14.4
	406291				14.4
5	458679	AW975460	Hs.143563	ESTs	14.4
	450152	AI138635	Hs.22958	ESTs	14.4
	403899				14.2
	454490	AW797778		gb:CM2-UM0041-250200-104-d02 UM0041 Homo	14.2
	451807	W52854	Hs.27099	DKFZP564J0863 protein	14.0
10	452453	AI902519		gb:OV-BT009-101198-051 BT009 Homo sapien	13.8
	447499	AW262580	Hs.147674	KIAA1621 protein	13.8
	406598				13.6
	430939	AI269471	Hs.187018	ESTs	13.4
	443316	AI478463	Hs.18443	ESTs	13.4
15	408034	N26639	Hs.42192	Human EST clone 251800 mariner transpos	13.2
	428508	BE252383	Hs.184568	SBB131 protein	13.2
	447934	AW631440	Hs.165596	ESTs	13.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	13.1
	438199	AW016531	Hs.122147	ESTs	13.0
20	415511	AI732617	Hs.182362	ESTs	12.9
	426920	AA393351	Hs.132121	ESTs	12.8
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	12.6
	423321	AB013885	Hs.126926	beta-ureidopropionase	12.5
	403622				12.4
25	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	12.4
	422317	NM_001147	Hs.115181	angiotensin 2	12.2
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	12.2
	445717	AW664658	Hs.149332	ESTs	12.2
30	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the m	12.1
	405336				12.0
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	12.0
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	12.0
	414923	AW445008	Hs.77637	homeo box A4	11.9
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	11.8
35	433326	AI379486	Hs.159430	ESTs	11.8
	453955	AW579207		gb:RC1-DT0029-120100-011-h01 DT0029 Homo	11.8
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	11.6
	433231	AB040926	Hs.143552	KIAA1493 protein	11.6
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	11.6
40	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	11.4
	405609				11.4
	418912	NM_000685	Hs.89472	angiotensin receptor 1	11.4
	421306	AA806207	Hs.125889	ESTs	11.4
	428721	X02158	Hs.2303	erythropoietin	11.4
45	419255	AA235672	Hs.87491	ESTs	11.4
	450006	AI241555	Hs.60171	ESTs	11.3
	435420	AI928513	Hs.59203	ESTs	11.2
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	11.2
	424647	W67751	Hs.137308	ESTs	11.0
50	435758	AI242163	Hs.22670	chromodomain helicase DNA binding protei	11.0
	404347				10.8
	438664	AI911173	Hs.213722	ESTs	10.8
	429125	AA446854	Hs.271004	ESTs	10.7
	416560	R02818	Hs.14102	ESTs	10.6
55	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	10.6
	435085	AW130284	Hs.192752	ESTs, Moderately similar to NSD1 protein	10.6
	442409	BE208843	Hs.129544	ESTs, Weakly similar to ORF YLL027w [S.c	10.6
	450644	AW505496	Hs.281215	ESTs	10.6
	448298	AW137134	Hs.187203	ESTs	10.4
60	404115				10.2
	406242				10.2
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.2
	452588	AA889120	Hs.110637	homeo box A10	10.2
	457233	AI355009	Hs.221698	ESTs	10.2
65	416185	AW975861	Hs.291995	ESTs	10.2
	446152	AI292036	Hs.150028	ESTs	10.1
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	10.1
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (I	10.0
	442405	BE465247	Hs.129530	ESTs	9.9
70	419213	AW749146		gb:PM0-BT0340-170100-004-e03 BT0340 Homo	9.8
	420840	AI915836	Hs.294008	ESTs	9.8
	423355	AA324856	Hs.257510	ESTs	9.8
	444929	AI685841	Hs.161354	ESTs	9.8
	423811	AW299598	Hs.50895	homeo box C4	9.8
75	433527	AW235613	Hs.133020	ESTs	9.6
	429975	AI167145	Hs.165538	ESTs	9.6
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	9.5
	433703	AA210863	Hs.3532	nemo-like kinase	9.2
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	9.2
80	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	9.2
	406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	9.2
	419699	AA248998	Hs.31246	ESTs	9.2
	443740	R56434	Hs.21062	ESTs	9.2

5	422728	AW937826	Hs.103262	ESTs	9.2
	436961	AW375974	Hs.156704	ESTs	9.2
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	9.1
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	9.1
	424115	AA335497	Hs.293965	ESTs	9.0
	402045				9.0
	433426	H69125	Hs.133525	ESTs	9.0
	425493	AW363582	Hs.75323	prohibiti	9.0
10	447641	BE619186		gb:601472933F1 NIH_MGC_68 Homo sapiens c	9.0
	403095				9.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	8.8
	423126	AA322245	Hs.290165	ESTs	8.8
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	8.8
15	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.7
	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	8.6
	401439				8.6
	449532	W74653	Hs.271593	ESTs	8.6
	453197	A1916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.6
20	448450	BE612490		gb:601451884F1 NIH_MGC_66 Homo sapiens c	8.6
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN T	8.5
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	8.4
	402921				8.4
	428133	AW167727	Hs.11873	ESTs	8.4
25	419503	AA243642	Hs.137422	ESTs	8.4
	452644	AW452616	Hs.212481	ESTs	8.4
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	8.4
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	8.4
	418076	R61388	Hs.6724	ESTs	8.3
	402696				8.3
30	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor 1	8.3
	413998	AW103807	Hs.243933	ESTs	8.3
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	8.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fs, clone C	8.2
35	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	8.2
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	8.1
	413627	BE182082	Hs.246973	ESTs	8.0
	415713	AW968573		gb:EST380649 MAGE resequences, MAGJ Homo	8.0
	426695	AW118191	Hs.112729	ESTs	8.0
40	452284	AW451426	Hs.252740	ESTs	8.0
	454933	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	8.0
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.0
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	8.0
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	8.0
45	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	7.9
	433190	M26901	Hs.3210	renin	7.9
	432777	AA564991	Hs.269477	ESTs	7.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.8
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	7.7
50	434032	AW009951	Hs.206892	ESTs	7.7
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fs, clone NT	7.7
	439024	R96696	Hs.35598	ESTs	7.6
	437205	AL110232		gb:Homo sapiens mRNA; cDNA DKFZp564D2071	7.6
	446030	AF131805	Hs.13544	Homo sapiens clone 24850 mRNA sequence	7.4
55	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.4
	452883	X80031	Hs.150318	ESTs	7.4
	448253	H25899	Hs.201591	ESTs	7.4
	406030				7.4
	437084	A1911516	Hs.127811	ESTs	7.4
60	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRO subu	7.3
	432143	AL040183	Hs.123484	ESTs, Weakly similar to The KIAA0149 gen	7.3
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (93720	7.3
	425151	AA351814	Hs.298678	ESTs	7.2
	448582	A1538880	Hs.94812	ESTs	7.2
65	455068	A1807894	Hs.27910	centrosomal protein 2	7.2
	406504				7.2
	428395	AA427992	Hs.104885	ESTs, Weakly similar to zinc finger prot	7.2
	421102	A1470093	Hs.89217	ESTs	7.2
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	7.1
70	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	7.1
	415084	M19267	Hs.77899	tropomyosin 1 (alpha)	7.0
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	7.0
	439416	W58294	Hs.56254	ESTs	7.0
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	6.9
75	423349	AF010258	Hs.127428	homeo box A9	6.8
	413070	AA126776		gb:zm88c11.s1 Stratagene lung carcinoma	6.8
	449361	AW207890	Hs.201918	ESTs	6.8
	459309	AA040620	Hs.109144	ESTs	6.8
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.8
80	416462	W92845		gb:zh80f05.r1 Soares_fetal_liver_spleen_	6.8
	447835	AW591623	Hs.164129	ESTs	6.8
	403563				6.7
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	6.7
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	6.6

	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	6.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	6.6
	445575	Z25368	Hs.172004	lin	6.6
	446075	AW451457	Hs.279179	ESTs	6.6
5	405963				6.6
	423049	X59373	Hs.188023	ESTs	6.6
	436456	AW292677	Hs.65909	ESTs	6.5
	420273	AI652864	Hs.197257	ESTs	6.5
	420831	AA280824	Hs.190035	ESTs	6.4
10	423739	AA398155	Hs.97600	ESTs	6.4
	441559	AA384448	Hs.259733	ESTs	6.4
	433999	AA778212	Hs.191869	ESTs	6.4
	439703	AF086538	Hs.196245	ESTs	6.4
	433757	AI949974	Hs.152670	ESTs	6.3
15	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.3
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	6.3
	448515	H68441	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	6.3
	429357	AA779725	Hs.164589	ESTs	6.3
20	404939				6.3
	417071	N58820	Hs.275133	ESTs	6.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	6.2
	403111				6.2
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228.3 BC372	6.2
25	442353	BE379594	Hs.49136	ESTs	6.2
	451110	AI955040	Hs.301584	ESTs	6.1
	420092	AA814043	Hs.88045	ESTs	6.1
	441801	AW242799	Hs.211874	ESTs	6.0
	407500	U43279		gb:Human nucleoporin nup 36 mRNA, comple	6.0
30	450864	R64139	Hs.205225	ESTs	6.0
	455711	BE069465		gb:RC2-BT0388-290100-012-a11 BT0388 Homo	6.0
	405394				6.0
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	6.0
35	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	6.0
	414575	H11257	Hs.295233	ESTs	5.9
	435767	H73505	Hs.117874	ESTs	5.9
	445495	BE622641	Hs.38489	ESTs	5.9
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	5.9
40	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.9
	402421				5.8
	417038	T85230		gb:yd33f02.r1 Soares fetal liver spleen	5.8
	436461	AW511956	Hs.293261	ESTs	5.8
45	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	5.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.8
	417280	AW173116	Hs.262206	ESTs	5.7
	437259	AI377755	Hs.120695	ESTs	5.7
	425717	X07282	Hs.171495	retinoic acid receptor, beta	5.7
50	443514	AV655386	Hs.7645	fibrinogen, B beta polypeptide	5.7
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	5.6
	425305	AA363025	Hs.155572	Human clone Z3801 mRNA sequence	5.6
	430371	D87466	Hs.240112	KIAA0276 protein	5.6
	430499	AW969408	Hs.231991	ESTs	5.6
	427920	Z11502	Hs.181107	annexin A13	5.6
55	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	5.6
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	5.5
	410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	5.5
	415286	AW249540	Hs.72548	ESTs	5.5
60	443297	AI049864	Hs.133029	ESTs	5.5
	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.5
	441006	AW605267	Hs.7627	CGI-60 protein	5.4
	409348	AI401535	Hs.146090	ESTs	5.4
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	5.4
65	408938	AA059013	Hs.22607	ESTs	5.4
	456411	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.4
	443756	AW089799	Hs.153665	ESTs	5.4
	422232	D43945	Hs.113274	transcription factor EC	5.4
	424574	BE408618	Hs.150748	malonyl-CoA decarboxylase	5.3
70	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	5.3
	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	5.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	5.3
	450236	AW162998	Hs.24684	KIAA1376 protein	5.3
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone H	5.3
	427061	AB032971	Hs.173392	KIAA1145 protein	5.3
75	413841	M34276	Hs.75576	plasminogen	5.3
	432358	AI093491	Hs.72830	ESTs	5.2
	416805	F13271	Hs.79981	Human clone Z3560 mRNA sequence	5.2
	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	5.2
	443305	AI050693	Hs.133318	ESTs	5.2
80	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.1
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	429826	N93266	Hs.40747	ESTs	5.1
	436032	AA150797	Hs.109276	latexin protein	5.1

	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	5.1
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	5.1
5	440238	AW451970	Hs.155644	paired box gene 2	5.1
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	5.0
	425813	AA364136	Hs.210553	ESTs, Weakly similar to hypothetical pro	5.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	5.0
	430682	AW971949	Hs.291252	ESTs	5.0
10	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo	5.0
	429222	AI457692	Hs.99164	ESTs	5.0
	446317	AI287367	Hs.150906	ESTs	5.0
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.0
	407768	AW002841	Hs.29475	ESTs	5.0
15	437938	AI950087		gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapien	5.0
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	4.9
	426215	AW963419	Hs.155223	stanniocalcin 2	4.9
	448570	AI923944	Hs.30913	ESTs	4.9
	445034	AW293376	Hs.160323	ESTs	4.9
20	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.8
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	4.8
	438492	AW340048	Hs.293188	ESTs	4.8
	446417	AI299050		gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	4.8
	409578	BE041386		gb:hk88c02.x1 NCI_CGAP_Lu21 Homo sapiens	4.8
25	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenylylsulfate:g	4.8
	413795	AL040178	Hs.142003	ESTs	4.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	4.8
	452208	AA024792	Hs.31895	ESTs, Weakly similar to B9 [H.sapiens]	4.7
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586i1518 (f	4.7
30	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERAT	4.7
	439221	AA737106	Hs.32250	ESTs	4.7
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.7
	417355	D13168	Hs.82002	endothelin receptor type B	4.7
	414700	H63202	Hs.38163	ESTs	4.7
35	402739				4.6
	403170				4.6
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.6
	427899	AA829286	Hs.181062	serum amyloid A1	4.5
40	446302	AI285848	Hs.149757	ESTs	4.5
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	4.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	4.4
	421298	AW172431	Hs.13012	ESTs	4.4
45	420789	AI670057	Hs.199882	ESTs	4.4
	453558	AI417023	Hs.40478	ESTs	4.4
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	4.4
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	4.4
	410334	AW979261	Hs.291993	ESTs	4.4
50	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.4
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	4.4
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.3
	401157				4.3
	432004	BE018302	Hs.2894	placental growth factor, vascular endothe	4.3
55	426866	U02330	Hs.172816	neuregulin 1	4.3
	446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	4.3
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	4.2
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.2
	433578	BE336886	Hs.3416	adipose differentiation-related protein	4.2
60	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR.	4.2
	407182	AA312551	Hs.230157	ESTs	4.2
	416565	AW000960	Hs.44970	ESTs	4.2
	442230	BE219088	Hs.279547	ESTs	4.2
	440680	AA903098		gb:ok46f08.s1 NCI_CGAP_Lu2 Homo sapiens	4.2
65	413802	AW964490	Hs.32241	ESTs	4.2
	438370	AA843242	Hs.48523	ESTs	4.2
	432731	R31178	Hs.287820	fibronectin 1	4.2
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	4.2
	441484	AA935481	Hs.58972	ESTs	4.2
70	411213	AA676939	Hs.69285	neuropilin 1	4.2
	453045	AW418979	Hs.224502	ESTs	4.2
	407999	AI126271	Hs.49433	ESTs, Weakly similar to HYPOTHETICAL PRO	4.2
	409770	AW499536		gb:UI-HF-BR0p-aj-c-12-0-UI.r1 NIH_MGC_5	4.1
	449856	AA203155	Hs.18200	ESTs	4.1
75	430806	S69377	Hs.247978	T-cell acute lymphocytic leukemia 2	4.1
	412872	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	4.1
	430719	AA488988	Hs.293796	ESTs	4.1
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	4.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	4.1
80	444670	H58373	Hs.37494	ESTs	4.1
	448090	AI608821	Hs.270289	ESTs	4.1
	408830	AK001709	Hs.48403	hypothetical protein FLJ10847	4.1
	419088	AI538323	Hs.77496	small nuclear ribonucleoprotein polypept	4.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.1

	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	4.1
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	4.1
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3)	4.1
5	438859	AI559626	Hs.164973	ESTs, Weakly similar to AF231024 1 proto	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
	441592	AW137071	Hs.127211	ESTs	4.0
	411836	AW901879		gb:QVQ-NN1021-280400-212-110 NN1021 Homo	4.0
	426384	AI472078		gb:ij85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	4.0
10	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	4.0
	413583	AL120806	Hs.5888	ESTs	4.0
	415610	L44319		gb:HUMEST1D10 Human thymus NSTH II Homo	4.0
	430009	AA894564	Hs.22242	ESTs	4.0
	449539	W80363	Hs.58446	ESTs	4.0
15	438929	AW195515	Hs.253177	ESTs	4.0
	416000	R82342	Hs.79856	ESTs	4.0
	429616	AI982722	Hs.120845	ESTs	4.0
	458471	AV648609	Hs.194240	ESTs	4.0
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	4.0
20	459046	AA910339	Hs.26216	Homo sapiens cDNA: FLJ22811 fis, clone K	3.9
	438177	BE327015	Hs.281391	ESTs	3.9
	422438	AA445925	Hs.270896	ESTs	3.9
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ135598 fis, clone PL	3.9
	449611	AI970394	Hs.197075	ESTs	3.9
25	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	3.9
	452881	AW135220	Hs.241921	ESTs	3.9
	414729	BE466928	Hs.281901	ESTs	3.9
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.9
	405908				3.8
30	445452	H92975	Hs.246046	ESTs, Weakly similar to RET1_HUMAN RETIN	3.8
	447961	W32791	Hs.170405	ESTs	3.8
	446639	AI016826	Hs.132501	ESTs	3.8
	401189				3.8
	429548	AW138872	Hs.135288	ESTs	3.8
35	431523	N55759	Hs.163674	ESTs	3.8
	430014	H59354	Hs.182485	actinin, alpha 4	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	3.8
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interlero	3.8
40	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.8
	433522	AI821730	Hs.116524	ESTs	3.8
	443843	AW878864	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	3.7
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.7
	434613	AI821826	Hs.187786	ESTs, Moderately similar to ALUB_HUMAN !	3.7
45	410276	AI554545	Hs.68301	ESTs	3.7
	422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.7
	437949	U78519	Hs.41654	ESTs	3.7
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.7
50	409446	AI561173	Hs.67688	ESTs	3.7
	415263	AA948033	Hs.130853	ESTs	3.7
	450206	AI796450	Hs.201600	ESTs	3.7
	439444	AI277652	Hs.54578	ESTs	3.7
	437828	AW976806	Hs.291805	ESTs	3.7
55	453238	AA033991	Hs.269234	ESTs	3.7
	420041	AB005142	Hs.94592	Idotho	3.7
	448458	AW614367	Hs.171054	ESTs	3.7
	435080	AI831760	Hs.155111	ESTs	3.7
	444249	T87398	Hs.205816	ESTs	3.7
60	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	3.7
	417715	AW969587	Hs.86366	ESTs	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein	3.6
	430091	AB032958	Hs.233023	KIAA1132 protein	3.6
65	438030	X98427	Hs.122634	ESTs	3.6
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.6
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.6
	417860	AW408557	Hs.235498	Homo sapiens cDNA FLJ14075 fis, clone HE	3.6
	435794	H72108	Hs.13704	ESTs	3.6
70	449695	AA164569	Hs.34550	ESTs	3.6
	411485	AW848125		gb:IL3-CT0214-301299-048-G04 CT0214 Homo	3.6
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	3.6
	458201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, S	3.6
	440987	AA911705	Hs.130229	ESTs	3.6
75	425178	H16097	Hs.161027	ESTs	3.6
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	3.6
	436091	AA704705	Hs.181044	ESTs, Weakly similar to A Chain A, Human	3.6
	452671	AW861074	Hs.225833	ESTs	3.6
	437222	AL117588	Hs.299963	ESTs	3.6
80	437809	AL137723	Hs.5855	Homo sapiens mRNA; cDNA DKFZp434D0818 (f	3.5
	411545	AW850818		gb:IL3-CT0220-091199-026-A03 CT0220 Homo	3.5
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.5
	439882	AA847856	Hs.124565	ESTs	3.5
	419229	AI827237	Hs.282884	ESTs	3.5

	431889	AA521277	Hs.124946	ESTs	
	422660	AW297582	Hs.237062	ESTs	3.5
	415122	D60708	Hs.22245	ESTs	3.5
	444127	N63620	Hs.13281	ESTs	3.5
5	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	409044	AI129586	Hs.33033	ESTs	3.5
	453365	AA035211	Hs.17404	ESTs	3.5
	452355	N54926	Hs.29202	G protein-coupled receptor 34	3.5
10	423246	AL119114	Hs.23107	ESTs	3.5
	434131	AI858275	Hs.143659	ESTs	3.5
	425304	AA463844	Hs.31339	fibroblast growth factor 11	3.5
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.5
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	3.4
15	456311	AA225632	Hs.190016	ESTs	3.4
	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfamily	3.4
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter)	3.4
	401811				3.4
	404021				3.4
20	447175	AI365208	Hs.293606	ESTs	3.4
	453743	AL120480		gb:DKFZp761K098_r1 761 (synonym: hamy2)	3.4
	455070	AW854675		gb:MR1-CT0258-290300-206-a01 CT0258 Homo	3.4
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	449441	AI656040	Hs.196532	ESTs	3.4
25	441606	R37263	Hs.21065	ESTs	3.4
	446594	AI311917	Hs.16292	ESTs	3.4
	424684	AI432572	Hs.164221	ESTs	3.4
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.4
	427914	AA417350	Hs.20575	ESTs	3.4
30	438257	AW474419	Hs.224794	ESTs	3.4
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	3.4
	454690	AW854639		gb:MR1-CT0258-140100-203-d10 CT0258 Homo	3.3
	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	3.3
	407331	AI570416	Hs.99910	phosphofructokinase, platelet	3.3
35	440472	AA886169	Hs.169071	ESTs	3.3
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.3
	403797				3.3
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.3
	410623	AW958932	Hs.293833	ESTs	3.3
40	449338	H73444	Hs.394	adrenomedullin	3.3
	441024	AW081530	Hs.137088	ESTs	3.3
	405257				3.3
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	3.3
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.3
45	444471	AB020684	Hs.11217	KIAA0877 protein	3.3
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.3
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	3.3
	425236	AW067800	Hs.155223	stanniocalcin 2	3.3
	428824	W23624	Hs.173059	ESTs	3.2
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	3.2
	425260	L47726	Hs.1870	phenylalanine hydroxylase	3.2
	443830	AI142095	Hs.143273	ESTs	3.2
	415245	N59650	Hs.27252	ESTs	3.2
	405953				3.2
55	430812	L10405	Hs.247992	DNA binding protein for surfactant prote	3.2
	418946	AI798841	Hs.132103	ESTs	3.2
	424750	D29956	Hs.152818	ubiquitin specific protease 8	3.2
	435342	AW979168	Hs.163270	ESTs	3.2
	458860	AW873557	Hs.212739	ESTs	3.2
60	430172	AA468591	Hs.161889	ESTs	3.2
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	3.2
	451221	AI949701	Hs.210589	ESTs	3.2
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	3.2
	433727	C16221	Hs.112608	ESTs	3.2
65	424897	D63216	Hs.153684	frizzled-related protein	3.2
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.1
	418030	BE207573	Hs.83321	neuromedin B	3.1
	417919	AI928203	Hs.86379	ESTs	3.1
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.1
70	409663	AI743750	Hs.65862	ESTs	3.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	3.1
	424980	L42172	Hs.154078	lipopolysaccharide-binding protein	3.1
	421633	AF121860	Hs.106260	sorting nexin 10	3.1
	436002	R68529	Hs.120967	ESTs	3.1
75	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	3.1
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	3.1
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.1
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	3.1
	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.1
80	456386	W28481		gb:47e1 Human retina cDNA randomly prime	3.1
	451130	AI762250	Hs.211347	ESTs	3.1
	439702	AW085525	Hs.134182	ESTs	3.1
	453331	AI240665	Hs.8895	ESTs	3.1
	428841	AI418430	Hs.104935	ESTs	3.1

5	449899	AI610700	Hs.103280	ESTs	3.1
	436009	H57130	Hs.120925	ESTs	3.1
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clone HE	3.1
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	3.1
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.1
10	401260				3.1
	450705	U90304	Hs.25351	iroquois-class homeodomain protein	3.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	3.1
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	3.0
	403346				3.0
15	446319	AW207590	Hs.160711	ESTs	3.0
	432757	AF113013	Hs.278919	PRO0806 protein	3.0
	407921	AI378617	Hs.23100	Homo sapiens cDNA FLJ12592 fis, clone NT	3.0
	414618	AI204600	Hs.96978	ESTs	3.0
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
20	440113	AI916532	Hs.188272	ESTs	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	428945	AW192803	Hs.98974	ESTs	3.0
	458297	R54033	Hs.21245	ESTs	3.0
	424405	AI076838	Hs.12967	ESTs	3.0
25	411290	AW835544		gb:QV4-LT0016-271299-068-f03 LT0016 Homo	3.0
	459068	BE464396	Hs.118468	ESTs	3.0
	459065	AI373532	Hs.157910	ESTs	3.0
	437693	AI754443	Hs.185951	ESTs	3.0
	429418	AI381028	Hs.99283	ESTs	3.0
30	406117				3.0
	415492	R41674	Hs.16491	ESTs	3.0
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from	3.0
	453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (f	3.0
	408119	W26213		gb:22d10 Human retina cDNA randomly prim	3.0
35	438358	AL035992	Hs.210278	ESTs	3.0
	412372	R65998	Hs.118615	ESTs	3.0
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256022	3.0
	403782				3.0
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.0
40	456388	W28557		gb:48d8 Human retina cDNA randomly prime	3.0
	447922	Z92910	Hs.20019	hemochromatosis	3.0
	428857	AF008192	Hs.194283	putative GR6 protein	3.0
	406991	S82185		(NONE)	3.0
	432596	AJ224741	Hs.278461	matrilin 3	3.0
45	453202	AW085781	Hs.26270	Homo sapiens cDNA FLJ11588 fis, clone HE	3.0
	414132	AI801235	Hs.48480	ESTs	3.0
	409122	W07089	Hs.297873	ESTs	3.0
	405547				3.0
	422219	AW978073		gb:EST390182 MAGE resequences, MAGO Homo	3.0
50	417227	T57776	Hs.191094	ESTs	3.0
	448592	N69546	Hs.141706	ESTs	3.0
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.0
	400368	BE779978	Hs.69149	proline-serine-threonine phosphatase int	3.0
	455362	AW902635		gb:QV3-NN1024-100500-181-b02 NN1024 Homo	3.0
55	443578	R97191	Hs.134106	ESTs	3.0
	419348	AA236645	Hs.98274	ESTs	3.0
	439138	AI742605	Hs.193696	ESTs	3.0
	449547	H93543	Hs.117963	ESTs	3.0
	455180	AW863503		gb:MR3-SN0009-180400-110-c12 SN0009 Homo	3.0
60	444228	AV648612	Hs.282396	ESTs	3.0
	423496	U91963	Hs.129700	toll-like 1	3.0
	401707				3.0
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	3.0
	441677	AW271702	Hs.93739	ESTs	3.0
65	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	3.0
	431311	AA502552	Hs.188980	ESTs	3.0
	426326	BE165753	Hs.250528	ESTs, Weakly similar to unnamed protein	3.0
	412685	BE092186		gb:IL2-BT0734-200400-075-H05 BT0734 Homo	3.0
	414752	BE503505	Hs.248689	ESTs	3.0
70	403144				3.0
	407539	X91103		gb:H.sapiens mRNA for Hr44 protein.	3.0
	412379	AW947581		gb:RC0-MT0004-140300-031-d08 MT0004 Homo	3.0
	407937	AW297944	Hs.242811	ESTs	3.0
	456976	AI681882	Hs.270428	ESTs	3.0
75	417066	AA329572	Hs.172004	tin	3.0
	406007				3.0
	416940	N75620	Hs.43157	ESTs	3.0
	433322	H50621	Hs.134156	ESTs	3.0
	406088				3.0
80	416573	R10356	Hs.18865	ESTs, Weakly similar to AC007228 2 BC372	3.0
	423130	AW897586	Hs.21213	ESTs	3.0
	412721	AW183165	Hs.95600	ESTs	3.0
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	3.0
	422992	AF016833	Hs.122785	maltase-glucoamylase (alpha-glucosidase)	3.0
	406506				3.0
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	3.0
	422650	D42055	Hs.1565	neural precursor cell expressed, develop	3.0

5	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	3.0
	401078				3.0
	446645	AI336596	Hs.156294	ESTs	3.0
	446704	AI337228	Hs.197083	ESTs	3.0
	427072	H38046		gb:yp58c10.r1 Soares fetal liver spleen	3.0
TABLE 338:					
10	Pkey:	Unique Eos probe/identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
15	Pkey	CAT number	Accession		
	407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087		
	408119	1040172_1	W26213 H08055 Z44031 AW954559 R17434		
	409519	113722_1	AA075368 AA075369		
	409578	1140976_1	BE041386 AW419449 AW663595		
20	409594	114249_1	AA076118 AA975618 AA076220		
	409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497		
	409745	115237_1	AA077391 AJ347618 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450		
	409770	1154048_1	AW499536 AW499553 AW502138 AW499537 AW502136 AW501743		
	410008	116812_1	AA079552 BE142525 BE142527		
25	410049	1172307_1	AW579475 AW939654 AW939655		
	410534	1207247_1	AW905138 AW753008 R13818 Z43519		
	410754	1219733_1	T63840 AW801569 AW801568		
	411290	1237738_1	AW835544 AW835613 AW835711 AW835697 AW835703 BE092535 BE092199 411485 1247181_1 AW848125 AW848124 AW848203 AW848695		
			AW848633 AW848693 BE350771		
30	411545	1249138_1	AW850818 AW850833 AW851100		
	411836	1260619_1	AW901879 AW901875 AW866247 BE011294 BE504813		
	412209	1283610_1	AW901456 AW901450 AW901441		
	412359	129085_1	AW837985 AW837938 AA101955 AW837913 AW837935		
	412379	1292479_1	AW947581 AW947546 AW947545 AW947544		
35	412685	1321663_1	BE092186 BE092157 AW983859		
	412872	1333898_1	BE006341 BE006307 BE006311		
	413070	134815_1	AA126776 AA133984 BE148613 BE063475 AA358219		
	415610	1540554_1	L44319 F12851 T75057		
	415713	154859_1	AW988573 AA167225 AA491129		
40	416462	1595954_1	W92845 H57479		
	416548	1600181_1	H62953 N76608 N72413		
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499		
	417038	164390_1	T85230 AA192508 T89190		
	418053	171810_1	AA211493 AW817839 AW817836		
45	419213	182860_1	AW749146 AW749138 AW749123 AW749130 AA235142		
	419546	185766_1	AA244199 AA244272 H57440		
	420637	195241_1	AW976153 AA278945 AA747691		
	422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839		
	422219	213547_1	AW978073 AW978072 AA807550 AA306567		
50	422504	217160_1	AA311407 AW958321 N23583 R70050		
	423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496		
	426384	266211_1	AI472078 AA377209 AA865807		
	427072	274884_1	H38046 W69645 AA397968 H38047		
	428637	293660_1	AW979268 AA878419 AA431342 AA431628		
55	430183	31412_2	BE010038 AA676833 AJ311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909		
	431595	335512_1	AA508196 BE142920 AI280311 AI205616 D61709		
	432009	34025_1	AL137424 BE007148 T52277		
	437205	43463_1	AL110232 N94765		
	437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875		
60			AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794		
			AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898		
			AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512		
			AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874		
			AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N23388		
65			H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002639		
			R67840 AA300207 AW959581 T63226 F04005		
	438966	467436_1	AW979074 AA834841 AA828650		
	438993	467651_1	AA828995 AA834879 AI926361		
	440680	500121_1	AA903098 AW836693 BE160824 AW606818 AW582699 AW836766		
70	442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647		
	446346	673545_1	AI290205 AW235762 AI651268		
	446417	676384_1	AI299050 BE256910		
	447641	73043_1	BE619186 BE264952 R26042		
	448450	76399_1	BE612490 T05205 AA481187		
75	449034	794817_1	AI624049 AW117770 AI858360		
	450625	84032_1	AW970107 AA513951 AA010406		
	452453	918300_1	AI902519 AI902518 AI902516		
	453743	979613_1	AL120480 AW836448 AW176802		
	453955	989877_1	AW579207 AW936883 AW008026 N88905		
80	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293		
	454490	1217172_1	AW797778 AW797781 AW797780		
	454690	1229106_1	AW854639 AW854719 AW854718 BE145880 AW854692 BE145866 AW816154 AW854698 AW854654 AW813335 AW854699		
	454933	1245515_1	BE141714 AW845993 AW845989		
	455070	1252209_1	AW854675 AW854685 AW854716 AW854690 AW854615 AW854624 AW854623 AW854641 AW854632 AW854695 AW854661		
	455180	1258658_1	AW863503 AW863362		
	455275	1272255_1	AW977806 AW887923 AW886321		

455362 1284507_1 AW902635 AW902574 BE011167 BE011329 AW902808 AW902651
 455711 1352369_1 BE069465 BE069505
 456386 1842693_-1 W28481
 456388 1842839_-1 W28557
 456411 185688_1 AA603305 AA244095 AA244183
 459587 94893_1 AA031956
 459595 969956_1 AL040421

TABLE 33C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401078	3687273	Plus	105052-105171
401157	9438289	Minus	114133-114247,114567-114645
401189	9690246	Minus	90815-90929
401260	8076883	Minus	86008-86355
401352	9931258	Minus	26064-26208
401439	8246737	Plus	92993-94026
401707	2951946	Plus	21972-22104
401811	6730720	Plus	107002-107209
401976	3095020	Minus	17594-17709,21068-21175
402045	7923943	Plus	5964-6128
402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
402696	7328818	Minus	23600-23731
402739	9212192	Plus	60456-61019
402921	7981303	Minus	52242-52384,55599-55858,57124-57309,59633-59761,59957-60123
403095	8954339	Plus	150025-150240,151564-151690
403111	8980970	Plus	175012-175159
403144	9454649	Minus	166200-166628
403170	9838134	Plus	40955-41356
403345	8569726	Plus	77890-78069
403346	8569726	Plus	92752-93015
403563	8101139	Plus	2800-3501
403622	8569879	Plus	1941-2388,2580-2761
403782	8078608	Plus	41326-41633
403797	8099896	Minus	123065-125008
403899	7381715	Minus	9144-9350
404021	8655966	Plus	192534-193489
404115	9621489	Plus	232707-232982
404200	6010176	Minus	7066-7210
404347	9838195	Plus	74493-74829
404939	6862697	Plus	175318-175476
405257	7329310	Plus	73121-73273
405336	6094635	Plus	33267-33563
405394	6624123	Minus	31900-32373
405547	1054740	Plus	124361-124520,124914-125050
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
405908	6758795	Plus	97969-98715
405943	6758796	Plus	20605-20812
405953	7960374	Minus	65101-65574
405963	8247786	Plus	4056-4699
406007	8247802	Minus	13484-13829
406030	8312328	Minus	96123-96547
406088	9123919	Minus	65772-66270
406117	9142932	Plus	54304-54584
406242	7417725	Minus	36736-36951
406291	5686274	Plus	9562-9867
406411	9256407	Plus	7400-7527
406414	9256407	Plus	49593-49850
406504	7711360	Minus	107068-107277
406506	7711374	Minus	6843-8077
406598	8248614	Plus	56373-56849

TABLE 34A: ABOUT 197 GENES UP-REGULATED IN KIDNEY CANCER

Table 34A lists about 197 genes up-regulated in kidney cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 33A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenetID: Unigenet number
 Unigenet Title: Unigenet gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor to normal tissue

Pkey	ExAccn	UnigenetID	Unigenet Title	PSDomain	R1
421471	U90545	Hs.104635	solute carrier	TM,SS	1007.4
452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,Xlink,CUB	336.4
421727	Y13153	Hs.107318	kynurenine 3-mo	TM,SS,Monooxygenase	323.6

5	426471	M22440	Hs.170009	transforming gr	TM,SS,EGF	224.6
	441031	AI110684	Hs.7645	fibrinogen, B b	fibrinogen_C	174.0
	411642	NM_014932	Hs.71132	neurologin 1	TM,SS,COesterase	172.4
	452838	U65011	Hs.30743	preferentially	TM	161.4
	425984	AW836277	Hs.165636	hypothetical pr	TM	151.0
	453165	S74727	Hs.32042	aspartoacylase	TM	134.8
	452431	U88879	Hs.29499	tol-like recep	TM,SS,TIR,LRRCT	130.6
10	423508	AW604297	Hs.129711	hepatitis A vir	TM,SS,ig	120.4
	407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	111.8
	415076	NM_000857	Hs.77890	guanylate cycla	TM,guanylate_cyc	97.0
	447046	AA326187	Hs.17170	G protein-coupl	TM,7tm_1	90.2
	423109	M59305	Hs.123655	natriuretic pep	TM,SS,ANF_receptor	78.0
	422544	AB018259	Hs.118140	KIAA0716 gene p	TM	74.8
15	429352	AK001512	Hs.200097	hypothetical pr	TM	73.0
	453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	72.2
	403345				TM,alpha-amylase	69.6
	430440	X52599	Hs.2561	nerve growth fa	TM,SS,NGF	69.0
20	408609	AA330431	Hs.640	calcitonin rece	TM,SS,7tm_2	57.4
	449101	AA205847	Hs.23016	G protein-coupl	TM,7tm_1	52.0
	423685	BE350494	Hs.49753	Homo sapiens mR	TM,Myosin_tail	48.0
	452891	N75582	Hs.212875	ESTs, Weakly si	SS	44.0
	408430	S79876	Hs.44926	dipeptidylpepti	TM,SS,DPPIV_N_term,Peptidase_S9	42.6
	412887	X91906	Hs.89872	chloride channe	TM,CBS,voltage_CLC	40.6
25	428822	W28418	Hs.301148	potassium volta	TM	40.2
	434208	T92641	Hs.127648	hypothetical pr	TM,SS	38.2
	400792	AA635062	Hs.50094	Homo sapiens mR	TM,BIR,CARD,zf-C3HC4	38.6
	444743	AA045648	Hs.11817	nudix (nucleosi	TM,muIT	38.4
	406411				TM,vwa,FG-GAP	37.6
30	423657	AL045128	Hs.1691	glucan (1,4-alp	TM,alpha-amylase	37.5
	424871	NM_004525	Hs.153595	low density lip	TM,SS,EGF,kid_receptL_a,kid_receptL_b	32.8
	449625	NM_014253	Hs.23796	odx (odd Oz/ten	SH2,EGF	30.5
	423020	AA383092	Hs.1608	replication pro	TM	29.6
	422420	U03398	Hs.1524	tumor necrosis	TM,TNF	29.6
35	414245	BE148072	Hs.75850	WAS protein fam	TM,WH2	28.8
	410247	AF181721	Hs.61345	RU2S	TM	27.4
	406414				TM,vwa,FG-GAP	27.2
	435951	AF269162	Hs.41267	c21orf7 form A -	TM	27.2
40	419948	AB041035	Hs.93847	NADPH oxidase 4	TM,SS,Ferri_reduct	26.4
	448595	AB014544	Hs.21572	KIAA0644 gene p	TM,SS,LRRCT,LRR	25.8
	419569	AI971651	Hs.91143	jagged 1 (Alagi	TM,SS,DSL,EGF	25.6
	433242	AB040938	Hs.113940	KIAA1505 protei	SS	25.6
	416778	M16505	Hs.79876	steroid sulfata	TM,Sulfatase	23.0
	401352				TM	22.6
45	404200				SS	19.6
	446591	H44186	Hs.15456	PDZ domain cont	TM,PDZ	19.2
	431806	AF186114	Hs.270737	tumor necrosis	TM,SS	18.0
	423909	AJ223183	Hs.135194	immunoglobulin	TM,SS,ig	17.6
50	446364	AB006624	Hs.14912	KIAA0286 protei	TM	17.4
	425695	NM_005401	Hs.159238	protein tyrosin	TM,Band_41,Y_phosphatase	17.0
	410947	AK000305	Hs.67055	hypothetical pr	TM	16.8
	421002	AF116030	Hs.100932	transcription f	TM,KRAB,zf-C2H2	16.5
	421659	NM_014459	Hs.106511	protocadherin 1	TM,SS,cadherin	16.0
55	458679	AW975460	Hs.143563	ESTs	SS	14.4
	406598				SS	13.6
	428508	BE252383	Hs.184668	SBB131 protein	TM,PX	13.2
	423321	AB013885	Hs.126926	beta-ureidoprop	TM,SS,CN_hydrolase	12.5
	422317	NM_001147	Hs.115181	angiotensin 2	fibrinogen_C	12.2
60	428227	AA321649	Hs.2248	small inducible	IL8	12.0
	414923	AW445008	Hs.77637	homeo box A4	TM,homeobox	11.9
	433231	AB040926	Hs.143552	KIAA1493 protei	SS	11.6
	443672	AA323362	Hs.9667	butyrobetaine (TM	11.4
	405609				TM,Myosin_tail,myosin_head	11.4
65	418912	NM_000685	Hs.89472	angiotensin rec	TM,7tm_1	11.4
	449802	AW901804	Hs.23984	hypothetical pr	TM	11.2
	404347				SS	10.8
	429945	NM_006729	Hs.226483	diaphanous (Dro	TM,FH2	10.6
	435085	AW130284	Hs.192752	ESTs, Moderate	TM	10.6
	404115				SS	10.2
70	420757	X78592	Hs.99915	androgen recept	TM,Androgen_recep,hormone_rec,zf-C4	10.2
	446298	AF187813	Hs.14637	kidney- and liv	TM,Acetyltransf	10.1
	433703	AA210863	Hs.3532	nemo-like kinas	TM,plkinase	9.2
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	9.2
	451621	AJ879148	Hs.26770	fatty acid bind	TM,SS,lipocalin	9.2
75	402045				TM,SS	9.0
	403095				SS,PAX,homeobox	8.8
	401439				TM	8.6
	407721	Y12735	Hs.38018	dual-specificit	TM,plkinase	8.4
80	402921				TM	8.4
	419503	AA243642	Hs.137422	ESTs	TM	8.4
	452259	AA317439	Hs.28707	signal sequence	TM	8.3
	402696				TM	8.1
	450001	NM_001044	Hs.406	solute carrier	TM,SS,SNF	7.8
	433190	M26901	Hs.3210	renin	SS,asp	7.8

	449444	AW818436	Hs.23590	solute carrier	TM,MCT	7.7
	444042	NM_004915	Hs.10237	ATP-binding cas	TM,ABC_tran	7.7
	452883	X80031	Hs.150318	ESTs	TM,C4.Collagen	7.4
	425151	AA351814	Hs.298678	ESTs	TM	7.2
5	455068	AI807894	Hs.27910	centrosomal pro	TM,SS	7.2
	406504				TM	7.2
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	7.0
	423349	AF010258	Hs.127428	homeo box A9	TM,homeobox	6.8
	408771	AW732573	Hs.47584	potassium volta	TM,K_tetra,ion_trans	6.8
10	445575	Z25368	Hs.172004	titin	TM	6.6
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) ang	TM,SS,fibrinogen_C	6.3
	404939				TM	6.3
	436209	AW850417	Hs.254020	ESTs, Moderate	TM,SS	6.2
15	403111				TM	6.2
	405394				TM	6.0
	454392	BE260893		gb:601150677F1	TM,SS	6.0
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.9
	402421				TM	5.8
20	425717	X07282	Hs.171495	retinoic acid r	TM,hormone_rec,zf-C4	5.7
	427920	Z11502	Hs.181107	annexin A13	TM,annexin	5.6
	407864	AF069291	Hs.40539	chromosome 8 op	TM,FHA,BRCT	5.5
	441006	AW605267	Hs.7627	CGI-60 protein	TM	5.4
	422232	D43945	Hs.113274	transcription f	TM,HLH	5.4
25	425782	U66468	Hs.159525	cell growth reg	SS	5.3
	450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	5.3
	413841	M34276	Hs.75576	plasminogen	SS,trypsin,kringle,PAN	5.3
	436032	AA150797	Hs.109276	latexin protein	TM	5.1
	447081	Y13896	Hs.17287	potassium inwar	TM,IRK	5.1
30	421126	M74587	Hs.102122	insulin-like gr	SS,thyroglobulin_1,IGFBP	5.1
	426651	AU076646	Hs.171683	nuclear recepto	TM,zf-C4,hormone_rec	5.0
	432328	AI572739	Hs.195471	6-phosphofructo	TM,6PF2K,PGAM	5.0
	409506	NM_006153	Hs.54589	NCK adaptor pro	TM,SH2,SH3	5.0
	410361	BE391804	Hs.62661	guanylate bindi	TM,SS,GBP	4.8
35	453891	AB037751	Hs.36353	Homo sapiens mR	TM	4.8
	447289	NM_004861	Hs.17958	cerebroside (3	TM,SS	4.8
	422357	AF016272	Hs.115418	cadherin 16, KS	TM,cadherin	4.8
	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zf-C3HC4	4.7
	402739				SS	4.6
40	443486	NM_003428	Hs.9450	zinc finger pro	TM,KRAB,zf-C2H2	4.6
	408380	AF123050	Hs.44532	diubiquitin	TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	4.6
	414812	X72755	Hs.77367	monokine induce	SS,IL8	4.4
	424063	NM_002019	Hs.138671	lms-related tyr	TM,SS,ptkinase,ig	4.4
	413384	NM_000401	Hs.75334	exostoses (mult	TM	4.4
45	457030	AJ301740	Hs.173381	dihydropyrimidi	TM,SS,Dihydroorotase	4.4
	410407	X66839	Hs.63287	carbonic anhydr	TM,SS,carb_anhydrase	4.3
	401157				TM,citrate_synt	4.3
	432004	BE018302	Hs.2894	placental growt	SS,PDGF	4.3
50	424704	AI263293	Hs.152096	cytochrome P450	SS,p450	4.2
	407065	Y10141		gb:H.sapiens DA	TM,SS,SNF	4.2
	411213	AA676939	Hs.69285	neurotrophin 1	TM,CUB,F5_F8_type_C,MAM	4.2
	430806	S69377	Hs.247978	T-cell acute ly	TM,HLH	4.1
	414696	AF002020	Hs.76918	Niemann-Pick di	TM,SS,Patched	4.1
55	408830	AK001709	Hs.48403	hypothetical pr	TM,UPF0013	4.1
	416655	AW968613	Hs.79428	BCL2/adenovirus	TM	4.1
	412494	AL133900	Hs.792	ADP-ribosylatio	TM,arf,zf-B_box,zf-C3HC4	4.0
	453195	BE241876	Hs.32352	hypothetical pr	TM	4.0
	428816	AA004986	Hs.193852	ATP-binding cas	TM,ABC_membrane,ABC_tran,COX15-CtaA	3.9
60	401189				TM,SET,PHD,HMG_box	3.8
	451988	AF263928	Hs.27410	papillomavirus	TM	3.8
	421013	M62397	Hs.1345	mutated in colo	TM	3.7
	420041	AB005142	Hs.94592	klortho	TM,SS,Glyco_hydro_1	3.7
	432579	AF043244	Hs.278439	nucleolar prote	TM	3.6
65	453496	AA442103	Hs.33084	solute carrier	TM,SS,sugar_tr	3.6
	446636	AC002563	Hs.15767	citron (rho-int	TM,CNH,DAG_PE-bind,PH,ptkinase,ptkinase_C	3.6
	426274	D38122	Hs.2007	tumor necrosis	TM,TNF	3.6
	452355	N54926	Hs.29202	G protein-coupl	TM,7tm_1	3.5
	453775	NM_002916	Hs.35120	replication fac	TM,SS,AAA	3.4
70	426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S8,P	3.4
	420737	L08096	Hs.98899	tumor necrosis	TM,TNF	3.4
	448733	NM_005629	Hs.187958	solute carrier	TM,SNF,ABC_tran,isodh,ptkinase,Ribosomal_L18ae	3.4
	413719	BE439580	Hs.75498	small inducible	SS,IL8	3.4
	427914	AA417350	Hs.20575	ESTs	TM,GAS2	3.4
	412642	BE244598	Hs.809	hepatocyte grow	kringle,PAN,trypsin	3.4
75	421893	NM_001078	Hs.109225	vascular cell a	TM,SS,ig	3.3
	417924	AU077231	Hs.82932	cyclin D1 (PRAD	TM,cyclin	3.3
	405257				TM	3.3
	450396	AU077002	Hs.24950	regulator of G-	TM,RGS	3.3
80	416892	L24498	Hs.80409	growth arrest a	TM,Ribosomal_L7Ae	3.3
	425236	AW067800	Hs.155223	stanniocalcin 2	SS	3.3
	430812	L10405	Hs.247992	DNA binding pro	TM,SS	3.2
	431842	NM_005764	Hs.271473	epithelial prot	TM,SS	3.2
	424897	D63216	Hs.153684	frizzled-relate	TM,Fz,NTR	3.2

5	414821	M63835	Hs.77424	Fc fragment of	TM,SS,ig	3.1
	418030	BE207573	Hs.83321	neuromedin B	SS	3.1
	421633	AF121860	Hs.106260	sorting nexin 1	TM,PX	3.1
	441285	NM_002374	Hs.167	microtubule-ass	SS,tubulin-binding	3.1
	418526	BE019020	Hs.85838	solute carrier	TM,MCT	3.1
	401260				TM,SS	3.1
	450705	U90304	Hs.25351	iroquois-class	TM,homeobox	3.1
	424415	NM_001975	Hs.146580	enolase 2, (gam	TM,SS,enolase	3.1
10	403346				TM,alpha-amylase	3.0
	432757	AF113013	Hs.278919	PRO0806 protein	TM	3.0
	434398	AA121098	Hs.3838	serum-inducible	TM,pkinase,POLO_box	3.0
	424539	L02911	Hs.150402	activin A recep	TM,Activin_rec,pkinase	3.0
	406117				SS	3.0
15	408119	W26213		gb:22d10 Human	TM,SS	3.0
	431984	AL080239	Hs.272284	Human DNA seque	TM	3.0
	403782				TM	3.0
	447822	Z92910	Hs.20019	hemochromatosis	TM,SS,ig,MHC_I,histone,SPRY,zf-B_box,zf-C3HC4	3.0
	428857	AF008192	Hs.194283	putative GR6 pr	SS	3.0
20	432596	AJ224741	Hs.278461	matrilin 3	SS	3.0
	453202	AW085781	Hs.26270	Homo sapiens cD	TM	3.0
	405547				TM,SS,ABC_membrane,ABC_tran	3.0
	423496	U91963	Hs.129700	tblloid-like 1	TM,SS,EGF,CUB,Astacin	3.0
	401707				SS	3.0
25	403144				TM,ion_trans,K_tetra	3.0
	418375	NM_003081	Hs.84389	synaptosomal-as	TM,NA	3.0
	422992	AF016833	Hs.122785	maltese-glucoam	TM,Glyco_hydro_31,trefoil	3.0
	406506				TM	3.0
	413472	BE242870	Hs.75379	solute carrier	TM,SDF	3.0
30	TABLE 34B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
35	Pkey	CAT number	Accession			
	408119	1040172_1	W26213 H08055 Z44031 AW954559 R17434			
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293			
40	TABLE 34C:					
	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
45	Nt_position:	Indicates nucleotide positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position		
	401157	9438289	Minus	114133-114247,114567-114645		
	401189	9690246	Minus	90815-90929		
50	401260	8076883	Minus	86008-86355		
	401352	9931258	Minus	26064-26208		
	401439	8246737	Plus	92993-94026		
	401707	2951946	Plus	21972-22104		
	402045	7923943	Plus	5964-6128		
55	402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924		
	402696	7328818	Minus	23600-23731		
	402739	9212192	Plus	60456-61019		
	402921	7981303	Minus	52242-52384,55599-55858,57124-57309,59633-59761,59957-60123		
	403095	8954339	Plus	150025-150240,151564-151690		
60	403111	8980970	Plus	175012-175159		
	403144	9454649	Minus	166200-166628		
	403345	8569726	Plus	77890-78069		
	403346	8569726	Plus	92752-93015		
	403782	8078608	Plus	41326-41633		
65	404115	9621489	Plus	232707-232982		
	404200	8010176	Minus	7066-7210		
	404347	9838195	Plus	74493-74829		
	404939	6862697	Plus	175318-175476		
	405257	7329310	Plus	73121-73273		
70	405394	6624123	Minus	31900-32373		
	405547	1054740	Plus	124361-124520,124914-125050		
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727		
	406117	9142932	Plus	54304-54584		
75	406411	9256407	Plus	7400-7527		
	406414	9256407	Plus	49593-49850		
	406504	7711360	Minus	107068-107277		
	406506	7711374	Minus	6843-8077		
	406598	8248614	Plus	56373-56849		

TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER

Table 35A lists about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th percentile for both the numerator and the denominator and using non-malignant kidney specimens in determining the denominator value.

Pkey:		Unique Eos probeset identifier number		
ExAccn:		Exemplar Accession number, Genbank accession number		
UnigeneID:		Unigene number		
Unigene Title:		Unigene gene title		
R1:		Ratio of tumor to normal tissue		
5				
	Pkey	ExAccn	UnigeneID	UnigeneTitle
	424704	AI263293	Hs.152096	cytochrome P450, subfamily 1J (arachido
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system
10	458079	AI796870	Hs.54277	ESTs
	433447	U29195	Hs.3281	neuronal pentraxin II
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy
15	435359	T60843	Hs.189679	ESTs
	450152	AI138635	Hs.22968	ESTs
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	440304	BE159984	Hs.125395	ESTs
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re
20	421155	H87879	Hs.102267	lysyl oxidase
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620
	414812	X72755	Hs.77367	monokine induced by gamma interferon
	426471	M22440	Hs.170009	transforming growth factor, alpha
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor
25	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5
	436961	AW375974	Hs.156704	ESTs
	447499	AW262580	Hs.147674	KIAA1621 protein
	438817	AI023799	Hs.163242	ESTs
	430630	AW269920	Hs.2621	cystatin A (stefin A)
30	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	424086	AI351010	Hs.102267	lysyl oxidase
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli
	415286	AW249540	Hs.72548	ESTs
	428157	AI738719	Hs.298668	ESTs
35	456804	AI421645	Hs.139851	caveolin 2
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively sp
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma
	433757	AI949974	Hs.152670	ESTs
40	400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot
	411642	NM_014932	Hs.71132	neurotigin 1
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA
	435767	H73505	Hs.117874	ESTs
45	427581	NM_014788	Hs.179703	KIAA0129 gene product
	448019	AW947164	Hs.195641	ESTs
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa
	447835	AW591623	Hs.164129	ESTs
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1
50	417308	H60720	Hs.81892	KIAA0101 gene product
	432731	R31178	Hs.287820	fibronectin 1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop
	419235	AW470411	Hs.288433	neurotrophin
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor
55	421485	AA243499	Hs.104800	hypothetical protein FLJ10134
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone H
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;
60	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re
	444969	AI203334	Hs.160628	ESTs
	426890	AA393167	Hs.41294	ESTs
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD
65	446627	AI973016	Hs.15725	hypothetical protein SBB148
	452960	AK001335	Hs.31137	Homo sapiens cDNA: FLJ22681 fis, clone H
	417280	AW173116	Hs.262206	ESTs
	422173	BE385828	Hs.250619	phorbol-like protein MDS019
	420552	AK000492	Hs.98806	hypothetical protein
70	425188	AK002052	Hs.155071	hypothetical protein FLJ11190
	427871	AW992405	Hs.59622	ESTs, Weakly similar to unknown [H.sapie
	446152	AI292036	Hs.150028	ESTs
	426560	AA381661	Hs.119878	ESTs
	419034	NM_002110	Hs.89555	hemopoietic cell kinase
75	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma
	426075	AW513691	Hs.270149	ESTs
	434398	AA121098	Hs.3838	serum-inducible kinase
80	450506	NM_004460	Hs.418	fibroblast activation protein, alpha
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma
	426108	AA622037	Hs.166468	programmed cell death 5
	416000	R82342	Hs.79856	ESTs
	450236	AW162998	Hs.24584	KIAA1376 protein
				11.7

	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	11.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	11.4
	442227	AW771958	Hs.175437	ESTs	11.4
5	414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYG pr	11.4
	447056	N67879	Hs.157695	ESTs	11.4
	444863	AW384082	Hs.301323	ESTs	11.3
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	11.3
	426780	BE242284	Hs.172199	adenylate cyclase 7	11.2
10	453160	AI263307	Hs.146228	ESTs	11.1
	449539	W80363	Hs.58446	ESTs	11.1
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	11.1
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	11.0
	408380	AF123050	Hs.44532	ubiquitin	11.0
15	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	11.0
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	11.0
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	10.8
	435380	AA679001	Hs.192221	ESTs	10.8
	447183	AI554733	Hs.173182	ESTs	10.7
20	438330	AW450572	Hs.257316	ESTs	10.7
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERAT	10.6
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.5
	452862	AW378065	Hs.8687	ESTs	10.5
	431512	BE270734	Hs.2795	lactate dehydrogenase A	10.4
25	421478	AI683243	Hs.97258	ESTs	10.3
	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fis, clone H	10.3
	411800	N39342	Hs.5184	TH1 drosophila homolog	10.3
	433862	D86960	Hs.3610	KIAA0205 gene product	10.3
	440694	AW445167	Hs.126036	ESTs	10.3
30	414504	AW069181	Hs.293523	ESTs, Weakly similar to transformation-r	10.2
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	10.2
	437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	10.2
	430097	AI523245	Hs.127638	ESTs	10.1
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	10.1
35	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	10.0
	424113	AI743880	Hs.12876	ESTs	9.9
	439981	AI348408	Hs.124675	ESTs, Weakly similar to unnamed protein	9.9
	411937	AW876626		gb:RC3-PT0028-120200-013-d08 PT0028 Homo	9.9
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	9.9
40	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	9.9
	424623	AW963062	Hs.165809	ESTs	9.8
	410762	AF226053	Hs.66170	HSKM-B protein	9.8
	433285	AW975944	Hs.237396	ESTs	9.8
	413795	AL040178	Hs.142003	ESTs	9.7
45	434392	AW983709	Hs.268051	ESTs	9.6
	435542	AA687376	Hs.269533	ESTs	9.6
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.6
	410339	AI916499	Hs.298258	ESTs	9.5
	452431	U88879	Hs.29499	loll-like receptor 3	9.5
50	405121	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	9.5
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	9.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	9.4
	449625	NM_014253	Hs.23796	odt (odd Ozten-m, Drosophila) homolog 1	9.4
	441024	AW081530	Hs.137088	ESTs	9.4
55	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	9.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2
	440074	AA863045	Hs.199057	ESTs, Weakly similar to T00050 hypothe	9.2
	421659	NM_014459	Hs.106511	protocadherin 17	9.2
	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	9.2
60	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	9.1
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	9.1
	419441	AW023731	Hs.274368	Homo sapiens mRNA: cDNA DKFZp586i1524 (f	9.1
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	9.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	9.0
65	446460	AW013999	Hs.150164	ESTs	9.0
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.9
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	8.9
	437259	AI377755	Hs.120695	ESTs	8.9
	420235	AA256756	Hs.31178	ESTs	8.7
70	436959	AL133076	Hs.5354	hypothetical protein FLJ12716	8.7
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.7
	435894	AI076667	Hs.188011	ESTs	8.6
	418693	AI750878	Hs.87409	thrombospondin 1	8.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	8.6
75	456249	AI206144	Hs.82508	HRIHFB2206 protein	8.6
	437672	AW748265	Hs.5741	flavohemoprotein b5-b5R	8.6
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	8.6
	417225	AA815048	Hs.24078	Homo sapiens cDNA FLJ12649 fis, clone NT	8.5
	435266	AK001942	Hs.4863	Homo sapiens cDNA FLJ11080 fis, clone PL	8.5
80	447974	R76886		gb:y164b03.s1 Soares placenta Nb2HP Homo	8.4
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	8.4
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	8.4
	435717	AF227905	Hs.105794	UDP-glucose:glycoprotein glucosyltransfe	8.3
	445784	AI253155	Hs.146065	ESTs	8.3

	454024	AA933527	Hs.16281	hypothetical protein FLJ23403	8.3
	443885	H91806	Hs.15284	ESTs	8.3
	403713				8.3
5	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	8.2
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	8.2
	444670	H58373	Hs.37494	ESTs	8.2
	408761	AA057264	Hs.238936	ESTs	8.2
	453033	AA325869	Hs.31463	KIAA0281 gene product	8.2
10	441224	AU076964	Hs.7753	calumenin	8.1
	441689	AI123705	Hs.106932	ESTs	8.1
	440283	AI732892	Hs.190489	ESTs	8.1
	429598	AA811257	Hs.269710	ESTs	8.1
	424775	AB014540	Hs.153026	SWAP-70 protein	8.1
15	451292	AB037716	Hs.26204	KIAA1295 protein	8.0
	453951	AI676235	Hs.24789	ESTs	8.0
	416200	AI188972	Hs.44257	Homo sapiens mRNA; cDNA DKFZp762O2215 (f	8.0
	431087	H12723	Hs.290791	ESTs	8.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	7.9
20	419474	AW968619	Hs.155849	ESTs	7.9
	418342	BE002723	Hs.293504	ESTs, Moderately similar to ALU1_HUMAN A	7.9
	408088	AW157022	Hs.4947	Homo sapiens cDNA: FLJ22584 fis, clone H	7.9
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	7.9
	440987	AA911705	Hs.130229	ESTs	7.9
25	412448	L12864	Hs.73895	tumor necrosis factor receptor superfam	7.9
	415737	AA167626	Hs.118743	ESTs	7.9
	412959	D87458	Hs.75090	KIAA0282 protein	7.8
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	7.8
	453331	AI240665	Hs.8895	ESTs	7.8
30	421991	NM_014918	Hs.110488	KIAA0990 protein	7.8
	443450	N66045	Hs.133529	ESTs	7.8
	431876	AA521183	Hs.269678	ESTs	7.8
	432582	AI623817	Hs.168457	ESTs	7.7
	445800	AA126419	Hs.301632	ESTs	7.7
35	424636	AA453734	Hs.10198	ESTs	7.7
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	7.7
	446873	AI554439	Hs.30724	ESTs	7.7
	400793	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	7.7
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	7.7
40	442028	AI239437	Hs.48945	ESTs	7.7
	442760	BE075297	Hs.10067	ESTs, Weakly similar to KIAA1205 protein	7.7
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	7.7
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	7.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	7.6
45	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 intra	7.6
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	7.6
	434666	AF151103	Hs.112259	T cell receptor gamma locus	7.6
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	7.6
	408418	AW963897	Hs.44743	KIAA1435 protein	7.6
50	418805	AI829520	Hs.227513	ESTs	7.5
	425354	U62027	Hs.155935	complement component 3a receptor 1	7.5
	408743	AL110246	Hs.47367	hypothetical protein from EUROIMAGE 7836	7.5
	444836	AI589825	Hs.173504	ESTs, Weakly similar to JCS238 galactosy	7.5
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	7.4
55	432753	NM_014075	Hs.278915	PRO0593 protein	7.4
	420061	AW024937	Hs.29410	ESTs	7.4
	432865	AI753709	Hs.152484	ESTs	7.4
	419070	AW979068	Hs.182503	ESTs	7.4
	430172	AA468591	Hs.161889	ESTs	7.4
60	446343	AW771414	Hs.8314	ESTs	7.4
	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	7.4
	453818	BE256832	Hs.10711	Homo sapiens cDNA FLJ13449 fis, clone PL	7.4
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	7.4
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	7.4
65	452240	AI591147	Hs.61232	ESTs	7.3
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	7.3
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	7.3
	450205	AI219748	Hs.11356	ESTs	7.3
	437212	AI765021	Hs.210775	ESTs	7.3
70	440193	AW902312	Hs.7037	pallid (mouse) homolog, pallidin	7.2
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	7.2
	451818	AI819018		gb:ts54f01.x1 NCI_CGAP_Kd8 Homo sapiens	7.2
	453013	AA031407		gb:zk15g12.r1 Soares_pregnant_Uterus_NbH	7.2
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	7.2
75	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	7.2
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kd5 Homo sapiens	7.2
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	7.2
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	7.2
80	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	7.2
	443462	AI064690	Hs.171176	ESTs	7.2
	422060	R20893	Hs.75613	CD36 antigen (collagen type I receptor,	7.2
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	7.1
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	7.1

5	458725	AW970192	Hs.171942	ras responsive element binding protein 1	7.1
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	7.1
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	435664	AI032087	Hs.269819	ESTs	7.0
	431708	AI698136	Hs.108873	ESTs	7.0
	426501	AW043782	Hs.293616	ESTs	7.0
	453548	AL079983	Hs.75442	albumin	7.0
	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	7.0
10	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	7.0
	431556	AF016028	Hs.260039	sarcospan (Kras oncogene-associated gene	6.9
	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	6.9
	418986	AI123555	Hs.81796	ESTs	6.9
	430290	AI734110	Hs.136355	ESTs	6.9
15	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	6.9
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.9
	414737	AI160386	Hs.125087	ESTs	6.9
	420479	AW183695	Hs.186572	ESTs	6.9
	432656	NM_000246	Hs.3076	MHC class II transactivator	6.9
20	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.9
	431870	AW449902	Hs.105500	ESTs	6.9
	415788	AW628686	Hs.78851	KIAA0217 protein	6.9
	430066	AI929659	Hs.237825	signal recognition particle 72kD	6.9
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	6.8
25	401539				6.8
	412782	AI189211	Hs.173044	ESTs	6.8
	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2	6.8
	437205	AL110232		gb:Homo sapiens mRNA; cDNA DKFZp564D2071	6.7
30	458814	AI498957	Hs.170861	ESTs	6.7
	452106	AI141031	Hs.21342	ESTs	6.7
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	6.7
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	6.7
	445527	W39694	Hs.83286	ESTs	6.7
	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	6.7
35	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.7
	430280	AA361258	Hs.237868	interleukin 7 receptor	6.7
	415989	AI267700	Hs.111128	ESTs	6.7
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	6.6
	425295	AA431366	Hs.37251	ESTs	6.6
40	438619	AB032773	Hs.6341	TUJ2B1-TY protein	6.6
	424916	AW867440	Hs.23096	ESTs	6.6
	429697	AW296451	Hs.24605	ESTs	6.6
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	6.6
	403549				6.6
45	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	6.6
	435798	BE395289	Hs.12720	elf4E-transporter	6.6
	447217	BE465754	Hs.17778	neuropilin 2	6.6
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	6.6
	410276	AI554545	Hs.68301	ESTs	6.6
50	435391	AA704588	Hs.58934	ESTs	6.6
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	6.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	6.5
	448789	BE539108	Hs.22051	Homo sapiens mRNA; cDNA DKFZp4340119 (fr	6.5
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	6.5
55	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	6.5
	444880	AW118683	Hs.154150	ESTs	6.5
	434131	AI858275	Hs.143659	ESTs	6.5
	446658	AI440137	Hs.164989	ESTs	6.5
	408150	BE620274	Hs.43112	Homo sapiens mRNA; cDNA DKFZp434B1620 (f	6.5
	403790				6.5
60	417129	AI381800	Hs.143275	Homo sapiens cDNA FLJ13233 fis, clone OV	6.5
	452119	AI656378	Hs.33461	ESTs	6.5
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	6.4
	458946	AA009716	Hs.42311	ESTs	6.4
65	452110	T47667	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G2463 (f	6.4
	449318	AW236021	Hs.108788	ESTs. Weakly similar to zeste [D.melanog	6.4
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.4
	402474				6.4
	430712	AW044647	Hs.196284	ESTs	6.4
70	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	6.4
	432683	AW995441	Hs.10475	ESTs	6.4
	423764	AF054589	Hs.132739	ESTs	6.4
	409571	AA504249	Hs.187585	ESTs	6.4
75	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	6.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.4
	432925	AA878324	Hs.192734	ESTs	6.4
	427528	AL077143	Hs.179565	minichromosome maintenance deficient (S.	6.4
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	6.4
	430335	D80007	Hs.239499	KIAA0185 protein	6.4
80	453370	AI470523	Hs.182356	ESTs. Moderately similar to translation	6.3
	421327	AA837295	Hs.188802	ESTs	6.3
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	6.3
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.3
	445279	R41900	Hs.22245	ESTs	6.3

	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	6.3
	421252	AA765930	Hs.130878	ESTs	6.3
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	6.3
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	6.2
5	419436	AA991639	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	6.2
	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	6.2
	409690	W45393	Hs.94642	ESTs, Highly similar to ATFα [H.sapiens]	6.2
	420101	AW500529	Hs.95180	Homo sapiens mRNA: cDNA DKFZp434A205 (tr	6.1
	435889	AJ249107	Hs.269901	ESTs	6.1
10	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	6.1
	448030	N30714	Hs.20161	HDCME31P protein	6.1
	442571	C06338	Hs.165464	ESTs	6.1
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	6.1
	415558	AA885143	Hs.125719	ESTs	6.1
15	408042	AL049233	Hs.42244	Homo sapiens mRNA: cDNA DKFZp564A023 (tr	6.1
	438086	AA336519	Hs.301167	Homo sapiens cDNA: FLJ21545 fis, clone C	6.1
	427390	AJ432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	6.0
	440749	W22335	Hs.7392	Homo sapiens mRNA: cDNA DKFZp761E0323 (f	6.0
	448822	BE149845	Hs.289038	Homo sapiens cDNA: FLJ20994 fis, clone C	6.0
20	424806	AA382523	Hs.105689	ESTs	6.0
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase	6.0
	452235	AL039743	Hs.28514	Homo sapiens mRNA: cDNA DKFZp434H092 (fr	6.0
	432415	T16971	Hs.289014	ESTs	6.0
	436345	AA873008	Hs.121572	ESTs	6.0
25	439451	AF086270	Hs.278554	heterochromatin-like protein 1	6.0
	434674	AA831879	Hs.136985	ESTs	6.0
	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	6.0
	446822	AB037794	Hs.16229	KIAA1373 protein	6.0
	423590	AW952412	Hs.65874	ESTs	6.0
30	424026	AF98295	Hs.123218	ESTs	5.9
	423246	AL119114	Hs.23107	ESTs	5.9
	420982	AW576160	Hs.100729	KIAA0692 protein	5.9
	435008	AF150262	Hs.162898	ESTs	5.9
	420092	AA814043	Hs.88045	ESTs	5.9
35	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	5.9
	450534	AJ570189	Hs.25132	KIAA0470 gene product	5.9
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.9
	425361	AA355933	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	5.9
40	425174	D87450	Hs.154978	KIAA0261 protein	5.9
	458287	AA987556	Hs.12867	ESTs	5.9
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	5.8
	443228	W24781	Hs.293798	ESTs	5.8
	419983	W55956	Hs.94030	Homo sapiens mRNA: cDNA DKFZp586E1624 (f	5.8
45	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.8
	415714	NM_002290	Hs.78672	laminin, alpha 4	5.8
	421689	N87820	Hs.106826	hypothetical protein	5.8
	431176	AJ026984	Hs.293662	ESTs	5.8
	443837	AJ984625	Hs.9884	spindle pole body protein	5.8
50	410623	AW958932	Hs.293833	ESTs	5.8
	421298	AW172431	Hs.13012	ESTs	5.8
	449052	AW029507	Hs.161102	ESTs	5.8
	433043	W57554	Hs.125019	ESTs, Highly similar to KIAA0886 protein	5.8
	439444	AJ277652	Hs.54578	ESTs	5.7
55	428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypotheti	5.7
	411928	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	5.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	5.7
	417315	AJ080042	Hs.180450	ribosomal protein S24	5.7
	422544	AB018259	Hs.118140	KIAA0716 gene product	5.7
60	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	5.7
	433505	AW504027	Hs.15301	Homo sapiens NY-REN-25 antigen mRNA, par	5.7
	410425	BE278367	Hs.63510	KIAA0141 gene product	5.7
	457292	AJ921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	5.7
	457100	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.7
65	436995	AJ160015	Hs.118112	ESTs	5.7
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.7
	441518	AW161697	Hs.294150	ESTs	5.7
	448807	AJ571940	Hs.7549	ESTs	5.7
	449556	AA002008	Hs.188633	ESTs	5.7
70	439211	AJ890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	5.7
	430440	X52599	Hs.2561	nerve growth factor, beta polypeptide	5.7
	413551	BE242639	Hs.75425	ubiquitin associated protein	5.7
	441633	AW958544	Hs.112242	ESTs	5.7
	427093	AA398118	Hs.97579	ESTs	5.6
75	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	5.6
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	5.6
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	5.6
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	5.6
	450447	AF212223	Hs.25010	hypothetical protein P15-2	5.6
80	434623	AB023163	Hs.4014	KIAA0946 protein; Huntingtin interacting	5.6
	420642	AK001520	Hs.99545	Homo sapiens cDNA FLJ10658 fis, clone NT	5.6
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.6
	420825	AJ656727		gbt1t53f12.x1 NCI_CGAP_GC6 Homo sapiens	5.6

	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	5.6
	452046	AB018345	Hs.27657	KIAA0802 protein	5.6
	408911	AW294772	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	5.6
5	414844	AA296874	Hs.77494	deoxyguanosine kinase	5.6
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	5.6
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSml8	5.6
	430339	W28608	Hs.239625	integral membrane protein 28	5.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	5.6
10	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	5.6
	441568	AI733322	Hs.127176	ESTs	5.6
	414575	H11257	Hs.295233	ESTs	5.5
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	5.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	5.5
15	453064	R40334	Hs.301395	Homo sapiens cDNA: FLJ21204 fis, clone C	5.5
	433409	AI278802	Hs.25661	ESTs	5.5
	407094	AF000574	Hs.22405	leukocyte immunoglobulin-like receptor,	5.5
	425234	AW152225	Hs.165909	ESTs	5.5
	447644	AW881622	Hs.108846	Homo sapiens cDNA FLJ12534 fis, clone NT	5.5
20	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	5.5
	446534	AI307356	Hs.175225	ESTs	5.5
	452355	N54926	Hs.29202	G protein-coupled receptor 34	5.5
	434715	BE005346	Hs.116410	ESTs	5.5
	440486	BE243513	Hs.7212	hypothetical protein PP1044	5.5
25	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase	5.5
	419172	AW338625	Hs.22120	ESTs	5.5
	444931	AV652066	Hs.75113	general transcription factor IIA	5.4
	413940	AI633205	Hs.159914	ESTs	5.4
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	5.4
30	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.4
	434361	AF129755	Hs.117772	ESTs	5.4
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	5.4
	445175	AV652851	Hs.300846	ESTs	5.4
	411213	AA676839	Hs.69285	neuropilin 1	5.4
35	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	5.4
	422667	H25642	Hs.133471	ESTs	5.4
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	5.4
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	5.4
	452060	W26980	Hs.153612	ATP-binding cassette, sub-family F (GCN2	5.4
40	419093	AI804054	Hs.112885	ESTs	5.4
	436267	AW450938	Hs.180115	ESTs	5.4
	405257				5.4
	431154	AW971228	Hs.290259	ESTs	5.4
	415511	AI732617	Hs.182362	ESTs	5.4
45	419175	AW270037	Hs.179507	KIAA0779 protein	5.4
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	5.3
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	5.3
	409995	AW960597	Hs.30164	ESTs	5.3
	414911	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4	5.3
50	455716	BE070263		gb:QV4-BT0407-280100-090-e07 BT0407 Homo	5.3
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.3
	419985	H66373	Hs.15973	ESTs, Highly similar to bA393U16.3 [H.s]	5.3
	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	5.3
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	5.3
	404176				5.3
55	431475	AI567669	Hs.287316	ESTs	5.3
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	5.3
	405475				5.3
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	5.3
60	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	5.3
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	5.3
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	5.3
	442837	AI022082	Hs.50492	ESTs	5.3
	437140	AA312799	Hs.283689	activator of CREM in testis	5.3
65	408989	AW361666	Hs.49500	KIAA0746 protein	5.3
	417355	D13168	Hs.82002	endothelin receptor type B	5.3
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.3
	437734	AA693951	Hs.180284	ESTs	5.3
	452234	AW084176	Hs.223296	ESTs	5.3
70	423057	AW961597	Hs.130816	ESTs	5.3
	439593	BE073597	Hs.124863	ESTs	5.3
	446501	AI302616	Hs.150819	ESTs	5.3
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	5.3
	427164	AB037721	Hs.173871	KIAA1300 protein	5.2
75	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	5.2
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	5.2
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	5.2
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.2
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	5.2
80	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.2
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.2
	451156	AI983569	Hs.232042	ESTs	5.2
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.2
	423024	AA593731	Hs.75613	CD36 antigen (collagen type I receptor,	5.2

5	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.2
	451149	AL047586	Hs.10283	ESTs	5.2
	429458	BE161832	Hs.292689	ESTs	5.2
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor I	5.2
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.2
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	5.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	5.2
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	5.2
10	438995	AI277986	Hs.164875	ESTs	5.1
	438582	AI521310	Hs.283365	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.1
	424859	U92014	Hs.153527	Homo sapiens pTM5 mariner-like transpos	5.1
	445563	AW873606	Hs.149006	ESTs	5.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	5.1
15	420567	AK000812	Hs.98874	similar to protein-rich protein 48	5.1
	420530	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	5.1
	455510	AA422029	Hs.143540	ESTs, Weakly similar to hyperpolarizatio	5.1
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	5.1
	438146	Z36842	Hs.57548	ESTs	5.1
20	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	5.1
	421633	AF121860	Hs.106260	sorting nexin 10	5.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.1
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine p	5.1
	456210	N49729	Hs.156875	ESTs	5.1
25	411893	R82845	Hs.273789	ESTs	5.1
	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (f	5.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.1
	426822	W78950	Hs.220823	ESTs	5.1
	444269	AI590346	Hs.146220	ESTs	5.1
30	437204	AL110216	Hs.12285	ESTs	5.1
	443180	R15875	Hs.70945	ESTs	5.1
	431510	AA580082	Hs.112264	ESTs	5.0
	446312	BE087853		gb:QV1-BT0681-290400-181-h05 BT0681 Homo	5.0
	449870	AI672487	Hs.15423	hypothetical protein HDCMCD4P	5.0
35	430462	AI584156	Hs.105640	ESTs	5.0
	457452	AW972675		gb:EST384766 MAGE resequences, MAGL Homo	5.0
	420397	NM_007018	Hs.97437	centrosomal protein 1	5.0
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.0
	426874	N67325	Hs.247132	ESTs	5.0
40	419746	AW867943	Hs.127216	Homo sapiens cDNA FLJ13465 fis, clone PL	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	5.0

TABLE 35B:

45	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

50	Pkey	CAT number	Accession
	411937	1266219_1	AW876626 AW876622 AW876624
	413497	1373771_1	BE177661 H06215 BE144709 BE144829
	420825	196769_1	AI656727 AI697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 BE000621 R68736 AW992695 AI768764 AW271284 AW974653 AI308951 AW055146 R93609 AW467031 AI096866 AI371871 AI126182 AI564756 AI361460 AI358914 AI419231 AW439733 R87059 AA628064 AW088970 AW008695 R68682 AI719136 R97752 AW196262
55	425331	250199_1	AW962128 AA355353 AA427363
	437205	43463_1	AL110232 N94765
	438966	467436_1	AW979074 AA834841 AA828650
	442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
	443161	561305_1	AI038316 AI344631 AI261653
60	446312	671114_1	BE087853 AI286184
	447197	711623_1	R36075 AI366546 R36167
	447974	745643_1	R76886 AI453674 R77049
	448212	755099_1	AI475858 AW969013
	451818	887271_1	AI819018 R05492 W27615
65	453013	94390_1	AA031407 N85751 AW974119 AA031408 AA572965
	455716	1352695_1	BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203
	457452	339381_1	AW972675 AA541366 AA523039
	407305	312657	AA715284

TABLE 35C:

70	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
75	NL_position:	Indicates nucleotide positions of predicted exons.

80	Pkey	Ref	Strand	NL_position
	401539	8072433	Minus	62028-62608
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	403549	8081591	Minus	137150-137362
	403713	6573831	Minus	152769-153155
	403790	8084957	Minus	87826-87947,89835-90002
	404176	9931122	Plus	52685-52800
	405257	7329310	Plus	73121-73273

405475 1931025 Plus 1548-1702

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TABLE 36A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER

Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 35A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor to normal tissue

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Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
424704	AI263293	Hs.152096	cytochrome P450	SS,p450	40.9
426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S8,P	35.6
458079	AI796870	Hs.54277	ESTs	TM	34.6
446921	AB012113	Hs.16530	small inducible	SS,IL8	25.9
452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,Xlink,CUB	24.8
414821	M63835	Hs.77424	Fc fragment of	TM,SS,ig	23.4
414812	X72755	Hs.77367	monokine induce	SS,IL8	22.1
426471	M22440	Hs.170009	transforming gr	TM,SS,EGF	21.3
449523	NM_000579	Hs.54443	chemokine (C-C	TM,7tm_1	20.7
428227	AA321649	Hs.2248	small inducible	IL8	19.5
456804	AI421645	Hs.139851	caveolin 2	TM,Caveolin	17.8
411642	NM_014932	Hs.71132	neurodin 1	TM,SS,COesterase	16.2
427581	NM_014788	Hs.179703	KIAA0129 gene p	TM	15.6
448520	AB002367	Hs.21355	doublecortin an	TM,kinase	14.8
417308	H60720	Hs.81892	KIAA0101 gene p	TM	14.8
421566	NM_000399	Hs.1395	early growth re	TM,zf-C2H2	14.6
422603	BE242587	Hs.118651	hematopoietical	TM,SS,homeobox	14.4
425984	AW836277	Hs.165636	hypothetical pr	TM	14.2
432606	NM_002104	Hs.3066	granzyme K (ser	TM,SS,trypsin	14.1
458809	AW972512	Hs.20985	sin3-associated	SS	13.7
446627	AI973016	Hs.15725	hypothetical pr	TM	13.6
452960	AK001335	Hs.31137	Homo sapiens cD	TM,Y_phosphatase	13.3
420552	AK000492	Hs.98806	hypothetical pr	TM,SS	13.0
425188	AK002052	Hs.155071	hypothetical pr	TM	12.6
419034	NM_002110	Hs.89555	hemopoietic cel	TM,kinase,SH2,SH3	12.3
442932	AA457211	Hs.8858	bromodomain adj	TM,bromodomain,PHD	12.3
434398	AA121098	Hs.3838	serum-inducible	TM,kinase,POLO_box	12.2
450506	NM_004460	Hs.418	fibroblast acti	SS,DPPIV_N_term,Peptidase_S9	12.1
425782	U66468	Hs.159525	cell growth reg	SS	12.0
426108	AA622037	Hs.166468	programmed cell	TM,DUF122	11.9
450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	11.7
452838	U65011	Hs.30743	preferentially	TM	11.2
426780	BE242284	Hs.172199	adenylate cycla	TM,guanylate_cyc	11.1
415323	BE269352	Hs.949	neutrophil cyto	TM,SH3,TPR	11.0
423508	AW604297	Hs.129711	hepatitis A vir	TM,SS,ig	11.0
408380	AF123050	Hs.44532	diubiquitin	TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	11.0
448410	AK000227	Hs.21126	hypothetical pr	TM	11.0
451277	AK001123	Hs.26176	hypothetical pr	TM	10.8
453165	S74727	Hs.32042	aspartoacylase	TM	10.8
418036	Z37976	Hs.83337	latent transfor	SS,TB,EGF	10.5
431512	BE270734	Hs.2795	lactate dehydro	TM,ldh	10.3
433862	D86960	Hs.3610	KIAA0205 gene p	TM,SS	10.3
431211	M86849	Hs.5566	gap junction pr	TM,connexin	10.2
432579	AF043244	Hs.278439	nucleolar prote	TM	10.0
439653	AW021103	Hs.6631	hypothetical pr	TM,SS	9.9
428862	NM_000346	Hs.2316	SRY (sex-determ	TM,HMG_box	9.8
410762	AF226053	Hs.66170	HSKM-B protein	SS,zf-MYND	9.8
452431	U88879	Hs.29499	tol-like recep	TM,SS,TIR,LRRC	9.5
405121	AB028989	Hs.88500	mitogen-activat	SS,vwa,vwd,TIL_Cys_knot,vwc	9.5
449625	NM_014253	Hs.23796	odc (odd Oz/ten	SH2,EGF	9.4
421659	NM_014459	Hs.106511	protocadherin 1	TM,SS,cadherin	9.2
427283	AL119796	Hs.174185	ectonucleotide	TM,SS,Phosphodiester,Somatostatin_B	9.1
407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	8.9
413554	AA319146	Hs.75426	secretogranin I	TM,SS,Granin	8.6
418693	AI750878	Hs.87409	thrombospondin	EGF,TSPN_tsp_1,tsp_3,vwc	8.6
437672	AW748265	Hs.5741	flavohemoprotei	TM,heme_1,oxidoreductase	8.6
430268	AK000737	Hs.237480	hypothetical pr	TM,SS	8.5
447850	AB018298	Hs.19822	SEC24 (S. cerev	TM	8.4
435717	AF227905	Hs.105794	UDP-glucose:gly	TM,Glyco_transf_8	8.3
433376	AI249361	Hs.74122	caspase 4, apop	TM,JICE_p20,JICE_p10,CARD	8.2
419490	NM_006144	Hs.90708	granzyme A (gra	TM,SS,trypsin	8.2
453033	AA325869	Hs.31463	KIAA0281 gene p	TM	8.2
432328	AI572739	Hs.195471	6-phosphofructo	TM,6PF2K,PGAM	7.9
413719	BE439580	Hs.75498	small inducible	SS,IL8	7.9
412448	L12964	Hs.73895	tumor necrosis	TM,SS,TNFR_c6	7.9
424247	X14008	Hs.234734	lysozyme (renal	SS,lvs	7.8
421991	NM_014918	Hs.110488	KIAA0990 protei	SS	7.8
400793	AA635062	Hs.50094	Homo sapiens mR	TM,BIR,CARD,zf-C3HC4	7.7

	414646	AA353776	Hs.901	CD48 antigen (B	TM,lg	7.6
	418372	AA311833	Hs.84318	replication pro	TM	7.6
	408418	AW963897	Hs.44743	KIAA1435 protei	TM,WD40,FYVE	7.6
5	425354	U62027	Hs.155935	complement comp	TM,7tm_1	7.5
	432753	NM_014075	Hs.278915	PRO0593 protein	TM,ptkinase	7.4
	447046	AA326187	Hs.17170	G protein-coupl	TM,7tm_1	7.4
	410577	X91911	Hs.64639	glioma pathogen	TM,SCP	7.4
	422631	BE218919	Hs.118793	hypothetical pr	TM	7.3
10	417022	NM_014737	Hs.80905	Ras association	TM,RA	7.2
	430105	X70297	Hs.2540	cholinergic rec	TM,neur_chan	7.2
	451621	AI879148	Hs.26770	fatty acid bind	TM,SS,lipocatin	7.2
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	7.2
	426028	NM_001110	Hs.172028	a disintegrin a	TM,SS,disintegrin,Reprolysin	7.2
15	434096	AW662958	Hs.75825	pleiomorphic ad	TM,zf-C2H2	7.1
	426423	NM_012446	Hs.169833	single-stranded	TM	7.1
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu	TM,dsm,helicase_C	7.1
	431556	AF016028	Hs.260039	sarcospan (Kras	TM	6.9
	420018	U56387	Hs.94376	proprotein conv	TM,SS,Peptidase_S8,P	6.9
20	444042	NM_004915	Hs.10237	ATP-binding cas	TM,ABC_tran	6.9
	432656	NM_000246	Hs.3076	MHC class II tr	TM,LRR	6.9
	430066	AI929659	Hs.237825	signal recognit	TM,TPR	6.9
	401539				TM,SS,zf-B_box,zf-C3HC4,Lysyl_oxidase	6.8
	416058	L08895	Hs.78995	MADS box transc	TM,SRF-TF	6.8
25	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu	TM,SAP	6.7
	424063	NM_002019	Hs.138671	fms-related tyr	TM,SS,ptkinase,lg	6.7
	418026	BE379727	Hs.83213	fatty acid bind	TM,SS,lipocatin	6.6
	438619	AB032773	Hs.6341	TU12B1-TY prote	TM	6.6
	408741	M73720	Hs.646	carboxypeptidas	SS,Zn_carbOpept,Propep_M14	6.6
	403549				TM,ptkinase	6.6
30	435798	BE395289	Hs.12720	elf4E-transport	TM	6.6
	453070	AK001465	Hs.31575	SEC63, endoplas	TM,SS,DnaJ	6.6
	452092	BE245374	Hs.27842	hypothetical pr	TM,SS,Acyltransferase	6.5
	437396	BE140396	Hs.21621	hypothetical pr	TM	6.4
	402474				TM,Peptidase_C1	6.4
35	401600	BE247275	Hs.151787	U5 snRNP-specif	TM,SS,HECT	6.4
	415076	NM_000857	Hs.77890	guanylate cycla	TM,guanylate_cyc	6.4
	430335	D80007	Hs.239499	KIAA0185 protei	TM,S1	6.3
	434203	BE262677	Hs.283558	hypothetical pr	TM	6.2
40	430287	AW182459	Hs.125759	ESTs, Weakly si	TM,SS	6.2
	417259	AW903838	Hs.81800	chondroitin sul	TM,Xlink,lectin_c,sushi,EGF,lg	6.1
	421202	AF193339	Hs.102506	eukaryotic tran	TM,SS	6.1
	452235	AL039743	Hs.28514	Homo sapiens mR	TM	6.0
	429653	NM_005955	Hs.211581	metal-regulator	TM,zf-C2H2	6.0
45	444484	AK002126	Hs.11260	hypothetical pr	TM	5.9
	410193	AJ132592	Hs.59757	zinc finger pro	TM,zf-C2H2	5.9
	425361	AA355933	Hs.132221	Homo sapiens cD	TM	5.9
	410361	BE391804	Hs.62661	guanylate bindi	TM,SS,GBP	5.8
	415714	NM_002290	Hs.78672	laminin, alpha	TM,SS,laminin_G,laminin_EGF	5.8
50	421689	N87820	Hs.106826	hypothetical pr	TM,SS,PHD	5.8
	443837	AI984625	Hs.9884	spindle pole bo	SS	5.8
	422544	AB018259	Hs.118140	KIAA0716 gene p	TM	5.7
	412584	X54870	Hs.74085	DNA segment on	TM,lectin_c	5.7
	410425	BE278367	Hs.63510	KIAA0141 gene p	TM	5.7
55	426283	NM_003937	Hs.169139	kynureninase (L	TM	5.7
	430440	X52599	Hs.2561	nerve growth fa	TM,SS,NGF	5.7
	413551	BE242639	Hs.75425	ubiquitin assoc	TM,SS,UBA	5.7
	418250	U29926	Hs.83918	adenosine monop	TMA_deaminase	5.6
	419839	U24577	Hs.93304	phospholipase A	SS	5.6
60	430253	AK001514	Hs.236844	hypothetical pr	TM	5.6
	450447	AF212223	Hs.25010	hypothetical pr	TM,ANF_receptor,guanylate_cyc,ptkinase	5.6
	414020	NM_002984	Hs.75703	small inducible	SS,IL8	5.6
	414844	AA296874	Hs.77494	deoxyguanosine	SS,dNK	5.6
	416498	U33632	Hs.79351	potassium chann	TM	5.6
65	430512	AF182294	Hs.241578	U6 snRNA-associ	SS	5.6
	419929	U90268	Hs.93810	cerebral cavern	SS,ank,Band_41	5.5
	407094	AF000574	Hs.22405	leukocyte immun	TM,SS,lg	5.5
	411653	AF070578	Hs.71168	Homo sapiens cl	TM,SS,Aa_trans	5.5
	452355	N54926	Hs.29202	G protein-coupl	TM,7tm_1	5.5
70	440486	BE243513	Hs.7212	hypothetical pr	TM	5.5
	444825	AW167613	Hs.248	mitogen-activat	TM,SS,ptkinase	5.5
	447072	D61594	Hs.17279	tyrosylprotein	SS	5.4
	453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	5.4
	411213	AA676939	Hs.69285	neuropilin 1	TM,CUB,F5_F8_type_C,MAM	5.4
75	429688	BE245169	Hs.211610	CUG triplet rep	TM,rm	5.4
	405257				TM	5.4
	414911	NM_000107	Hs.77602	damage-specific	TM,WD40	5.3
	430598	AK001764	Hs.247112	hypothetical pr	TM	5.3
	428753	AW939252	Hs.192927	hypothetical pr	TM,SS	5.3
80	406625	Y13647	Hs.119597	stearoyl-CoA de	TM,Desaturase	5.3
	405475				TM,sugar_tr	5.3
	430180	AA331406	Hs.75456	A kinase (PRKA)	TM	5.3
	417381	AF164142	Hs.82042	solute carrier	TM,xan_ur_permease	5.3
	433029	NM_014322	Hs.279926	opsin 3 (enceph	TM,7tm_1	5.3

	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zf-C3HC4	5.3
	412420	AL035668	Hs.73853	bone morphogene	SS,TGFb_propeptide,TGF-beta	5.2
	416975	NM_004131	Hs.1051	granzyme B (gra	SS,trypsin	5.2
5	451418	BE387790	Hs.26369	hypothetical pr	TM	5.2
	425322	U63630	Hs.155637	protein kinase,	TM,MCM,FAT,FATC,PI3_P14_kinase	5.2
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.2
	428593	AW207440	Hs.185973	degenerative sp	TM	5.2
	417696	BE241624	Hs.82401	CD69 antigen (p	TM,lectin_c	5.2
10	442991	BE281238	Hs.8886	hypothetical pr	TM	5.2
	420567	AK000812	Hs.98874	similar to prol	TM	5.2
	412676	NM_000165	Hs.74471	gap junction pr	TM,connexin	5.1
	423430	AF112481	Hs.128501	RAD54, S. cerev	TM,SNF2_N,helicase_C	5.1
	421633	AF121860	Hs.106260	sorting nexin 1	TM,PX	5.1
15	436943	AA773838	Hs.5353	caspase 10, apo	TM,ICE_p10,ICE_p20,DED	5.1
	414696	AF002020	Hs.76918	Niemann-Pick di	TM,SS,Patched	5.1
	446312	BE087853		gb:QV1-BT0681-2	TM	5.1
	420397	NM_007018	Hs.97437	centrosomal pro	TM	5.0
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	5.0
20	TABLE 36B*					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
25	Pkey	CAT number	Accession			
	446312	671114_1	BE087853 AI286184			
	TABLE 36C:					
30	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
	Nt_position:	Indicates nucleotide positions of predicted exons.				
35	Pkey	Ref	Strand	Nt_position		
	401539	8072433	Minus	62028-62608		
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757		
	403549	8081591	Minus	137150-137362		
40	405257	7329310	Plus	73121-73273		
	405475	1931025	Plus	1548-1702		
	TABLE 37A: ABOUT 280 GENES DOWN-REGULATED IN KIDNEY CANCER					
45	Table 37A lists about 280 genes significantly down-regulated in kidney cancer compared to normal kidney. These were selected as for Table 35A, except that the numerator and denominator were switched.					
	Pkey:	Unique Eos probeset identifier number				
	ExAccon:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
50	Unigene Title:	Unigene gene title				
	R1:	Ratio of normal to tumor tissue				
	Pkey	ExAccon	UnigeneID	UnigeneTitle	R1	
55	425260	L47726	Hs.1870	phenylalanine hydroxylase	50.20	
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	48.14	
	440243	BE301029	Hs.226422	ESTs	42.54	
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	40.14	
	441120	AI632015	Hs.164492	ESTs	34.56	
	432488	AA551010	Hs.216640	ESTs	33.16	
60	416854	H40164	Hs.80296	Purkinje cell protein 4	32.06	
	438452	AI220911	Hs.288959	Homo sapiens cDNA: FLJ20920 fis, clone A	29.54	
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	28.26	
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	28.16	
	446795	AI797713	Hs.156471	ESTs	27.23	
65	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	26.98	
	432128	AA127221	Hs.117037	ESTs	26.54	
	448178	AI479482	Hs.170789	ESTs	25.42	
	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-activat	23.99	
	426770	AI948618	Hs.150178	ESTs	23.78	
70	428839	AI767756	Hs.82302	ESTs	23.04	
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	22.38	
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	22.28	
	437575	AW954355	Hs.36529	ESTs	22.14	
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	22.12	
75	447350	AI375572	Hs.172634	ESTs	20.40	
	425920	AL049977	Hs.162209	claudin 8	20.30	
	446293	AI420213	Hs.149722	ESTs	19.48	
	425075	AA506324	Hs.1852	acid phosphatase, prostate	19.10	
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	18.74	
80	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (18.56	
	441550	F13386	Hs.7888	Homo sapiens clone 23736 mRNA sequence	17.40	
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	17.30	
	406667	M12523	Hs.75442	albumin	17.06	
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	16.54	

	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	16.11
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	15.84
	443324	R44013	Hs.164225	ESTs	15.68
5	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	15.46
	436637	A1783629	Hs.26766	ESTs	15.18
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	14.52
	434874	N62448	Hs.135906	ESTs	14.46
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	13.84
10	453685	AL110309		gb:DKFZp564L0278_r1 564 (synonym: hfor2)	13.48
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.24
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	13.05
	428931	AA994979	Hs.98967	ATPase, H(+) -transporting, lysosomal, no	12.97
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	12.66
15	431713	AK000388	Hs.267997	EHM2 gene	12.66
	436679	A1127483	Hs.120451	ESTs, Weakly similar to unnamed protein	12.36
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	12.32
	425707	AF115402	Hs.11713	ET4-like factor 5 (ets domain transcript)	11.92
	440504	A1948966	Hs.130017	ESTs, Weakly similar to VATX_HUMAN VACUO	11.66
20	417275	X63578	Hs.81849	parvalbumin	11.48
	410929	H47233	Hs.30643	ESTs	11.40
	427167	A1239607	Hs.99196	ESTs	11.34
	445591	A1471866	Hs.149095	ESTs	11.30
	443622	A1911527	Hs.11805	ESTs	11.23
25	438935	H40665	Hs.31564	ESTs	11.16
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	11.00
	415539	A1733881	Hs.72472	ESTs	10.84
	438081	H49546	Hs.298964	ESTs	9.76
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	9.74
30	407280	A1241296	Hs.145609	ESTs	9.71
	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	9.61
	442448	A1733144	Hs.129611	ESTs	9.52
	442308	AA989402	Hs.45194	ESTs	9.51
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	9.35
35	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	9.32
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxy	9.31
	459247	N46243	Hs.110373	ESTs	9.20
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	9.16
	410247	AF181721	Hs.61345	RU2S	9.10
40	430573	AA744550	Hs.136345	ESTs	9.08
	457411	AW085961	Hs.130093	ESTs	8.99
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.92
	435024	A1863518	Hs.127743	ESTs, Weakly similar to V-ATPase G-subun	8.76
	435056	AW023337	Hs.5422	glycoprotein M6B	8.74
45	426451	A1908165	Hs.169946	GATA-binding protein 3	8.50
	450648	A1703366	Hs.26766	ESTs	8.38
	426255	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	8.31
	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	8.28
	451027	AW519204	Hs.40808	ESTs	8.10
50	435823	R07856	Hs.16355	ESTs	8.06
	429269	AA449013	Hs.99203	ESTs	8.02
	438199	AW016531	Hs.122147	ESTs	7.94
	442176	AA983764	Hs.128910	ESTs	7.94
	450164	A1239923	Hs.30098	ESTs	7.86
55	445627	AW818475	Hs.7363	ESTs	7.85
	445779	A1253104	Hs.189267	ESTs	7.82
	407178	AA195651	Hs.104106	ESTs	7.68
	426966	A1493134	Hs.159125	ESTs	7.68
	445659	AW300508	Hs.149229	ESTs	7.50
60	403204				7.46
	448037	AW195634	Hs.170401	ESTs	7.30
	413589	AW452631	Hs.258811	coatomer protein complex, subunit gamma	7.26
	446063	A1720140	Hs.151079	ESTs	7.26
	424626	AA344308	Hs.128427	ESTs	7.25
65	403381				7.16
	414807	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	7.12
	432102	AW015506	Hs.130730	ESTs	7.12
	442315	AA173992	Hs.7956	ESTs	7.10
	453698	AA037615	Hs.42746	ESTs	7.02
70	415003	M11437	Hs.77741	kininogen	6.95
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	6.92
	452883	X80031	Hs.150318	ESTs	6.88
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8	6.76
	410781	A1375672	Hs.165028	ESTs	6.74
75	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.66
	441031	A1110684	Hs.7645	fibrinogen, B beta polypeptide	6.66
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	6.64
	437553	A1829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	6.63
	445286	U03886	Hs.264	GS2 gene	6.54
80	408427	AW194270	Hs.177236	ESTs	6.52
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.46
	457001	J03258	Hs.2062	vitamin D (1,25-dihydroxyvitamin D3) re	6.46
	420205	AA256395	Hs.88156	ESTs	6.42
	441364	AW450466	Hs.126830	ESTs	6.36

	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	6.34
	405373				
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	6.32
5	440094	AI651558	Hs.270372	ESTs	6.32
	442764	AI762254	Hs.131122	ESTs	6.27
	424433	H04607	Hs.9218	ESTs	6.21
	415025	AW207091	Hs.72307	ESTs	6.20
	428927	AA441837	Hs.90250	ESTs	6.16
10	439145	H67346	Hs.269187	ESTs	6.16
	424683	N87519	Hs.27196	ESTs	6.06
	415314	N88802	Hs.5422	glycoprotein M6B	6.04
	424025	AI701852	Hs.301296	ESTs	5.94
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	5.90
15	417332	AW972717	Hs.288462	Homo sapiens cDNA: FLJ21511 f1s, clone C	5.89
	440102	AI672443	Hs.131190	ESTs	5.86
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	5.84
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	5.82
	446224	AW450551	Hs.13308	ESTs	5.82
20	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	5.74
	436802	N34486	Hs.170504	ESTs	5.72
	412452	AA215731	Hs.283446	ESTs, Weakly similar to ALAT_HUMAN ALANI	5.72
	445611	AW418497	Hs.145583	ESTs	5.70
	440038	AA861627	Hs.243989	ESTs	5.66
25	424028	AF055084	Hs.153692	KIAA0686 protein	5.66
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUO	5.61
	425907	AA365752	Hs.155965	ESTs	5.60
	428523	AW974540	Hs.98626	ESTs	5.60
	429918	AW873986	Hs.119383	ESTs	5.58
30	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	5.58
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 f1s, clone PL	5.56
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	5.56
	418504	BE159718	Hs.85335	Homo sapiens mRNA: cDNA DKFZp564D1462 (f	5.52
	440656	AA902650	Hs.192742	Homo sapiens cDNA FLJ12785 f1s, clone NT	5.51
35	432286	AW327432	Hs.255843	ESTs	5.50
	451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	5.48
	422746	NM_004484	Hs.119651	glypican 3	5.46
	416426	AA180256	Hs.210473	ESTs, Weakly similar to GELS_HUMAN GELSO	5.43
	414449	AA557660	Hs.76152	decorin	5.37
40	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.36
	451835	T63643	Hs.209715	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.34
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	5.32
	408604	D51408	Hs.21925	ESTs	5.22
	456576	AA287443		gb:zs52c10.r1 NCL_CGAP_GC81 Homo sapiens	5.18
45	433212	BE218049	Hs.121820	ESTs	5.18
	452114	N22687	Hs.8236	ESTs	5.16
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 f1s, clone K	5.14
	443005	AI027184	Hs.200918	ESTs	5.14
	408554	AA836381	Hs.7323	ESTs	5.14
50	438609	T62870	Hs.291991	ESTs	5.12
	429343	AK000785	Hs.199480	epsin 3	5.10
	452223	AA425467	Hs.8035	ESTs	5.10
	446925	AW974605	Hs.176669	ESTs	5.10
	407664	AW063476	Hs.279080	ESTs	5.09
55	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	5.08
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	5.06
	435343	AW194962	Hs.199028	ESTs	5.04
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	5.04
	442317	AI915599	Hs.129225	ESTs	5.04
60	404319				5.02
	433637	AW024214	Hs.135405	ESTs	5.02
	440205	T86950	Hs.188465	ESTs	4.92
	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	4.84
65	453125	AW779544	Hs.115497	Homo sapiens cDNA: FLJ22655 f1s, clone H	4.83
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	4.80
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.78
	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	4.75
	449050	AW302858	Hs.187333	ESTs	4.74
	422237	M13149	Hs.1498	histidine-rich glycoprotein	4.69
70	442476	AF069475		gb:AF069475 Homo sapiens astrocytoma lib	4.67
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	4.64
	440624	AF017987	Hs.7306	secreted fibrinogen-related protein 1	4.58
	403046				4.58
	450838	R65841	Hs.28653	ESTs	4.51
75	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	4.48
	453500	AI478427	Hs.43125	ESTs	4.47
	405701				4.40
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.37
80	451032	W03692	Hs.25832	Homo sapiens mRNA: cDNA DKFZp564P116 (fr	4.37
	426200	AA371876	Hs.234786	KIAA0707 protein	4.37
	418836	AI655499	Hs.161712	ESTs	4.35
	447754	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 f1s, clone MA	4.34
	438209	AL120659	Hs.6111	KIAA0307 gene product	4.32
	404559				4.23
					4.22

	413272	AA127923	Hs.293256	ESTs	4.21
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	4.19
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	4.18
5	445512	AI241246	Hs.148903	EST	4.17
	445177	AI215070	Hs.16135	ESTs	4.16
	448475	BE613134	Hs.247474	Homo sapiens cDNA: FLJ21032 fis, clone C	4.14
	402072				4.09
	439285	AL133916	Hs.298998	ESTs	4.02
10	429621	AI823386	Hs.130874	Homo sapiens cDNA FLJ14181 fis, clone NT	3.99
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	3.97
	453511	AL031224	Hs.33102	transcription factor AP-2 beta (activati	3.94
	452620	AA436504	Hs.119286	ESTs	3.92
	425642	X91220	Hs.158462	solute carrier family 12 (sodium/chlorid	3.91
15	435884	AA701443	Hs.192868	ESTs	3.90
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	3.89
	419677	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	3.88
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.84
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	3.82
20	442306	AI820660	Hs.129205	ESTs	3.82
	438453	D17056	Hs.288959	Homo sapiens cDNA: FLJ20920 fis, clone A	3.81
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	3.80
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	3.79
	413841	M34276	Hs.75576	plasminogen	3.77
25	431161	AA493591		gb:nh01a12.s1 NCI_CGAP_Thy1 Homo sapiens	3.76
	428544	AA430034	Hs.191611	ESTs	3.74
	453903	AW299606	Hs.232777	ESTs	3.74
	434061	AW024973	Hs.283675	NPD009 protein	3.73
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	3.73
30	440080	AW051597	Hs.143707	ESTs	3.71
	440230	AI732970	Hs.126246	ESTs	3.70
	428735	AJ279246	Hs.192657	NPHS2 gene (podocin)	3.68
	421832	NM_016098	Hs.108725	HSPC040 protein	3.66
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	3.65
	453055	AW291436	Hs.31917	ESTs	3.65
35	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	3.59
	440232	AI766925	Hs.112554	ESTs	3.57
	432099	U20760	Hs.272429	calcium-sensing receptor (hypocalciuric	3.57
	445924	AI264671	Hs.164166	ESTs	3.56
40	411356	H45377		gb:yn99h03.r1 Soares adult brain N2bSHB5	3.56
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.55
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	3.53
	416298	NM_003891	Hs.1011	protein Z, vitamin K-dependent plasma gl	3.53
	423603	AB007880	Hs.129883	KIAA0420 gene product	3.53
45	436610	AW611912	Hs.120414	ESTs	3.50
	425905	AB032959	Hs.161700	KIAA1133 protein	3.48
	403625				3.47
	425210	AA054679	Hs.155150	ribonuclease P (14kD)	3.45
50	430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113 1 promi	3.42
	448877	AI583696	Hs.253313	ESTs	3.40
	456686	AI554303	Hs.35982	Homo sapiens cDNA FLJ12776 fis, clone NT	3.38
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone NT	3.37
	453574	AI767947	Hs.50841	ESTs, Weakly similar to tufelin [M.musc	3.32
	438535	L09078		gb:Homo sapiens mRNA fragment	3.31
55	414040	N58513	Hs.32171	ESTs	3.30
	451416	AW631469	Hs.203213	ESTs	3.30
	444564	AI167877	Hs.143716	ESTs	3.29
	408001	AA046458	Hs.95296	ESTs	3.27
	406666	V00495	Hs.75442	albumin	3.24
60	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.24
	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.23
	423968	AF098277	Hs.136529	solute carrier family 23 (nucleobase tra	3.21
	427209	H06509	Hs.92423	KIAA1566 protein	3.20
	403442				3.20
65	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.19
	425548	AA890023	Hs.1906	prolactin receptor	3.17
	414502	AL133721	Hs.224680	ESTs	3.16
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)-	3.14
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	3.11
70	433942	AW272166	Hs.123465	ESTs	3.11
	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	3.10
	448819	AI589190	Hs.188372	ESTs	3.10
	423041	BE170842	Hs.123123	chloride channel Ka	3.10
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	3.10
75	406664	L34041	Hs.25478	glycerol-3-phosphate dehydrogenase 1 (so	3.10
	449850	AW206292	Hs.199751	ESTs	3.08
	427450	AB014526	Hs.178121	KIAA0626 gene product	3.08
	454788	AW820691		gb:RCS-ST0300-300100-012-H06 ST0300 Homo	3.06
	444895	AI674383	Hs.301192	ESTs	3.06
80	457782	N54493		gb:yy40g05.s1 Soares fetal liver spleen	3.05
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	3.05
	427041	AI693661	Hs.97557	ESTs	3.01
	434788	AF154121	Hs.102867	sodium-dependent high-affinity dicarboxy	3.01
	419003	T78640	Hs.268595	ESTs	3.01

TABLE 37B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
411356	1240273_1	H45377 H21137 AW838640
413752	1386338_1	BE161807 BE161584 BE161700 BE161748
431161	328713_1	AA493591 AA829120 AA533792
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
442476	543547_1	AF069475 AF069477 AF069476
453685	977734_1	AL110309 AW088119 H22881
454554	1223842_1	AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156
		AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431
		BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330
		AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998
		BE061745 BE061753
454788	1234694_1	AW820691
455887	1380836_1	BE154173 BE154098 BE154096
456576	201378_1	AA287443 AA419385 BE084078 A1478347
457782	405265_1	N54493 AA679039 N76605
407198		H91679

TABLE 37C:

Pkey: Unique Eos probeset identifier number
 Ref: reference gi ID
 Strand: strand identification
 Nt_position: chromosomal nucleotide position

Pkey	Ref	Strand	Nt_position
402072	8117363	Plus	71983-72128
403046	3540153	Minus	55707-55859,56369-56511
403204	7622392	Plus	16214-16439
403381	9438267	Minus	26009-26178
403442	7210003	Plus	174560-175270
403625	8569879	Plus	6551-7111
404319	9211467	Plus	54436-54608
404559	8748893	Minus	73499-73651,89575-89739
405373	2076718	Plus	21294-21575
405701	4263751	Plus	93243-93364

TABLE 38A: ABOUT 860 GENES UP-REGULATED IN KIDNEY CANCER COMPARED TO NORMAL ADULT TISSUES

Table 38A lists about 860 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 70th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenetID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccon	UnigenetID	Unigene Title	R1
435013	H91923	Hs.110024		15.71
447768	X86400	Hs.19520	Hs.19520:FXFD domain-containing ion tran	14.07
445178	A1792241	Hs.129614	Hs.129614:kidney-specific membrane prote	12.56
432542	AW083920	Hs.16098	Hs.16098:claudin 2	12.41
443595	AF169312	Hs.9613	NM_016109:Homo sapiens angiotensin-like	11.77
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.39
436878	BE465204	Hs.47448	Hs.47448:ESTs	10.18
440304	BE159984	Hs.125395	Hs.125395:ESTs	9.95
407065	Y10141			9.58
413049	NM_002151	Hs.823	NM_002151:Homo sapiens hepsin (transmembr	9.51
425983	AK000226	Hs.165619	Hs.165619:mucin and cadherin-like	8.88
423161	AL049227	Hs.124776	Hs.124776:Homo sapiens mR: cD DKFZp564N1	8.77
430569	AF241254	Hs.178098	Hs.178098:angiotensin I converting enzyme	8.45
416768	AA363733	Hs.1032	NM_002909:Homo sapiens regenerating isle	7.94
422357	AF016272	Hs.115418	NM_004062:Homo sapiens cadherin 16, KSP.	7.78
420737	L08096	Hs.99899	NM_001252:Homo sapiens tumor necrosis fa	7.78
409745	AA077391		AA077391:7B14E12 Chromosome 7 Fetal Brai	7.74
413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	7.32
426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	7.20
406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	7.03
419508	AW997938	Hs.90786	Hs.90786:ATP-binding cassette, sub-famil	6.57
428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	6.36
436895	AF037335	Hs.5338	NM_001218:Homo sapiens carbonic anhydras	6.31
431842	NM_005764	Hs.271473	NM_005764:Homo sapiens epithelial protei	6.20
430014	H59354	Hs.374303	Hs.374303:hypothetical protein MGC20576	6.20
423803	NM_005709	Hs.132945	NM_005709:Homo sapiens PDZ-73 protein (P	6.19

	434779	AF153815	Hs.50151	Hs.50151:potassium inwardly-rectifying c	6.11
	435767	H73505	Hs.117874	Hs.117874:ESTs	6.08
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.02
5	425280	U31519	Hs.1872	Hs.1872:phosphoenolpyruvate carboxykinase	5.81
	426559	AB001914	Hs.170414	NM_002570:Homo sapiens paired basic amin	5.73
	451564	AU076698	Hs.132760	NM_001467:Homo sapiens glucose-6-phospha	5.69
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	5.68
	444151	AW972917	Hs.128749	Hs.128749:alpha-methylacyl-CoA racemase	5.66
	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
10	432579	AF043244	Hs.278439	NM_003946:Homo sapiens nucleolar protein	5.45
	448733	NM_005629	Hs.187958	NM_005629:Homo sapiens solute carrier fa	5.42
	446650	AB016625	Hs.15813	NM_003060:Homo sapiens solute carrier fa	5.36
	417089	HS2280	Hs.18612	Hs.18612:Homo sapiens cD: FLJ21909 fis,	5.35
	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamyltransferase 1	5.32
15	423081	AF262992	Hs.123159	Hs.123159:sperm associated antigen 4	5.30
	421893	NM_001078	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
	435886	BE265839	Hs.12126	Hs.12126:hepatocellular carcinoma-associ	5.20
	410276	AI554545	Hs.359201	Hs.359201:ESTs	5.20
	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygase (dec	5.14
20	446404	AA019961	Hs.26216	Hs.26216:Homo sapiens cD: FLJ22811 fis,	5.13
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.09
	449444	AW818436	Hs.351306	NM_004696:Homo sapiens solute carrier fa	5.05
	438106	BE245551	Hs.6079	NM_014863:Homo sapiens B cell RAG associ	5.02
	400419	AF084545		AF084545:Homo sapiens versican Vint isofo	5.01
25	453920	AI133148	Hs.36602	NM_000204:Homo sapiens I factor (complem	4.99
	447881	BE620886	Hs.355279	Hs.355279:Homo sapiens cD FLJ23711 fis,	4.97
	422253	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
	439024	R96696	Hs.35598	Hs.35598:ESTs	4.88
	414799	AI752416	Hs.77326	NM_000598:Homo sapiens insulin-like grow	4.80
30	426530	U24578	Hs.278625	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
	404240				4.71
	414617	AI339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.68
35	448249	AW855331	Hs.337124	Hs.337124:ESTs	4.67
	447818	W79940	Hs.21906	Hs.21906:Homo sapiens clone 24670 mR seq	4.66
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.66
	422424	AI186431	Hs.296638	NM_004864:Homo sapiens prostate differen	4.62
	417335	R70429	Hs.81988	NM_001343:Homo sapiens disabled homolog	4.62
40	425873	NM_013390	Hs.160417	NM_013390:Homo sapiens transmembrane pro	4.58
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.58
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.56
	414763	U97276	Hs.77266	NM_002626:Homo sapiens quiescin Q6 (QSCN	4.48
	443358	H65417	Hs.17757	Hs.17757:pleckstrin homology domain-cont	4.45
45	440091	AI767388	Hs.37890	Hs.37890:Homo sapiens, clone IMAGE:48275	4.43
	447131	NM_004585	Hs.17466	NM_004585:Homo sapiens retinoic acid rec	4.43
	406973	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.42
	427740	BE242604	Hs.180616	NM_005505:Homo sapiens CD36 antigen (col	4.40
	436258	AW867491	Hs.107125	Hs.107125:plasmalemma vesicle associated	4.38
50	452884	C05964	Hs.31841	Hs.31841:ESTs	4.37
	444006	BE395085	Hs.10086	NM_016639:Homo sapiens type I transmembr	4.36
	422627	BE336857	Hs.118787	NM_000358:Homo sapiens transforming grow	4.35
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.34
	419011	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	4.34
	404277				4.33
55	435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
	431779	AW971178	Hs.268571	NM_001645:Homo sapiens apolipoprotein C-	4.29
	406645	M57466	Hs.814	Hs.814:major histocompatibility complex,	4.28
	421485	AA243499	Hs.104800	Hs.104800:hypothetical protein FLJ10134	4.26
60	426812	AF105365	Hs.172613	NM_005598:Homo sapiens solute carrier fa	4.25
	407910	AA650274	Hs.41296	NM_013281:Homo sapiens fibronectin leuci	4.22
	438030	X98427	Hs.122634	Hs.122634:ESTs	4.22
	430661	AC005551	Hs.130714	Hs.130714:ESTs, Moderately similar to AF	4.21
	444381	BE387335	Hs.283713	Hs.283713:hypothetical protein BC014245	4.20
65	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-Ii	4.16
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	4.15
	418323	NM_002118	Hs.1162	NM_002118:Homo sapiens major histocompat	4.12
	449853	AF006823	Hs.24040	NM_002246:Homo sapiens potassium channel	4.11
	415198	AW009480	Hs.943	NM_004221:Homo sapiens tural killer cell	4.11
70	418751	BE389014	Hs.372548	Hs.372548:phosphoinositide-3-kinase, regul	4.09
	414166	AW888941	Hs.75789	NM_006096:Homo sapiens N-myc downstream	4.07
	424125	M31669	Hs.1735	Hs.1735:inhibin, beta B (activin AB beta	4.00
	416926	H03109	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.92
	419175	AW270037	Hs.362996	Hs.362996:KIAA0779 protein	3.92
75	424218	AF031824	Hs.143212	NM_003650:Homo sapiens cystatin F (leuko	3.91
	412870	N22788	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.88
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.87
	446872	X97058	Hs.16362	NM_004154:Homo sapiens pyrimidinergic re	3.87
	449961	AW265634	Hs.133100	Hs.133100:ESTs	3.87
80	424517	AI539443	Hs.137447	Hs.137447:Homo sapiens cD FLJ12169 fis,	3.86
	425262	D87119	Hs.155418	Hs.155418:GS3955 protein	3.83
	443639	BE269042	Hs.9661	NM_002801:Homo sapiens proteasome (proso	3.82
	448133	AA723157	Hs.73769	NM_000802:Homo sapiens folate receptor 1	3.81
	418030	BE207573	Hs.83321	Hs.83321:neuromedin B	3.81

5	412939	AW411491	Hs.75069	NM_005412:Homo sapiens serine hydroxymet	3.80
	409162	H25530	Hs.50868	NM_002555:Homo sapiens solute carrier fa	3.79
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.78
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.77
	430413	AW842182	Hs.241392	NM_002985:Homo sapiens small inducible c	3.76
	422282	AF019225	Hs.114309	Hs.114309:apolipoprotein L 1	3.76
	420747	BE294407	Hs.99910	Hs.99910:phosphofructokinase, platelet	3.76
	414875	H42679	Hs.77522	NM_006120:Homo sapiens major histocompat	3.75
10	418793	AW382987	Hs.88474	Hs.88474:prostaglandin-endoperoxide synt	3.74
	446291	BE397753	Hs.14623	NM_006332:Homo sapiens interferon, gamma	3.71
	417289	D86962	Hs.81875	Hs.81875:growth factor receptor-bound pr	3.69
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	3.68
	448569	BE382657	Hs.21486	NM_007315:Homo sapiens sigl transducer a	3.68
15	437270	R18087	Hs.323769	Hs.323769:cisplatin resistance related p	3.67
	408452	AA054683	Hs.192455	Hs.192455:ESTs, Moderately similar to hy	3.67
	443986	AI381750	Hs.283437	Hs.283437:HT-GN29 protein	3.66
	418869	AW516565		AW516565:xq01d05.x1 Soares_NHCC_cervica	3.65
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.62
20	428699	AW578252	Hs.190161	NM_014020:Homo sapiens LR8 protein (LR8)	3.62
	418299	AA279530	Hs.83968	NM_000211:Homo sapiens integrin, beta 2	3.61
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
	415765	NM_005424	Hs.78824	NM_005424:Homo sapiens tyrosine kase wit	3.58
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.57
25	424893	AW295112	Hs.153648	Hs.153648:protein tyrosine phosphatase,	3.57
	426046	AA833655	Hs.206868	Hs.206868:Homo sapiens cD FLJ14056 fis,	3.57
	424415	NM_001975	Hs.146580	NM_001975:Homo sapiens enolase 2, (gamma	3.57
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.56
	443834	AI741510	Hs.173548	Hs.173548:ESTs	3.54
30	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53
	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52
	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	3.52
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	3.50
35	414311	AI693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50
	415149	X12451	Hs.78056	NM_001912:Homo sapiens cathepsin L (CTSL	3.50
	424321	W74048	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
	414825	X06370	Hs.77432	NM_005228:Homo sapiens epidermal growth	3.48
	408194	AA601038	Hs.191797	Hs.191797:ESTs	3.48
40	410600	AW575742	Hs.351676	Hs.351676:ESTs, Weakly similar to T02670	3.47
	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47
	436856	AI469355	Hs.127310	Hs.127310:hypothetical protein BC014917	3.47
	419660	BE280337	Hs.194693	NM_003982:Homo sapiens solute carrier fa	3.47
	413566	AW604451	Hs.285814	Hs.285814:growth factor receptor-bound p	3.47
45	412104	AW205197	Hs.240951	Hs.240951:kcd cuticle homolog 2 (Drosoph	3.46
	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
	412276	BE262621	Hs.73798	NM_002415:Homo sapiens macrophage migrat	3.45
	449338	H73444	Hs.394	NM_001124:Homo sapiens adrenomedullin (A	3.44
50	430304	AL122071	Hs.238927	Hs.238927:Homo sapiens mR; cD DKFZp434H1	3.43
	415388	AF018081	Hs.78409	(locuslink)NM_030582:Homo sapiens collag	3.43
	432210	AI567421	Hs.273330	Hs.273330:agrin	3.43
	418177	N44967	Hs.351554	Hs.351554:Homo sapiens cD FLJ32092 fis,	3.42
	414888	AL039185	Hs.77558	Hs.77558:thyroid hormone receptor intera	3.42
55	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.41
	414803	X03100	Hs.914	Hs.914:major histocompatibility complex,	3.41
	419201	M22324	Hs.1239	NM_001150:Homo sapiens alanyl (membrane)	3.41
	445139	AB037848	Hs.12365	Hs.12365:cytotagmin XIII	3.41
	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41
60	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	3.40
	439737	AI751438	Hs.41271	Hs.41271:Homo sapiens mR full length ins	3.39
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.39
	431590	AB037789	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.38
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.36
65	416700	AW498958	Hs.343475	NM_001909:Homo sapiens cathepsin D (lyso	3.36
	440516	S42303	Hs.161	NM_001792:Homo sapiens cadherin 2, type	3.35
	423720	AL044191	Hs.23388	Hs.23388:hypothetical protein DKFZp434F0	3.32
	421902	BE392717		BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
70	421502	AF111856	Hs.105039	NM_006424:Homo sapiens solute carrier fa	3.32
	416729	U46165	Hs.1027	NM_004165:Homo sapiens Ras-related assoc	3.30
	430302	AL137502	Hs.238679	Hs.238679:Rag D protein	3.30
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cD FLJ14761 fis,	3.29
	406825	AI982529	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.29
75	446272	BE268912	Hs.14601	NM_005335:Homo sapiens hematopoietic cel	3.28
	437145	AF007216	Hs.5462	NM_003759:Homo sapiens solute carrier fa	3.27
	444071	AI627808	Hs.110524	Hs.110524:ESTs	3.27
	414662	AL036058	Hs.76807	Hs.76807:major histocompatibility comple	3.27
	436576	AI458213	Hs.77542	Hs.77542:ESTs, Weakly similar to S26650	3.26
80	424675	NM_005512	Hs.151641	NM_005512:Homo sapiens glycoprotein A re	3.25
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.25
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.25
	414788	X78342	Hs.77313	NM_003674:Homo sapiens cyclin-dependent	3.25
	414249	AI797994	Hs.279929	Hs.279929:gp25L2 protein	3.24

	430396	D49742	Hs.241363	NM_004132:Homo sapiens hyaluron binding	3.23
	424456	AA341017	Hs.25549	Hs.25549:hypothetical protein FLJ20898	3.23
	452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor kise	3.22
	425390	AJ092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
5	416033	NM_012201	Hs.78979	NM_012201:Homo sapiens golgi apparatus p	3.19
	450931	N25156	Hs.25648	Hs.25648:tumor necrosis factor receptor	3.19
	428065	AI634046	Hs.157313	Hs.157313:ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
	439318	AW837046	Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
10	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.17
	409936	AK001691	Hs.57655	Hs.57655:dudulin 2	3.16
	436001	AW903849	Hs.173840	Hs.173840:similar to endothelial cell-se	3.16
	451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
	420256	U84722	Hs.76206	NM_001795:Homo sapiens cadherin 5, type	3.16
	407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.15
15	428593	AW207440	Hs.185973	NM_003676:Homo sapiens degenerative sper	3.15
	410026	AI912061	Hs.55016	Hs.55016:EPS8-related protein 2	3.15
	445333	BE537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
	448143	AF039704	Hs.20478	NM_000391:Homo sapiens ceroid-lipofuscin	3.14
20	423007	AA320134	Hs.196029	Hs.196029:Homo sapiens mR for KIAA1657 p	3.14
	416511	NM_006762	Hs.79356	NM_006762:Homo sapiens Lysosomal-associa	3.14
	439237	AW408158	Hs.318893	Hs.318893:ESTs, Weakly similar to Z195_H	3.13
	446899	NM_005397	Hs.16426	NM_005397:Homo sapiens podocalyxin-like	3.13
25	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.13
	434398	AA121098	Hs.3838	NM_006622:Homo sapiens serum-inducible k	3.12
	441283	AA927670	Hs.131704	Hs.131704:ESTs	3.12
	418945	BE246762	Hs.89499	NM_000698:Homo sapiens arachidole 5-lipo	3.12
	418458	AA332941	Hs.85226	NM_000235:Homo sapiens lipase A, lysosom	3.12
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.11
30	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11
	411089	AA456454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
	432990	AL036071	Hs.279899	NM_003820:Homo sapiens tumor necrosis fa	3.11
	425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine	3.10
35	443601	AI078554	Hs.42658	Hs.42658:Homo sapiens cD FLJ30167 fis, c	3.10
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	3.10
	413672	BE156536	Hs.353632	Hs.353632:ESTs, Moderately similar to hy	3.09
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09
	414586	AA306160	Hs.16488	NM_002298:Homo sapiens lymphocyte cytosol	3.08
	423712	W46802	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08
40	438552	AJ245820	Hs.6314	NM_012410:Homo sapiens type I transmembr	3.06
	448364	T08958	Hs.297214	Hs.297214:HSPC141 protein	3.06
	426437	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
	437679	NM_014214	Hs.5753	NM_014214:Homo sapiens inositol(myo)-1(o	3.06
	422262	AL022315	Hs.113987	NM_006498:Homo sapiens lectin, galactosi	3.06
45	410480	R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
	453613	F06838	Hs.374476	Hs.374476:ESTs	3.05
	408051	AI623351	Hs.172148	Hs.172148:ESTs	3.05
50	432278	AL137506	Hs.274256	Hs.274256:hypothetical protein FLJ23563	3.04
	407949	W21874	Hs.247057	Hs.247057:ESTs, Weakly similar to 210926	3.04
	418090	U57059	Hs.83429	NM_003810:Homo sapiens tumor necrosis fa	3.04
	433165	AA578904	Hs.292437	Hs.292437:ESTs	3.03
55	425809	AA370362	Hs.57958	Hs.57958:EGF-TM7-latrophilin-related pro	3.03
	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447831	AI433293	Hs.164115	Hs.164115:ESTs	3.02
	413278	BE563085	Hs.833	NM_005101:Homo sapiens interferon-stimul	3.01
	418870	AF147204	Hs.89414	Hs.89414:chemokine (C-X-C motif), recept	3.00
60	456376	AA663904	Hs.89862	Hs.89862:TNFRSF1A-associated via death d	3.00
	439738	BE246502	Hs.9598	Hs.9598:sema domain, immunoglobulin doma	3.00
	444416	AW288085	Hs.11156	NM_016494:Homo sapiens hypothetical prot	3.00
	406656	M16714	Hs.89643	Hs.89643:transketolase (Wernicke-Korsako	3.00
	406826	AW516005	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
65	418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
	421742	AW970004	Hs.107528	NM_016108:Homo sapiens androgen induced	2.99
	406824	AW515961	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	435605	AF151815	Hs.4973	NM_015680:Homo sapiens hypothetical prot	2.98
	410491	AA465131	Hs.64001	Hs.64001:Homo sapiens clone 25218 mR seq	2.98
70	427648	AI376722	Hs.180062	NM_004159:Homo sapiens proteasome (proso	2.98
	411125	AA151647	Hs.68877	NM_000101:Homo sapiens cytochrome b-245,	2.98
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.98
	429373	NM_014694	Hs.200594	NM_014694:Homo sapiens KIAA0605 gene pro	2.98
	445701	AF055581	Hs.13131	NM_005475:Homo sapiens lymphocyte adapt	2.97
75	414649	AI672727	Hs.76753	NM_000118:Homo sapiens endoglin (Oster-R	2.97
	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.97
	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.97
	407792	AI077715	Hs.39384	NM_014344:Homo sapiens four jointed box	2.97
	445707	AI248720	Hs.114390	Hs.114390:ESTs	2.96
80	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
	418478	U38945	Hs.1174	Hs.1174:cyclin-dependent kinase inhibitor	2.95
	411441	AL042355	Hs.70202	Hs.70202:WD repeat domain 10	2.95
	443426	AF098158	Hs.9329	Hs.9329:chromosome 20 open reading frame	2.94
	450876	AF189062	Hs.285976	Hs.285976:LAG1 longevity assurance homol	2.94

5	426359	AA376409	Hs.10862	Hs.10862:Homo sapiens cD: FLJ23313 fis,	2.94
	425421	L11669	Hs.157145	NM_001120:Homo sapiens tetracycline tran	2.93
	449879	H03573	Hs.287830	Hs.287830:Homo sapiens mR: cD DKFZp434E1	2.93
	454075	R43826	Hs.16313	Hs.16313:Kruppel-like zinc finger protei	2.93
	421595	AB014520	Hs.301685	Hs.301685:KIAA0620 protein	2.93
	457949	W69171	Hs.334814	Hs.334814:hypothetical protein FLJ14868	2.92
	443987	AW163123	Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
10	430259	BE550182	Hs.375142	Hs.375142:RalGEF-like protein 3, mouse h	2.92
	415906	AJ751357	Hs.288741	Hs.288741:Homo sapiens cD: FLJ22256 fis,	2.91
	429762	A1346255	Hs.216354	NM_006913:Homo sapiens ring finger prote	2.91
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.91
	427080	AW068287	Hs.301175	NM_002872:Homo sapiens ras-related C3 bo	2.91
15	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxase 2 (PON2	2.90
	431476	BE612705	Hs.256697	Hs.256697:histidine triad nucleotide bin	2.89
	406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cD FLJ31548 fis, c	2.89
	456362	AW973003	Hs.179909	Hs.179909:nuclear receptor coactivator 6	2.88
20	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	2.88
	456974	M12529	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.88
	418174	L20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88
	446055	AJ815981	Hs.12909	Hs.12909:mucopolip 1	2.88
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EF1),	2.87
25	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87
	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143	AW747996	Hs.160999	Hs.160999:ESTs, Weakly similar to 17885	2.87
	407151	H25836	Hs.301527	Hs.301527:ESTs, Moderately similar to un	2.86
	449349	AJ825386	Hs.352579	Hs.352579:Homo sapiens, chromosome 20 op	2.86
30	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86
	417355	D13168	Hs.82002	Hs.82002:endothelin receptor type B	2.86
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	2.86
	408877	AA479033	Hs.130315	Hs.130315:ESTs	2.85
35	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
	412014	AJ620650	Hs.43761	Hs.43761:gap junction protein, alpha 7,	2.84
	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	2.84
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.84
	439941	AJ392640	Hs.18272	Hs.18272:solute carrier family 38, membe	2.84
40	436496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation 1	2.84
	422100	AJ096988	Hs.111554	NM_005737:Homo sapiens ADP-ribosylation	2.83
	439730	AF035292	Hs.6654	Hs.6654:KIAA0657 protein	2.83
	447217	BE465754	Hs.17778	NM_003872:Homo sapiens neuropilin 2 (NRP	2.83
45	428343	AL043021	Hs.12705	Hs.12705:similar to HYPOTHETICAL 43.1 KO	2.82
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mR: cD DKFZp564O24	2.82
	415523	AL042003	Hs.296847	NM_003119:Homo sapiens spastic paraplegi	2.81
	439668	AJ091277	Hs.302634	Hs.302634:frizzled homolog 8 (Drosophila	2.81
	414570	Y00285	Hs.76473	NM_000876:Homo sapiens insulin-like grow	2.80
50	426535	AJ077012	Hs.288582	NM_006287:Homo sapiens tissue factor pat	2.80
	409649	AA159216	Hs.55505	Hs.55505:hypothetical protein FLJ20442	2.80
	406655	M21533	Hs.277477	Hs.277477:major histocompatibility compl	2.79
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytosol	2.79
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cD FLJ14201 fis,	2.78
55	451356	AA748418	Hs.164577	Hs.164577:ESTs	2.78
	450708	AA376654	Hs.350065	Hs.350065:Homo sapiens cD FLJ30634 fis,	2.78
	433681	AJ004377	Hs.200360	Hs.200360:Homo sapiens cD FLJ13027 fis,	2.77
	442599	AF078037	Hs.324051	NM_006663:Homo sapiens RalA-associated i	2.76
	414509	AW161311	Hs.76294	NM_001780:Homo sapiens CD63 antigen (mel	2.76
	431394	AK000692	Hs.252351	Hs.252351:HERV-H LTR-associating 2	2.76
60	417331	AW411297	Hs.81972	Hs.81972:SHC (Src homology 2 domain cont	2.76
	415995	NM_004573	Hs.355888	NM_004573:Homo sapiens phosphatidase C,	2.75
	414911	NM_000107	Hs.77602	NM_000107:Homo sapiens damage-specific D	2.75
	425976	C75094	Hs.334514	Hs.334514:chromosome 6 open reading fram	2.75
	407893	BE408359	Hs.43621	Hs.43621:hypothetical protein MBC3205	2.75
65	407903	AJ287341	Hs.154029	Hs.154029:bHLH factor Hes4	2.75
	416062	AA724811	Hs.334791	Hs.334791:similar to neural tetraspanin	2.75
	428494	AA233439	Hs.184634	Hs.184634:hypothetical protein FLJ20005	2.75
	421506	BE302796	Hs.105097	NM_003258:Homo sapiens thymidine kase 1,	2.74
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif,	2.74
70	424527	AW138558	Hs.334873	Hs.334873:carboxypeptidase M	2.74
	439678	AW263124	Hs.350547	Hs.350547:nuclear receptor co-repressor/	2.74
	425188	AK002052	Hs.155071	Hs.155071:chromosome 20 open reading fra	2.74
	428013	AF151020	Hs.181444	NM_016456:Homo sapiens hypothetical prot	2.73
	439333	AW384710	Hs.132986	Hs.132986:Homo sapiens cD FLJ31588 fis,	2.73
75	450935	BE514743	Hs.355753	NM_005851:Homo sapiens tumor suppressor	2.73
	421532	AW138207	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.73
	440502	AJ824113	Hs.78281	Hs.78281:regulator of G-protein siglting	2.73
	444981	AW855398	Hs.12210	Hs.12210:tumor endothelial marker 6	2.72
	439219	N33883	Hs.41322	Hs.41322:ESTs	2.72
80	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
	433179	AW362945	Hs.162459	Hs.162459:ESTs	2.72
	424528	AW073971	Hs.238954	Hs.238954:ESTs, Weakly similar to putati	2.71
	411213	AA676939	Hs.69285	NM_003873:Homo sapiens neuropilin 1 (NRP	2.70
	433012	NM_004045	Hs.279910	NM_004045:Homo sapiens ATX1 antioxidant	2.70

	425345	AU077297	Hs.155894	NM_002827:Homo sapiens protein tyrosine	2.69
	428923	BE047698	Hs.188785	Hs.188785:ESTs	2.69
	427923	AW274357	Hs.301406	Hs.301406:hypothetical protein PP3501	2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.69
5	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.68
	416207	NM_014745	Hs.79077	NM_014745:Homo sapiens KIAA0233 gene pro	2.68
	420372	AW960049	Hs.293660	Hs.293660:gene overexpressed in astrocyt	2.68
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	2.67
10	425069	AA687465	Hs.298184	Hs.298184:potassium voltage-gated channe	2.67
	418558	AW082266	Hs.86131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67
	426251	M24283	Hs.168383	NM_000201:Homo sapiens intercellular adh	2.66
	406701	AA780613	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.66
	431681	AK000378	Hs.267566	Hs.267566:hypothetical protein FLJ20371	2.66
15	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
	433101	AW572317	Hs.12082	Hs.12082:TIGA1	2.66
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	2.66
	427868	AI360119	Hs.181013	NM_002629:Homo sapiens phosphoglycerate	2.66
	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, alpha 2	2.66
20	424762	AL119442	Hs.183684	Hs.183684:eukaryotic translation initiat	2.66
	422048	NM_012445	Hs.288126	NM_012445:Homo sapiens spondin 2, extrac	2.65
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.65
	450184	W31096	Hs.237617	Hs.237617:dipeptidylpeptidase 9	2.65
	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein	2.65
25	414217	AI309298	Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SLIT-ROBO Rho GTPase-activating	2.64
	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	2.63
	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein BC011406	2.63
30	430223	NM_002514	Hs.235935	NM_002514:Homo sapiens neuroblastoma ov	2.63
	417526	AA568906	Hs.82240	NM_004177:Homo sapiens syntaxin 3A (STX3	2.63
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.63
	449843	R85337	Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62
	417389	BE260964	Hs.82045	NM_002391:Homo sapiens midline (neurite	2.62
35	446312	BE087853	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.62
	435099	AC004770	Hs.4756	Hs.4756:flap structure-specific endonuc	2.62
	417920	S47833	Hs.82927	NM_004037:Homo sapiens adenosine monopho	2.62
	435702	AI033647	Hs.121001	Hs.121001:Homo sapiens, clone MGC:45521	2.62
	422959	AV647015	Hs.349256	Hs.349256:paired immunoglobulin-like rec	2.62
40	419938	AU076772	Hs.1279	NM_001733:Homo sapiens complement compon	2.62
	450954	AI904740	Hs.25691	NM_005856:Homo sapiens receptor (calcito	2.61
	421753	BE314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
	443577	AU078033	Hs.177170	Hs.177170:ESTs, Weakly similar to ALU8_H	2.61
	453886	R66282	Hs.20247	Hs.20247:ESTs	2.61
45	421883	X55079	Hs.1437	NM_000152:Homo sapiens glucosidase, alph	2.60
	440457	BE387593	Hs.21321	Hs.21321:granule cell differentiation pr	2.60
	410295	AA741357	Hs.356624	Hs.356624:ESTs	2.59
	420679	X57152	Hs.99853	NM_001436:Homo sapiens fibrillarin (FBL)	2.59
	451558	NM_001089	Hs.26630	NM_001089:Homo sapiens ATP-binding casse	2.59
50	444672	Z95636	Hs.11669	Hs.11669:aminin, alpha 5	2.59
	408669	AI493591	Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	426194	T50872	Hs.2001	Hs.2001:thromboxane A synthase 1 (plate	2.59
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	2.59
	456371	S76825	Hs.89695	Hs.89695:insulin receptor	2.59
55	429098	AF030249	Hs.196176	NM_001398:Homo sapiens enoyl Coenzyme A	2.59
	414443	AU077268	Hs.76144	NM_002609:Homo sapiens platelet-derived	2.59
	428484	AF104032	Hs.184501	NM_003486:Homo sapiens solute carrier fa	2.59
	453309	AI791809	Hs.32949	NM_005218:Homo sapiens defensin, beta 1	2.59
	412867	AU076861	Hs.74637	NM_003217:Homo sapiens testis enhanced g	2.58
60	432827	Z58128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
	412669	AW880841	Hs.96908	NM_006034:Homo sapiens p53-induced prote	2.58
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.58
	452866	R26969	Hs.268016	Hs.268016:Homo sapiens cD: FLJ21243 fis,	2.58
	435129	AI381659	Hs.267086	Hs.267086:ESTs	2.57
65	424482	BE268621	Hs.149155	NM_003374:Homo sapiens voltage-dependent	2.57
	410494	M36564	Hs.64016	NM_000313:Homo sapiens protein S (alpha)	2.56
	433895	AI287912	Hs.3628	NM_004834:Homo sapiens mitogen-activated	2.56
	442566	R37337	Hs.12111	Hs.12111:ESTs	2.56
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
70	442622	NM_000435	Hs.8546	NM_000435:Homo sapiens Notch homolog 3 (2.56
	430346	AK000331	Hs.297641	Hs.297641:retinoblastoma-associated fact	2.55
	419344	U94905	Hs.277445	Hs.277445:diacylglycerol kase, zeta (104	2.55
	426500	NM_014638	Hs.170156	NM_014638:Homo sapiens KIAA0450 gene pro	2.55
	408048	NM_007203	Hs.42322	NM_007203:Homo sapiens A kase (PRKA) anc	2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-like	2.54
75	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.54
	422451	AA310753	Hs.42491	Hs.42491:ESTs, Moderately similar to hyp	2.53
	435906	AI686379	Hs.110796	Hs.110796:SAR1 protein	2.53
80	400231				2.53
	417849	AW291587	Hs.82733	NM_007361:Homo sapiens nidogen 2 (NID2),	2.53
	427380	NM_005534	Hs.177559	NM_005534:Homo sapiens interferon gamma	2.52
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading tra	2.52
	438000	AI825880	Hs.5985	Hs.5985:non-kise Cdc42 effector protein	2.52

	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) protease i	2.52
	422396	W21872	Hs.7907	Hs.7907:L-fucose kase	2.52
	420787	AA564248	Hs.351292	Hs.351292:Homo sapiens cD FLJ32605 fis,	2.51
5	430590	AW383947	Hs.246381	NM_001251:Homo sapiens CD68 antigen (CD6	2.51
	447026	BE313144	Hs.324844	Hs.324844:hypothetical protein IMAGE3455	2.51
	439223	AW238299	Hs.250618	Hs.250618:UL16 binding protein 2	2.50
	435151	AA348482	Hs.4788	Hs.4788:nicastatin	2.50
	448202	AB002292	Hs.20695	NM_014629:Homo sapiens Rho guanine nucle	2.50
10	449943	AF104266	Hs.24212	Hs.24212:latrophilin	2.50
	425743	BE396495	Hs.159428	Hs.159428:BCL2-associated X protein	2.50
	444681	AJ243937	Hs.288316	Hs.288316:chromosome 6 open reading fram	2.50
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.50
	426865	D63476	Hs.172813	NM_003899:Homo sapiens Rho guanine nucle	2.50
15	432306	Y18207	Hs.303090	NM_005398:Homo sapiens protein phosphata	2.49
	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kase C su	2.49
	421905	AJ660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	2.49
	419493	AF001212	Hs.90744	NM_002815:Homo sapiens proteasome (proso	2.49
	422530	AW972300	Hs.118110	NM_004335:Homo sapiens bone marrow strom	2.48
20	442821	BE391929	Hs.8752	NM_014255:Homo sapiens transmembrane pro	2.48
	416919	T97839	Hs.80464	NM_006402:Homo sapiens hepatitis B virus	2.48
	443105	X96753	Hs.9004	NM_001897:Homo sapiens chondroitin sulfat	2.48
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
	428028	U52112	Hs.182018	NM_001569:Homo sapiens interleukin-1 rec	2.47
25	424307	AW293399	Hs.356377	Hs.356377:Homo sapiens, clone IMAGE:3633	2.46
	434511	R28982	Hs.18106	Hs.18106:ESTs, Weakly similar to T06291	2.46
	454390	AB020713	Hs.56966	Hs.56966:KIAA0906 protein	2.46
	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.46
	424673	AA345051	Hs.294092	Hs.294092:Homo sapiens mR full length in	2.46
30	422003	AA361760	Hs.296326	Hs.296326:ESTs, Weakly similar to A33533	2.46
	432126	AA865239	Hs.37196	Hs.37196:putative G protein coupled rece	2.46
	445937	AJ452943	Hs.321231	NM_003779:Homo sapiens UDP-GalbetaGluc	2.46
	409354	N68188	Hs.159472	Hs.159472:Homo sapiens cD: FLJ22224 fis,	2.46
	401179				2.46
35	418151	AA864238	Hs.83583	NM_005731:Homo sapiens actin related pro	2.45
	422648	D86983	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (prefo	2.45
	431222	X56777	Hs.273790	NM_007155:Homo sapiens zo pellucida glyc	2.45
	411529	AA430348	Hs.317596	Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45
40	426825	AL133415	Hs.297753	NM_003380:Homo sapiens vimentin (VIM), m	2.45
	422242	AJ251760	Hs.273385	NM_016592:Homo sapiens GS complex locus	2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44
	426410	BE298446	Hs.305890	Hs.305890:BCL2-like 1	2.44
	421064	AJ245432	Hs.101382	NM_006291:Homo sapiens tumor necrosis fa	2.44
45	428157	AJ738719	Hs.198427	NM_000189:Homo sapiens hexokase 2 (HK2),	2.44
	424398	BE397787	Hs.146393	NM_014685:Homo sapiens homocysteine-indu	2.44
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	2.44
	426031	AA295251	Hs.166066	Hs.166066:cisplatin resistance associate	2.43
	409817	BE295464	Hs.56607	Hs.56607:Williams-Beuren syndrome chromo	2.43
50	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.43
	426761	AJ015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	2.43
	429332	AF030403	Hs.199263	NM_013233:Homo sapiens serine threonine	2.43
	425923	NM_005026	Hs.162808	NM_005026:Homo sapiens phosphoinositide-	2.43
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.43
55	433339	AF019226	Hs.8036	Hs.8036:RAB3D, member RAS oncogene famil	2.42
	420539	AA282735	Hs.44004	Hs.44004:AD031 protein	2.42
	413243	AA769266	Hs.193657	Hs.193657:ESTs	2.42
	435029	AF167706	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
	422374	AW732869	Hs.1519	Hs.1519:protein kase, cAMP-dependent, re	2.42
60	444501	AW247624	Hs.11342	NM_004148:Homo sapiens ninjurin 1 (NINJ1	2.42
	414919	AW087337	Hs.194461	Hs.194461:ESTs	2.42
	419355	AA428520	Hs.90061	NM_006667:Homo sapiens progesterone rece	2.42
	436042	AF284422	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
	418245	AA088767	Hs.83883	Hs.83883:transmembrane, prostate androge	2.42
65	444215	AB033075	Hs.10669	Hs.10669:development and differentiation	2.41
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.41
	423701	AA329856	Hs.143022	Hs.143022:ESTs	2.41
	441783	BE313412	Hs.7961	Hs.7961:Homo sapiens clone 25012 mR sequ	2.41
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.41
70	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
	407894	AJ278313	Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449	W16752	Hs.32981	Hs.32981:sema domain, immunoglobulin dom	2.40
	408688	AJ634522	Hs.152925	Hs.152925:KIAA1268 protein	2.40
75	422448	AW372922	Hs.116774	Hs.116774:integrin, alpha 1	2.39
	416269	AA177138	Hs.161671	Hs.161671:ESTs	2.39
	452679	Z42387	Hs.83883	Hs.83883:transmembrane, prostate androge	2.38
	432981	NM_002733	Hs.3136	NM_002733:Homo sapiens protein kase, AMP	2.38
	419846	NM_015977	Hs.285681	Hs.285681:Williams Beuren syndrome chrom	2.38
80	422110	AJ376736	Hs.111779	Hs.111779:secreted protein, acidic, cyst	2.38
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.38
	433969	AW207279	Hs.271786	Hs.271786:ESTs, Weakly similar to PC4395	2.37
	451267	AJ033894	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.37
	447526	AL048753	Hs.303649	NM_002982:Homo sapiens small inducible c	2.37

5	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	2.37
	420255	NM_007289	Hs.1298	NM_007289:Homo sapiens membrane metallo-	2.37
	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens src family associ	2.36
	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.36
	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) protease i	2.36
	408212	AA297567	Hs.43728	NM_015696:Homo sapiens weakly similar to	2.36
	430478	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L,	2.36
	405102				2.35
10	423583	AL122055	Hs.129836	Hs.129836:KIAA1028 protein	2.35
	426125	X87241	Hs.166994	NM_005245:Homo sapiens FAT tumor suppres	2.35
	425204	NM_002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
	421079	AW404994	Hs.101695	Hs.101695:NCK adaptor protein 2	2.35
	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
15	412958	BE391579	Hs.75087	NM_006712:Homo sapiens FAST kise (FASTK)	2.34
	430363	M28713	Hs.274464	NM_000398:Homo sapiens diaphorase (DH) (2.34
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (D)	2.34
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso)	2.34
20	449027	AJ271216	Hs.22880	Hs.22880:diptidylpeptidase III	2.34
	429457	BE243065	Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.34
25	430702	U56979	Hs.278568	NM_000186:Homo sapiens H factor 1 (compl	2.33
	456804	AJ421645	Hs.139851	NM_001233:Homo sapiens caveolin 2 (CAV2)	2.33
	453648	W21493	Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33
	450812	AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
	402575				2.33
30	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32
	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine	2.32
	442968	AK000606	Hs.8868	NM_004871:Homo sapiens golgi SP receptor	2.32
	410639	BE269047	Hs.65234	Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32
35	450160	BE048099	Hs.183738	Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32
	407223	H96850		H96850:yo03b12.s1 Soares melanocyte 2NbH	2.32
	426780	BE242284	Hs.172199	NM_001114:Homo sapiens adenylate cyclase	2.32
	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
40	453107	NM_016113	Hs.279746	NM_016113:Homo sapiens transient recepto	2.31
	422963	M79141	Hs.13234	Hs.13234:ESTs, Weakly similar to hypothe	2.31
	433618	AA602539	Hs.345494	Hs.345494:ESTs, Moderately similar to ZN	2.31
	438584	AA811347		AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	2.31
	446126	AW085909	Hs.356618	Hs.356618:ESTs, Weakly similar to PC4259	2.31
45	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
	433230	AW136134	Hs.220277	Hs.220277:ESTs, Weakly similar to expres	2.30
	410168	AW834050	Hs.351432	Hs.351432:tensin	2.30
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mR cD DKFZp564D01	2.30
	418452	BE379749	Hs.85201	NM_005127:Homo sapiens C-type (calcium d	2.30
50	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848	AJ417193	Hs.288912	Hs.288912:BBP-like protein 2	2.29
	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
	422562	AI962060	Hs.118397	NM_001129:Homo sapiens AE binding protei	2.28
55	432828	AB042326	Hs.287402	Hs.287402:chondroitin 4-sulfotransferase	2.28
	412948	BE243313	Hs.334851	NM_006148:Homo sapiens LIM and SH3 prote	2.28
	426068	AF029778	Hs.166154	NM_002226:Homo sapiens jagged 2 (JAG2),	2.28
	456919	NM_003900	Hs.182248	NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.28
60	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cD FLJ30677 fis,	2.28
	413211	AW967107	Hs.109274	Hs.109274:hypothetical protein MGCA365	2.28
	422051	AW327546	Hs.111024	Hs.111024:solute carrier family 25 (mito	2.27
	438438	AA257992	Hs.50651	Hs.50651:Janus kise 1 (a protein tyrosin	2.27
65	436278	BE396290	Hs.5097	NM_004710:Homo sapiens syptogyrin 2 (SYN	2.27
	454080	AI199711	Hs.576	NM_000147:Homo sapiens fucosidase, alpha	2.27
	426542	AF190746	Hs.170310	NM_017424:Homo sapiens cat eye syndrome	2.27
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27
	402901				2.26
70	412898	AI129903	Hs.74669	NM_006634:Homo sapiens vesicle-associate	2.26
	413020	R98736		R98736:yr31h09.r1 Soares fetal liver spl	2.26
	413939	AL047051	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.26
	408681	AW953853	Hs.281462	Hs.281462:hypothetical protein FLJ14251	2.25
	412330	NM_005100	Hs.788	NM_005100:Homo sapiens A kise (PRKA) anc	2.25
75	442083	R50192	Hs.165062	Hs.165062:ESTs	2.25
	418271	NM_000919	Hs.83920	NM_000919:Homo sapiens peptidylglycine a	2.25
	433376	AI249361	Hs.74122	NM_001225:Homo sapiens caspase 4, apopto	2.25
	438562	AI566826	Hs.25890	Hs.25890:ESTs, Weakly similar to transdu	2.25
	443883	AA114212	Hs.9930	NM_001235:Homo sapiens serine (or cystei	2.25
80	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.24
	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24
	407904	W44735	Hs.107260	Hs.107260:putative UDP-Galc:polypeptide	2.24
	429690	AW956329	Hs.23721	Hs.23721:ESTs	2.24

443813	AA876372	Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667D09	2.24
427458	BE208364	Hs.29283	Hs.29283:ESTs, Weakly similar to LKHU pr	2.24
454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
425751	T19239	Hs.1940	NM_001885:Homo sapiens crystallin, alpha	2.23
456437	AI924228	Hs.115185	Hs.115185:ESTs	2.23
413019	BE281604	Hs.75140	NM_002337:Homo sapiens low density lipop	2.23
418862	BE550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23
435284	AA879470	Hs.96849	Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
429630	M85289	Hs.211573	NM_005529:Homo sapiens heparan sulfate p	2.23
427609	AK000436	Hs.179791	Hs.179791:RAB20, member RAS oncogene fam	2.23
421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.23
446616	R65964	Hs.334873	Hs.334873:carboxypeptidase M	2.23
407232	X04526		X04526:Human liver mR for beta-subunit s	2.23
423798	AF047033	Hs.132904	Hs.132904:solute carrier family 4, sodiu	2.23
446755	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	2.22
431393	AW971493	Hs.134269	Hs.134269:ESTs, Weakly similar to 200439	2.22
431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.22
428782	X12830	Hs.193400	NM_000655:Homo sapiens interleukin 6 rec	2.22
446006	NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
436418	AJ245874	Hs.4245	Hs.4245:chromosome 11 hypothetical prote	2.22
423869	BE409301	Hs.134012	NM_006688:Homo sapiens C1q-related facto	2.21
437730	AW071087	Hs.239176	Hs.239176:insulin-like growth factor 1 r	2.21
444020	R92962	Hs.35052	Hs.35052:ESTs	2.21
413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR; cD DKFZp667B0	2.21
412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
448988	Y09763	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21
426841	AI052358	Hs.131741	Hs.131741:ESTs	2.21
408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.21
451711	AK000461	Hs.26890	Hs.26890:cat eye syndrome chromosome reg	2.20
414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20
448883	BE614989	Hs.7503	Hs.7503:hypothetical protein FLJ14153	2.20
411296	BE207307	Hs.10114	Hs.10114:growth suppressor 1	2.20
452268	NM_003512	Hs.28777	NM_003512:Homo sapiens H2A histone fami	2.20
416810	AF035606	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
441415	H21497	Hs.7471	Hs.7471:BBP-like protein 1	2.20
444212	AW503976	Hs.10649	NM_004848:Homo sapiens basement membrane	2.19
428044	AA093322	Hs.301404	NM_006743:Homo sapiens R binding motif p	2.19
430017	AA263172	Hs.35	NM_002832:Homo sapiens protein tyrosine	2.19
424490	AJ278016	Hs.55565	Hs.55565:ankyrin repeat domain 3	2.19
431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.19
453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19
448262	AW880830	Hs.186273	Hs.186273:ESTs	2.19
416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	2.19
442045	C05768	Hs.8078	Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19
423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimul	2.19
428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
424503	NM_002205	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.19
437696	Z83844	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18
405204				2.18
426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.18
417418	NM_002468	Hs.82116	NM_002468:Homo sapiens myeloid different	2.18
412773	H15785	Hs.74573	NM_012268:Homo sapiens similar to vaccin	2.18
409402	AF208234	Hs.695	NM_000100:Homo sapiens cystatin B (stefi	2.18
443791	N64458	Hs.143345	Hs.143345:ESTs	2.18
435049	AL122067	Hs.4746	Hs.4746:hypothetical protein FLJ21324	2.18
418389	AA830613	Hs.293849	Hs.293849:ESTs	2.18
450712	AI732130	Hs.270496	Hs.270496:ESTs, Weakly similar to ALUB_H	2.18
422007	AI739435	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.18
453676	AW853745	Hs.286035	Hs.286035:hypothetical protein FLJ22686	2.18
415718	F30631	Hs.200237	Hs.200237:ESTs	2.18
452688	AA721140	Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18
415988	BE407713	Hs.78943	NM_000386:Homo sapiens bleomycin hydrola	2.18
409453	AI885516	Hs.95612	Hs.95612:ESTs	2.17
417512	X76534	Hs.82226	NM_002510:Homo sapiens glycoprotein (tra	2.17
427202	BE272922	Hs.173936	NM_000628:Homo sapiens interleukin 10 re	2.17
440983	M20681	Hs.7594	NM_006931:Homo sapiens solute carrier fa	2.17
416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.17
429642	X68264	Hs.211579	NM_006500:Homo sapiens melanoma adhesio	2.17
427213	AW007211	Hs.348389	Hs.348389:hypothetical protein FLJ12876	2.17
437763	AA469369	Hs.5831	NM_003254:Homo sapiens tissue inhibitor	2.17
454000	AA040620	Hs.5672	Hs.5672:golgi membrane protein SB140	2.17
424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (rel amy	2.16
403857				2.16
406648	AA563730	Hs.277477	Hs.277477:major histocompatibility compl	2.16
400265				2.16
442379	NM_004613	Hs.8265	NM_004613:Homo sapiens transglutaminase 2	2.16
441892	AB028981	Hs.8021	Hs.8021:KIAA1058 protein	2.16
417446	AL118671	Hs.82163	NM_000898:Homo sapiens monoamine oxidase	2.16
418386	AA361739	Hs.84549	NM_002494:Homo sapiens DH dehydrogese (u	2.16
414053	BE391635	Hs.75725	NM_003564:Homo sapiens transgelin 2 (TAG	2.16

	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
	447660	AW160386	Hs.163667	Hs.163667:ESTs, Weakly similar to CA1H_H	2.16
	408279	AF216965	Hs.44095	Hs.44095:cyclin M3	2.16
5	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.16
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.16
	415651	AF057307	Hs.78575	Hs.78575:prosaposin (variant Gaucher dis	2.15
	425302	U79115	Hs.155566	NM_003805:Homo sapiens CASP2 and RIPK1 d	2.15
	425996	W67330	Hs.374451	Hs.374451:ESTs	2.15
10	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.15
	422070	AF149785	Hs.111126	Hs.111126:pituitary tumor-transforming 1	2.15
	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initial	2.15
	435551	AF212365	Hs.5470	Hs.5470:interleukin 17B receptor	2.15
15	437741	BE561610	Hs.5809	Hs.5809:putative transmembrane protein;	2.15
	441192	AA526626	Hs.7736	NM_016504:Homo sapiens mitochondrial rib	2.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	2.14
20	425252	AW391162	Hs.349306	Hs.349306:hypothetical protein FLJ31951	2.14
	427600	AW630918	Hs.179774	NM_002818:Homo sapiens proteasome (proso	2.14
	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.14
	407797	AK000524	Hs.39850	Hs.39850:uridine kise-like 1	2.14
25	443044	N28522	Hs.8935	NM_014298:Homo sapiens quindite phospho	2.14
	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cD FLJ32174 fis,	2.14
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	2.14
	458097	AW341135	Hs.58104	Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
30	411925	AW014588	Hs.72925	NM_003475:Homo sapiens chromosome 11 ope	2.14
	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.14
	428586	M36712	Hs.2299	Hs.2299:CD8 antigen, beta polypeptide 1	2.14
	429379	NM_014840	Hs.200598	NM_014840:Homo sapiens KIAA0537 gene pro	2.13
35	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	2.13
	443895	AW979048	Hs.292566	Hs.292566:YEA4 protein	2.13
	428145	BE243327	Hs.182626	NM_012264:Homo sapiens chromosome 22 ope	2.13
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cD: FLJ21933 fis,	2.13
	456534	X91195	Hs.100623	Hs.100623:protein phosphatase 1, regulat	2.13
40	419972	AL041465	Hs.182982	Hs.182982:gdgln-67	2.13
	424950	AA602917	Hs.156974	Hs.156974:ESTs	2.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	2.13
	431449	M55994	Hs.256278	NM_001066:Homo sapiens tumor necrosis fa	2.13
	418758	AW959311	Hs.172012	Hs.172012:hypothetical protein DKFZp434J	2.13
45	434202	BE382411	Hs.3764	NM_000858:Homo sapiens guanylate kise 1	2.13
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.12
	452700	AI859390	Hs.288940	Hs.288940:transmembrane protein B (five	2.12
	438033	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing fi	2.12
	400847				2.12
50	447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12
	417052	NM_000712	Hs.81029	NM_000712:Homo sapiens biliverdin reduct	2.12
	413284	AU077055	Hs.289107	NM_001166:Homo sapiens baculoviral IAP r	2.11
	434558	AW264102	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.11
	404030				2.11
55	410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	2.11
	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kise	2.11
	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.11
	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical prot	2.11
	426433	L38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3	2.11
60	442439	UD9759	Hs.246857	NM_002752:Homo sapiens mitogen-activated	2.11
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.11
	400208				2.11
	455705	AW161061	Hs.356580	Hs.356580:ESTs, Weakly similar to zinc I	2.11
65	417599	AA204688	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.10
	416728	AB024597	Hs.79658	NM_001894:Homo sapiens casein kise 1, ep	2.10
	439920	H05430	Hs.288433	Hs.288433:neurotrimin	2.10
	422309	U79745	Hs.114924	NM_004694:Homo sapiens solute carrier fa	2.10
	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517				2.10
70	421872	AA369753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kise, rec	2.10
	431214	AA294921	Hs.348024	NM_002881:Homo sapiens v-ral simian leuk	2.10
	412856	BE386745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442064	AI422867	Hs.88594	Hs.88594:Homo sapiens, clone IMAGE:43329	2.10
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.10
75	426728	NM_007118	Hs.367689	NM_007118:Homo sapiens triple functio d	2.10
	419596	BE379320	Hs.91448	NM_007026:Homo sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.09
80	424658	NM_002406	Hs.151513	NM_002406:Homo sapiens mannosyl (alpha-1	2.09
	432805	X94630	Hs.3107	Hs.3107:CD97 antigen	2.09
	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09

	445584	AF217518	Hs.8360	Hs.8360:PTD012 protein	2.09
	402559				2.09
5	418043	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kise	2.09
	448888	AW196663	Hs.200242	Hs.200242:caspace recruitment domain fam	2.09
	436910	AA926944	Hs.261587	Hs.261587:GCN2 eIF2alpha kise	2.09
	422573	AW297985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin	2.08
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.08
	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08
10	410301	AW502935	Hs.740	Hs.740:PTK2 protein tyrosine kise 2	2.08
	449538	AI559444	Hs.104679	Hs.104679:Homo sapiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541:netrin 4	2.08
	411779	AA292811	Hs.72050	NM_003551:Homo sapiens non-metastatic ce	2.08
	427704	AW971063	Hs.292882	Hs.292882:ESTs	2.07
15	413518	BE149455	Hs.75415	NM_004048:Homo sapiens beta-2-microglobu	2.07
	447345	BE247767	Hs.18166	Hs.18166:KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613061	Hs.337772	Hs.337772:hypothetical protein BC009331	2.07
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.07
20	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
	403966				2.07
	409115	AI223335	Hs.50651	NM_002227:Homo sapiens Janus kise 1 (a p	2.07
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	2.07
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.06
25	413980	NM_002437	Hs.75659	NM_002437:Homo sapiens Mpv17 transgene,	2.06
	439414	NM_001183	Hs.6551	NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06
	429849	U33053	Hs.2499	NM_002741:Homo sapiens protein kise C-6	2.06
	402424				2.06
30	406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, lysoso	2.05
	426086	T94907	Hs.188572	Hs.188572:ESTs	2.05
	419726	U50330	Hs.1274	NM_006129:Homo sapiens bone morphogeneti	2.05
	452344	AI264357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
35	442498	U54617	Hs.8364	NM_002612:Homo sapiens pyruvate dehydrog	2.05
	422114	AW194851	Hs.111801	NM_015908:Homo sapiens ansete resistance	2.05
	413420	AW410235	Hs.75348	NM_006263:Homo sapiens proteasome (proso	2.05
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	2.05
	409932	AI376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
40	434848	BE256304	Hs.32148	Hs.32148:AD-015 protein	2.04
	453852	AW961818	Hs.374424	Hs.374424:ESTs	2.04
	427637	AK000816	Hs.179986	NM_005803:Homo sapiens flotillin 1 (FLOT	2.04
	400264				2.04
	430016	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	2.04
45	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
	440975	AW499914	Hs.7579	Hs.7579:importin 9	2.04
	432280	BE440142	Hs.2943	NM_003135:Homo sapiens sigl recognition	2.04
	409504	AA304961	Hs.699	NM_000942:Homo sapiens peptidylprolyl is	2.04
	412146	M92444	Hs.73722	NM_001641:Homo sapiens APEX nuclease (mu	2.04
50	434203	BE262677	Hs.283558	Hs.283558:hypothetical protein PRO1855	2.04
	422754	AA316476	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
	413086	AA126841	Hs.183834	Hs.183834:ESTs	2.03
	424340	AA339036	Hs.7033	Hs.7033:ESTs	2.03
55	450440	AB024334	Hs.25001	NM_012479:Homo sapiens tyrosine 3-monoox	2.03
	424682	NM_002870	Hs.151536	NM_002870:Homo sapiens RAB13, member RAS	2.03
	415740	N80486	Hs.39911	Hs.39911:Homo sapiens miR for FLJ00089 pr	2.03
	412749	AA378417	Hs.74564	NM_003145:Homo sapiens sigl sequence rec	2.03
	408393	AW015318	Hs.23165	Hs.23165:ESTs	2.03
60	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.03
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cD FLJ10196 fis, c	2.03
	414883	AA926960	Hs.348669	NM_001826:Homo sapiens CDC28 protein kis	2.03
	447298	BE617527	Hs.239818	Hs.239818:phosphoinositide-3-kise, catal	2.02
	459580	AA022888	Hs.176065	Hs.176065:ESTs	2.02
65	422785	AI824114	Hs.289088	Hs.289088:heat shock 90kD protein 1, alp	2.02
	452696	AI826645	Hs.211534	Hs.211534:Homo sapiens cD FLJ31665 fis,	2.02
	452056	AW955065	Hs.101150	Hs.101150:KIAA1949 protein	2.02
	450690	AA296696	Hs.333418	NM_014164:Homo sapiens FXYD domain-conta	2.02
	423527	AI206965	Hs.105861	Hs.105861:engulfment and cell motility 3	2.01
70	429545	AI824164	Hs.356130	Hs.356130:ESTs	2.01
	439180	AI393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.01
	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.01
	436014	AF281134	Hs.283741	Hs.283741:exosome component Rrp46	2.01
	453329	T97205	Hs.193400	Hs.193400:interleukin 6 receptor	2.01
75	407347	AA829847		TZ3514:seq3329 1-NIB Homo sapiens cD clo	2.01
	435370	AI964074	Hs.225838	Hs.225838:ESTs	2.01
	430657	AA482910	Hs.370602	Hs.370602:ESTs. Weakly similar to hypoth	2.01
	427157	U51166	Hs.173824	NM_003211:Homo sapiens thymine-D glycosy	2.01
	424833	NM_003894	Hs.153405	NM_003894:Homo sapiens period homolog 2	2.01
80	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat simian leuk	2.01
	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.01
	417426	NM_002291	Hs.82124	NM_002291:Homo sapiens laminin, beta 1 (2.01
	412790	NM_014767	Hs.74583	NM_014767:Homo sapiens KIAA0275 gene pro	2.01
	445892	AV655500	Hs.93961	Hs.93961:Homo sapiens miR, cD DKFZp667D09	2.01

TABLE 38B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409745	MH1944_5	B1030997 AA921874 AW188822 B1027862 AJ347618 AJ361453 AJ088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 N64410 AA248866 AA248779 W02010 AL390180 AA359908 BE177778 BE177779 AW893733 BF756318 AA229762 AA230035 AA677593 AA618150 AA557952 BG171436 BE079601 BE079534 AA299964 BE392717 BE883402 BE079532 BE018148 BF889427 W00396 B1030997 AA921874 AW188822 B1027862 AJ347618 AJ361453 AJ088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 AW173494 AJ804346 AA669490 AW837178 T77002 F13038 T63141 AJ821021 BF370092 BF370127 BF370060 T62998 BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AJ299772 AW518149 AJ144456 AW628070 AJ629032 AJ358810 AJ880433 AJ440472 AJ357070 AJ865365 AW014799 AJ767973 AW518041 AA909398 AW768606 AF086037 H89360 H89546 AW936378 AW936544 AW813513 AW934714 AW749864 AW749902 BE162498 BE161005 BE162499 BE161006 AA190449 AW513465 BE162500 BE161007 AW974073 T56957

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403346	8569726	Plus	92752-93015
401621	8570184	Minus	193-608
403344	8569726	Plus	70823-70990
404240	5002624	Minus	116132-116407,116653-116922
401964	3126781	Minus	13510-13725,13847-14015
404277	1834458	Minus	91665-91946
405121	8102330	Minus	35816-36004,36587-36684
402493	9797670	Minus	205146-205240,205428-205542
402121	9188523	Plus	25692-25895
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
403887	7710553	Minus	69533-69868
403328	8469086	Minus	120428-120703
401241	4827300	Minus	30503-30844,31056-31248
401736	3219338	Plus	1771-1894
405029	7533975	Minus	37929-38224
404171	9930793	Plus	173667-173783,176876-177055
401797	6730720	Plus	6973-7118
401234	9929642	Plus	120173-120337
404170	9930793	Plus	168836-169248
406122	9144087	Minus	30940-31386

TABLE 39A: 856 GENES UP-REGULATED IN RENAL CANCER COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT RENAL TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Table 39A lists about 856 genes up-regulated in renal cancer compared to normal adult tissues and to non-malignant renal tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" renal cancer to "average" normal adult tissues was greater than or equal to 2.0, the ratio of "average" renal cancer to "average" non-malignant renal tissues was greater than or equal to 2.0, the "average" renal cancer level was set to the 90th percentile value amongst various renal specimens, the "average" normal adult tissue level was set to the 70th percentile value amongst various non-malignant tissues, the "average" non-malignant renal tissues level was set to the 50th percentile value amongst various non-malignant renal tissues, the "average" renal cancer value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
435013	H91923	Hs.110024		15.71
447768	X86400	Hs.19520	Hs.19520:FXFD domain-containing ion tran	14.07
445178	AJ792241	Hs.129614	Hs.129614:kidney-specific membrane prote	12.56
432542	AW083920	Hs.16098	Hs.16098:claudin 2	12.41
443595	AF169312	Hs.9613	NM_016109:Homo sapiens angiopoietin-like	11.77
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.39
436878	BE465204	Hs.47448	Hs.47448:ESTs	10.18
440304	BE159984	Hs.125395	Hs.125395:ESTs	9.95
407065	Y10141			9.58

5	413049	NM_002151	Hs.823	NM_002151:Homo sapiens hepsin (transmemb	9.51
	425983	AK000226	Hs.165619	Hs.165619:mucin and cadherin-like	8.88
	423161	AL049227	Hs.124776	Hs.124776:Homo sapiens mR: cD DKFZp564N1	8.77
	430569	AF241254	Hs.178098	Hs.178098:angiotensin I converting enzyme	8.45
	416768	AA363733	Hs.1032	NM_002909:Homo sapiens regenerating isle	7.94
	422357	AF016272	Hs.115418	NM_004062:Homo sapiens cadherin 16, KSP-	7.78
	420737	L08096	Hs.99899	NM_001252:Homo sapiens tumor necrosis fa	7.78
	409745	AA077391		AA077391:7B14E12 Chromosome 7 Fetal Brai	7.74
10	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	7.32
	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	7.20
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	7.03
	419508	AW997938	Hs.90786	Hs.90786:ATP-binding cassette, sub-famil	6.57
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	6.36
15	436895	AF037335	Hs.5338	NM_001218:Homo sapiens carbonic anhydras	6.31
	431842	NM_005764	Hs.271473	NM_005764:Homo sapiens epithelial protei	6.20
	430014	H59354	Hs.374303	Hs.374303:hypothetical protein MGC20576	6.20
	423803	NM_005709	Hs.132945	NM_005709:Homo sapiens PDZ-73 protein (P	6.19
	434779	AF153815	Hs.50151	Hs.50151:potassium inwardly-rectifying c	6.11
20	435767	H73505	Hs.117874	Hs.117874:ESTs	6.08
	422664	AA316933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.02
	425280	U31519	Hs.1872	Hs.1872:phosphoenolpyruvate carboxylase	5.81
	426559	AB001914	Hs.170414	NM_002570:Homo sapiens paired basic amin	5.73
25	451564	AU076698	Hs.132760	NM_001467:Homo sapiens glucose-6-phospha	5.69
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	5.68
	444151	AW972917	Hs.128749	Hs.128749:alpha-methylacyl-CoA racemase	5.66
	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
	432579	AF043244	Hs.278439	NM_003946:Homo sapiens nucleolar protein	5.45
30	448733	NM_005629	Hs.187958	NM_005629:Homo sapiens solute carrier fa	5.42
	446650	AB016625	Hs.15813	NM_003060:Homo sapiens solute carrier fa	5.36
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cD: FLJ21909 fis,	5.35
	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamyltransferase 1	5.32
	423081	AF262992	Hs.123159	Hs.123159:sperm associated antigen 4	5.30
	421893	NM_001078	Hs.109225	NM_001078:Homo sapiens vascular cell adh	5.23
35	435886	BE265839	Hs.12126	Hs.12126:hepatocellular carcinoma-associ	5.20
	410276	AI554545	Hs.359201	Hs.359201:ESTs	5.20
	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygase (dec	5.14
	446404	AA019961	Hs.26216	Hs.26216:Homo sapiens cD: FLJ22811 fis,	5.13
40	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.09
	449444	AWB18436	Hs.351306	NM_004696:Homo sapiens solute carrier fa	5.05
	438106	BE245551	Hs.6079	NM_014863:Homo sapiens B cell RAG associ	5.02
	400419	AF084545		AF084545:Homo sapiens versican Vint isof	5.01
	453920	AI133148	Hs.36602	NM_000204:Homo sapiens I factor (complem	4.99
45	447881	BE620886	Hs.355279	Hs.355279:Homo sapiens cD FLJ23711 fis,	4.97
	422253	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
	439024	R96696	Hs.35598	Hs.35598:ESTs	4.88
	414799	AI752416	Hs.77326	NM_000598:Homo sapiens insulin-like grow	4.80
	426530	U24578	Hs.278625	NM_000592:Homo sapiens complement compon	4.77
	410055	AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4.72
50	404240				4.71
	414617	AI339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.68
	448249	AW855331	Hs.337124	Hs.337124:ESTs	4.67
	447818	W79940	Hs.21906	Hs.21906:Homo sapiens clone 24670 mR seq	4.66
55	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.66
	422424	AI186431	Hs.296638	NM_004864:Homo sapiens prostate differen	4.62
	417335	R70429	Hs.81988	NM_001343:Homo sapiens disabled homolog	4.62
	425873	NM_013390	Hs.160417	NM_013390:Homo sapiens transmembrane pro	4.58
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.58
60	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.56
	414763	U97276	Hs.77266	NM_002826:Homo sapiens quiescin Q6 (OSCN	4.48
	443358	H65417	Hs.17757	Hs.17757:pleckstrin homology domain-cont	4.45
	440091	AI767388	Hs.37890	Hs.37890:Homo sapiens, clone IMAGE:48275	4.43
	447131	NM_004585	Hs.17466	NM_004585:Homo sapiens retinoic acid rec	4.43
65	406973	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.42
	427740	BE242604	Hs.180616	NM_005505:Homo sapiens CD36 antigen (col	4.40
	435258	AW867491	Hs.107125	Hs.107125:plasmalemma vesicle associated	4.38
	452884	C05964	Hs.31841	Hs.31841:ESTs	4.37
	444006	BE395085	Hs.10086	NM_016639:Homo sapiens type I transmembr	4.36
	422627	BE336857	Hs.118787	NM_000358:Homo sapiens transforming grow	4.35
70	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.34
	419011	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	4.34
	404277				4.33
	435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
75	431779	AW971178	Hs.268571	NM_001645:Homo sapiens apolipoprotein C-	4.29
	406645	M57466	Hs.814	Hs.814:major histocompatibility complex,	4.28
	421485	AA243499	Hs.104800	Hs.104800:hypothetical protein FLJ10134	4.26
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	4.25
	407910	AA650274	Hs.41296	NM_013281:Homo sapiens fibronectin leuci	4.22
80	438030	X98427	Hs.122634	Hs.122634:ESTs	4.22
	430661	AC005551	Hs.130714	Hs.130714:ESTs, Moderately similar to AF	4.21
	444381	BE387335	Hs.283713	Hs.283713:hypothetical protein BC014245	4.20
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-II	4.16
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	4.15
	418323	NM_002118	Hs.1162	NM_002118:Homo sapiens major histocompat	4.12

	449853	AF006823	Hs.24040	NM_002246:Homo sapiens potassium channel	4.11
	415198	AW009480	Hs.943	NM_004221:Homo sapiens tural killer cell	4.11
	418751	BE389014	Hs.372548	Hs.372548:phosphoinositide-3-kinase, regul	4.09
	414166	AW888941	Hs.75789	NM_006096:Homo sapiens N-myc downstream	4.07
5	424125	M31669	Hs.1735	Hs.1735:inhibin, beta B (activin AB beta	4.00
	416926	H03109	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.92
	419175	AW270037	Hs.362996	Hs.362996:KIAA0779 protein	3.92
	424218	AF031824	Hs.143212	NM_003650:Homo sapiens cystatin F (leuko	3.91
	412870	N22788	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.88
10	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.87
	446872	X97058	Hs.16362	NM_004154:Homo sapiens pyrimidineric re	3.87
	449961	AW265634	Hs.133100	Hs.133100:ESTs	3.87
	424517	AI539443	Hs.137447	Hs.137447:Homo sapiens cD FLJ12169 fis,	3.86
	425262	D87119	Hs.155418	Hs.155418:GSJ955 protein	3.83
15	443639	BE269042	Hs.9661	NM_002801:Homo sapiens proteasome (proso	3.82
	448133	AA723157	Hs.73769	NM_000802:Homo sapiens folate receptor 1	3.81
	418030	BE207573	Hs.83321	Hs.83321:neuromedin B	3.81
	412939	AW411491	Hs.75069	NM_005412:Homo sapiens serine hydroxymet	3.80
	409162	M25530	Hs.50868	NM_002555:Homo sapiens solute carrier fa	3.79
20	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.78
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.77
	430413	AW842182	Hs.241392	NM_002985:Homo sapiens small inducible c	3.76
	422282	AF019225	Hs.114309	Hs.114309:apolipoprotein L, 1	3.76
	420747	BE294407	Hs.99910	Hs.99910:phosphofructokinase, platelet	3.76
25	414875	H42679	Hs.77522	NM_006120:Homo sapiens major histocompat	3.75
	418793	AW382987	Hs.88474	Hs.88474:prostaglandin-endoperoxide synt	3.74
	446291	BE397753	Hs.14623	NM_006332:Homo sapiens interferon, gamma	3.71
	417289	D86962	Hs.81875	Hs.81875:growth factor receptor-bound pr	3.69
30	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	3.68
	448569	BE382657	Hs.21486	NM_007315:Homo sapiens sigl transducer a	3.68
	437270	R18087	Hs.323769	Hs.323769:cisplatin resistance related p	3.67
	408452	AA054683	Hs.192455	Hs.192455:ESTs, Moderately similar to hy	3.67
	443986	AI381750	Hs.283437	Hs.283437:HTGN29 protein	3.66
35	418869	AW516565	AW516565:xq01d05.x1 Soares_NHCeC_cervica	3.65	
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.62
	428699	AW578252	Hs.190161	NM_014020:Homo sapiens LR8 protein (LR8)	3.62
	418299	AA279530	Hs.83968	NM_000211:Homo sapiens integrin, beta 2	3.61
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
40	415765	NM_005424	Hs.78824	NM_005424:Homo sapiens tyrosine kinase wit	3.58
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.57
	424893	AW295112	Hs.153648	Hs.153648:protein tyrosine phosphatase,	3.57
	426046	AA833655	Hs.206868	Hs.206868:Homo sapiens cD FLJ14056 fis,	3.57
	424415	NM_001975	Hs.146580	NM_001975:Homo sapiens enolase 2, (gamma	3.57
45	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.56
	443834	AI741510	Hs.173548	Hs.173548:ESTs	3.54
	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53
	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52
50	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	3.52
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	3.50
	414311	AI693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50
	415149	X12451	Hs.78056	NM_001912:Homo sapiens cathepsin L (CTSL	3.50
	424321	W74048	Hs.1765	Hs.1765:lymphocyte-specific protein tyro	3.49
55	414825	X06370	Hs.77432	NM_005228:Homo sapiens epidermal growth	3.48
	408194	AA601038	Hs.191797	Hs.191797:ESTs	3.48
	410600	AW575742	Hs.351676	Hs.351676:ESTs, Weakly similar to T02670	3.47
	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47
60	436856	AI469355	Hs.127310	Hs.127310:hypothetical protein BC014917	3.47
	419660	BE280337	Hs.194693	NM_003982:Homo sapiens solute carrier fa	3.47
	413566	AW604451	Hs.285814	Hs.285814:growth factor receptor-bound p	3.47
	412104	AW205197	Hs.240951	Hs.240951:ked cuticle homolog 2 (Drosoph	3.46
	444488	AW192879	Hs.355660	Hs.355660:peptide-histidine transporter	3.46
	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
65	412276	BE262621	Hs.73798	NM_002415:Homo sapiens macrophage migrat	3.45
	449338	H73444	Hs.394	NM_001124:Homo sapiens adrenomedullin (A	3.44
	430304	AL122071	Hs.238927	Hs.238927:Homo sapiens mR: cD DKFZp434H1	3.43
	415388	AF018081	Hs.78409	(locuslink)NM_030582:Homo sapiens collag	3.43
	432210	AI567421	Hs.273330	Hs.273330:agrin	3.43
	418177	N44967	Hs.351554	Hs.351554:Homo sapiens cD FLJ32092 fis,	3.42
70	414888	AL039185	Hs.77558	Hs.77558:thyroid hormone receptor intera	3.42
	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.41
	414803	X03100	Hs.914	Hs.914:major histocompatibility complex,	3.41
	419201	M22324	Hs.1239	NM_001150:Homo sapiens alanyl (membrane)	3.41
	445139	AB037848	Hs.12365	Hs.12365:syplotagrin XIII	3.41
75	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	3.40
	439737	AI751438	Hs.41271	Hs.41271:Homo sapiens mR full length ins	3.39
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.39
	431590	AB037789	Hs.263395	Hs.263395:sema domain, transmembrane dom	3.38
80	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.36
	416700	AW498958	Hs.343475	NM_001909:Homo sapiens cathepsin D (lyso	3.36
	440516	S42303	Hs.161	NM_001792:Homo sapiens cadherin 2, type	3.35
	423720	AL044191	Hs.23388	Hs.23388:hypothetical protein DKFZp434F0	3.32

	421902	BE392717		BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	409220	BE243323	Hs.51233	Hs.51233:tumor necrosis factor receptor	3.32
	421502	AF111856	Hs.105039	NM_006424:Homo sapiens solute carrier fa	3.32
5	416729	U46165	Hs.1027	NM_004165:Homo sapiens Ras-related assoc	3.30
	430302	AL137502	Hs.238679	Hs.238679:Rag D protein	3.30
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cD FLJ14761 fs,	3.29
	406825	AI982529	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.29
	446272	BE268912	Hs.14501	NM_005335:Homo sapiens hematopoietic cel	3.28
10	437145	AF007216	Hs.5462	NM_003759:Homo sapiens solute carrier fa	3.27
	444071	AI627808	Hs.110524	Hs.110524:ESTs	3.27
	414662	AL036058	Hs.76807	Hs.76807:major histocompatibility comple	3.27
	436576	AI458213	Hs.77542	Hs.77542:ESTs, Weakly similar to S26650	3.26
	424675	NM_005512	Hs.151641	NM_005512:Homo sapiens glycoprotein A re	3.25
15	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.25
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.25
	414788	X78342	Hs.77313	NM_003674:Homo sapiens cyclin-dependent	3.25
	414249	AI797994	Hs.279929	Hs.279929:gp25L2 protein	3.24
	430396	D49742	Hs.241363	NM_004132:Homo sapiens hyaluron binding	3.23
20	424456	AA341017	Hs.25549	Hs.25549:hypothetical protein FLJ20898	3.23
	452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor like	3.22
	425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
	416033	NM_012201	Hs.78979	NM_012201:Homo sapiens golgi apparatus p	3.19
	450931	N25156	Hs.25648	Hs.25648:tumor necrosis factor receptor	3.19
25	428065	AI634046	Hs.157313	Hs.157313:ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
	439318	AW837046	Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.17
	409936	AK001691	Hs.57655	Hs.57655:dudulin 2	3.16
30	436001	AW903849	Hs.173840	Hs.173840:similar to endothelial cell-se	3.16
	451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
	420256	U84722	Hs.76206	NM_001795:Homo sapiens cadherin 5, type	3.16
	407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.15
	428593	AW207440	Hs.185973	NM_003676:Homo sapiens degenerative sper	3.15
35	410026	AI912061	Hs.55016	Hs.55016:EPS8-related protein 2	3.15
	445333	BE537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
	448143	AF039704	Hs.20478	NM_000391:Homo sapiens ceroid-lipofuscin	3.14
	423007	AA320134	Hs.196029	Hs.196029:Homo sapiens mR for KIAA1657 p	3.14
	416511	NM_006762	Hs.79356	NM_006762:Homo sapiens Lysosomal-associa	3.13
40	439237	AW408158	Hs.318893	Hs.318893:ESTs, Weakly similar to Z195_H	3.13
	446899	NM_005397	Hs.16426	NM_005397:Homo sapiens podocalyxin-like	3.13
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.13
	434398	AA121098	Hs.3838	NM_006622:Homo sapiens serum-inducible k	3.12
	441283	AA927670	Hs.131704	Hs.131704:ESTs	3.12
45	418945	BE246762	Hs.89499	NM_000698:Homo sapiens arachidate 5-lipo	3.12
	418458	AA332941	Hs.85226	NM_000235:Homo sapiens lipase A, lysosom	3.12
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.11
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.11
50	411089	AA456454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
	432990	AL036071	Hs.279899	NM_003820:Homo sapiens tumor necrosis fa	3.11
	425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine	3.10
	443601	AI078554	Hs.42658	Hs.42658:Homo sapiens cD FLJ30167 fs, c	3.10
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	3.10
	413672	BE156536	Hs.353632	Hs.353632:ESTs, Moderately similar to hy	3.09
55	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09
	414586	AA306160	Hs.16488	NM_007298:Homo sapiens lymphocyte cytosol	3.08
	423712	W46802	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08
	438552	AJ245820	Hs.6314	NM_012410:Homo sapiens type I transmembr	3.06
	448364	T08958	Hs.297214	Hs.297214:HSPC141 protein	3.06
60	426437	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06
	437679	NM_014214	Hs.5753	NM_014214:Homo sapiens inositol(myo)-1(o	3.06
	422262	AL022315	Hs.113987	NM_006498:Homo sapiens lecltin, galactosi	3.06
	410480	R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
65	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
	453613	F06838	Hs.374476	Hs.374476:ESTs	3.05
	408051	AI623351	Hs.172148	Hs.172148:ESTs	3.05
	432278	AL137506	Hs.274256	Hs.274256:hypothetical protein FLJ23563	3.04
	407949	W21874	Hs.247057	Hs.247057:ESTs, Weakly similar to Z10926	3.04
70	418090	U57059	Hs.83429	NM_003810:Homo sapiens tumor necrosis fa	3.04
	433165	AA578904	Hs.292437	Hs.292437:ESTs	3.03
	425809	AA370362	Hs.57958	Hs.57958:EGF-TM7-latrophiin-related pro	3.03
	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447831	AI433293	Hs.164115	Hs.164115:ESTs	3.02
75	413278	BE563085	Hs.833	NM_005101:Homo sapiens interferon-stimul	3.01
	418870	AF147204	Hs.89414	Hs.89414:chemokine (C-X-C motif), recept	3.00
	456376	AA663904	Hs.89862	Hs.89862:TNFRSF1A-associated via death d	3.00
	439738	BE246502	Hs.95598	Hs.95598:sema domain, immunoglobulin doma	3.00
	444416	AW288085	Hs.11156	NM_016494:Homo sapiens hypothetical prot	3.00
80	406656	M16714	Hs.89643	Hs.89643:transketolase (Wernicke-Korsako	3.00
	406826	AW516005	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
	421742	AW970004	Hs.107528	NM_016108:Homo sapiens androgen induced	2.99
	406824	AW515961	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99

	435605	AF151815	Hs.4973	NM_015680:Homo sapiens hypothetical prot	2.98
	410491	AA465131	Hs.64001	Hs.64001:Homo sapiens clone 25218 mR seq	2.98
	427648	AI376722	Hs.180062	NM_004159:Homo sapiens proteasome (proso	2.98
	411125	AA151647	Hs.68877	NM_000101:Homo sapiens cytochrome b-245,	2.98
5	435550	AI224456	Hs.324507	Hs.324507: hypothetical protein FLJ20986	2.98
	429373	NM_014694	Hs.200594	NM_014694:Homo sapiens KIAA0605 gene pro	2.98
	445701	AF055581	Hs.13131	NM_005475:Homo sapiens lymphocyte adapto	2.97
	414649	AI672727	Hs.76753	NM_000118:Homo sapiens endoglin (Osler-R	2.97
	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.97
10	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.97
	407792	AI077715	Hs.39384	NM_014344:Homo sapiens four jointed box	2.97
	445707	AI248720	Hs.114390	Hs.114390:ESTs	2.96
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
	418478	U38945	Hs.1174	Hs.1174:cyclin-dependent kinase inhibitor	2.95
15	411441	AL042355	Hs.70202	Hs.70202:WD repeat domain 10	2.95
	443426	AF098158	Hs.9329	Hs.9329:chromosome 20 open reading frame	2.94
	450876	AF189062	Hs.285976	Hs.285976:LAG1 longevity assurance homol	2.94
	426359	AA376409	Hs.10862	Hs.10862:Homo sapiens cD: FLJ23313 fis,	2.94
	425421	L11669	Hs.157145	NM_001120:Homo sapiens tetracycline tran	2.93
20	449879	H03573	Hs.287830	Hs.287830:Homo sapiens mR: cD DKFZp434E1	2.93
	454075	R43826	Hs.16313	Hs.16313:Krueppel-like zinc finger protei	2.93
	421595	AB014520	Hs.301685	Hs.301685:KIAA0620 protein	2.93
	457949	W69171	Hs.334814	Hs.334814: hypothetical protein FLJ14868	2.92
	443987	AW163123	Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
25	430259	BE550182	Hs.375142	Hs.375142:RafGEF-like protein 3, mouse h	2.92
	415906	AI751357	Hs.288741	Hs.288741:Homo sapiens cD: FLJ22256 fis,	2.91
	429762	AI346255	Hs.216354	NM_006913:Homo sapiens ring finger prote	2.91
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91
30	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.91
	427080	AW068287	Hs.301175	NM_002872:Homo sapiens ras-related C3 bo	2.91
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxase 2 (PON2	2.90
	431476	BE612705	Hs.256697	Hs.256697:histidine triad nucleotide bin	2.89
	406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
35	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cD FLJ31548 fis, c	2.89
	456362	AW973003	Hs.179909	Hs.179909:nuclear receptor coactivator 6	2.88
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	2.88
	456974	M12529	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.88
	418174	L20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88
	446055	AI815981	Hs.12909	Hs.12909:mucopolip 1	2.88
40	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EF1),	2.87
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87
	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143	AW747996	Hs.160999	Hs.160999:ESTs, Weakly similar to I78885	2.87
45	407151	H25836	Hs.301527	Hs.301527:ESTs, Moderately similar to un	2.86
	449349	AI825386	Hs.352579	Hs.352579:Homo sapiens, chromosome 20 op	2.86
	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86
	417355	D13168	Hs.82002	Hs.82002:endothelin receptor type B	2.86
50	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	2.86
	408877	AA479033	Hs.130315	Hs.130315:ESTs	2.85
	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
	412014	AI620650	Hs.43761	Hs.43761:gap junction protein, alpha 7,	2.84
	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	2.84
55	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.84
	439941	AI392640	Hs.18272	Hs.18272:solute carrier family 38, membe	2.84
	436496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84
	422100	AI096988	Hs.111554	NM_005737:Homo sapiens ADP-ribosylation	2.83
	439730	AF035292	Hs.6654	Hs.6654:KIAA0657 protein	2.83
60	447217	BE465754	Hs.17778	NM_003872:Homo sapiens neuropilin 2 (NRP	2.83
	428343	AL043021	Hs.12705	Hs.12705:similar to HYPOTHETICAL 43.1 KD	2.82
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mR: cD DKFZp564O24	2.82
	415523	AL042003	Hs.296847	NM_003119:Homo sapiens spastic paraplegi	2.81
	439668	AI091277	Hs.302634	Hs.302634:frizzled homolog 8 (Drosophila	2.81
65	414570	Y00285	Hs.76473	NM_000876:Homo sapiens insulin-like grow	2.80
	426535	AU077012	Hs.288582	NM_006287:Homo sapiens tissue factor pat	2.80
	409649	AA159216	Hs.55505	Hs.55505: hypothetical protein FLJ20442	2.80
	406655	M21533	Hs.277477	Hs.277477:major histocompatibility compl	2.79
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytooso	2.79
70	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cD FLJ14201 fis,	2.78
	451356	AA748418	Hs.164577	Hs.164577:ESTs	2.78
	450708	AA376654	Hs.350065	Hs.350065:Homo sapiens cD FLJ30634 fis,	2.78
	433681	AI004377	Hs.200360	Hs.200360:Homo sapiens cD FLJ13027 fis,	2.77
	442599	AF078037	Hs.324051	NM_006663:Homo sapiens RelA-associated i	2.77
75	414509	AW161311	Hs.76294	NM_001780:Homo sapiens CD63 antigen (mel	2.76
	431394	AK000692	Hs.252351	Hs.252351:HERV-H LTR-associating 2	2.76
	417331	AW411297	Hs.81972	Hs.81972:SHC (Src homology 2 domain cont	2.76
	415995	NM_004573	Hs.355888	NM_004573:Homo sapiens phospholipase C,	2.75
	414911	NM_000107	Hs.77602	NM_000107:Homo sapiens damage-specific D	2.75
80	425976	C75094	Hs.334514	Hs.334514:chromosome 6 open reading fram	2.75
	407893	BE408359	Hs.43621	Hs.43621: hypothetical protein MBC3205	2.75
	407903	AI287341	Hs.154029	Hs.154029:bHLH factor Hes4	2.75
	416062	AA724811	Hs.334791	Hs.334791:similar to neurol tetraspanin	2.75
	428494	AA233439	Hs.184634	Hs.184634: hypothetical protein FLJ20005	2.75

	421506	BE302796	Hs.105097	NM_003258:Homo sapiens thymidine kise 1,	2.74
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.74
	424527	AW138558	Hs.334873	Hs.334873:carboxypeptidase M	2.74
5	439578	AW263124	Hs.350547	Hs.350547:nuclear receptor co-repressor/	2.74
	425188	AK002052	Hs.155071	Hs.155071:chromosome 20 open reading fra	2.74
	428013	AF151020	Hs.181444	NM_016456:Homo sapiens hypothetical prot	2.73
	439333	AW384710	Hs.132986	Hs.132986:Homo sapiens cD FLJ31588 fis,	2.73
	450935	BE514743	Hs.355753	NM_005851:Homo sapiens tumor suppressor	2.73
10	421532	AW138207	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.73
	440502	AI824113	Hs.78281	Hs.78281:regulator of G-protein sigling	2.73
	444981	AW855398	Hs.12210	Hs.12210:tumor endothelial marker 6	2.72
	439219	N33883	Hs.41322	Hs.41322:ESTs	2.72
	416847	L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
15	433179	AW362945	Hs.162459	Hs.162459:ESTs	2.72
	424528	AW073971	Hs.238954	Hs.238954:ESTs, Weakly similar to puta	2.71
	411213	AA676939	Hs.69285	NM_003873:Homo sapiens neuropilin 1 (NRP	2.70
	433012	NM_004045	Hs.279910	NM_004045:Homo sapiens ATX1 antioxidant	2.70
	425345	AU077297	Hs.155894	NM_002827:Homo sapiens protein tyrosine	2.69
20	428923	BE047698	Hs.188785	Hs.188785:ESTs	2.69
	427923	AW274357	Hs.301406	Hs.301406:hypothetical protein PP3501	2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.68
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.68
	416207	NM_014745	Hs.79077	NM_014745:Homo sapiens KIAA0233 gene pro	2.68
25	420372	AW960049	Hs.293660	Hs.293660:gene overexpressed in astrocyt	2.68
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	2.67
	425069	AA687465	Hs.298184	Hs.298184:potassium voltage-gated channe	2.67
	418558	AW082266	Hs.86131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67
	426251	M24283	Hs.168383	NM_000201:Homo sapiens intercellular adh	2.66
30	406701	AA780613	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.66
	431681	AK000378	Hs.267566	Hs.267566:hypothetical protein FLJ20371	2.66
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
	433101	AW572317	Hs.12082	Hs.12082:TIGA1	2.66
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	2.66
35	427868	AI360119.comp	Hs.181013	NM_002629:Homo sapiens phosphoglycerate	2.66
	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, alpha 2	2.66
	424762	AL119442	Hs.183684	Hs.183684:eukaryotic translation initiat	2.66
	422048	NM_012445	Hs.288126	NM_012445:Homo sapiens spondin 2, extrac	2.65
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.65
40	450184	W31096	Hs.237617	Hs.237617:dipeptidylpeptidase 9	2.65
	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein	2.65
	414217	AI309298	Hs.279898	Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SLIT-ROBO Rho GTPase-activating	2.64
45	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gene pro	2.63
	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein BC011406	2.63
	430223	NM_002514	Hs.235835	NM_002514:Homo sapiens nephroblastoma ov	2.63
	417526	AA568906	Hs.82240	NM_004177:Homo sapiens syntaxin 3A (STX3	2.63
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.62
50	449843	R85337	Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62
	417389	BE260964	Hs.82045	NM_002391:Homo sapiens midline (neurite	2.62
	446312	BE087853	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.62
	435099	AC004770	Hs.4756	Hs.4756:flap structure-specific endonucle	2.62
	417920	S47833	Hs.82927	NM_004037:Homo sapiens adenosine monopho	2.62
55	435702	AI033647	Hs.121001	Hs.121001:Homo sapiens, clone MGC:4552 I	2.62
	422959	AV647015	Hs.349256	Hs.349256:paired immunoglobulin-like rec	2.62
	419938	AU076772	Hs.1279	NM_001733:Homo sapiens complement compon	2.62
	450954	AI904740	Hs.25691	NM_005856:Homo sapiens receptor (calcitri	2.61
	421753	BE314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fam	2.61
60	443577	AI078033	Hs.177170	Hs.177170:ESTs, Weakly similar to ALU8_H	2.61
	453886	R66282	Hs.20247	Hs.20247:ESTs	2.61
	421883	X55079	Hs.1437	NM_000152:Homo sapiens glucosidase, alph	2.60
	440457	BE387593	Hs.21321	Hs.21321:granule cell differentiation pr	2.60
	410295	AA741357	Hs.356624	Hs.356624:ESTs	2.59
65	420679	X57152	Hs.99853	NM_001436:Homo sapiens fibrillarin (FBL)	2.59
	451558	NM_001089	Hs.26630	NM_001089:Homo sapiens ATP-binding casse	2.59
	444672	Z95636	Hs.11669	Hs.11669:laminin, alpha 5	2.59
	408669	AI493591	Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	426194	T50872	Hs.2001	Hs.2001:thromboxane A synthase 1 (plate	2.59
70	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	2.59
	456371	S76825	Hs.89695	Hs.89695:insulin receptor	2.59
	429098	AF030249	Hs.196176	NM_001398:Homo sapiens enoyl Coenzyme A	2.59
	414443	AU077268	Hs.76144	NM_002609:Homo sapiens platelet-derived	2.59
	428484	AF104032	Hs.184601	NM_003486:Homo sapiens solute carrier fa	2.59
75	453309	AI791809	Hs.32949	NM_005218:Homo sapiens defensin, beta 1	2.58
	412867	AU076861	Hs.74637	NM_003217:Homo sapiens testis enhanced g	2.58
	432827	Z68128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
	412669	AW880841	Hs.96908	NM_006034:Homo sapiens p53-induced prote	2.58
80	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.58
	452866	R26969	Hs.268016	Hs.268016:Homo sapiens cD: FLJ21243 fis,	2.57
	435129	AI381659	Hs.267086	Hs.267086:ESTs	2.57
	424482	BE268621	Hs.149155	NM_003374:Homo sapiens voltage-dependent	2.57
	410494	M36564	Hs.64016	NM_000313:Homo sapiens protein S (alpha)	2.56
	433895	AI287912	Hs.3628	NM_004834:Homo sapiens myogen-activated	2.56

	442566	R37337	Hs.12111	Hs.12111:ESTs	2.56
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
	442622	NM_000435	Hs.8546	NM_000435:Homo sapiens Notch homolog 3 (2.56
5	430346	AK000331	Hs.297641	Hs.297641:retinoblastoma-associated fact	2.55
	419344	U94905	Hs.277445	Hs.277445:diacylglycerol kise, zeta (104	2.55
	426500	NM_014538	Hs.170156	NM_014538:Homo sapiens KIAA0450 gene pro	2.55
	408048	NM_007203	Hs.42322	NM_007203:Homo sapiens A kise (PRKA) anc	2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-like	2.54
10	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.54
	422451	AA310753	Hs.42491	Hs.42491:ESTs, Moderately similar to hyp	2.53
	435906	AI686379	Hs.110796	Hs.110796:SAR1 protein	2.53
	400231				2.53
15	417849	AW291587	Hs.82733	NM_007361:Homo sapiens nidogen 2 (NID2),	2.53
	427380	NM_005534	Hs.177559	NM_005534:Homo sapiens interferon gamma	2.52
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.52
	438000	AI825880	Hs.5985	Hs.5985:non-kise Cdc42 effector protein	2.52
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) protease i	2.52
20	422396	W21872	Hs.7907	Hs.7907:L-fucose kise	2.52
	420787	AA564248	Hs.351292	Hs.351292:Homo sapiens cD FLJ32605 fis,	2.51
	430590	AW383947	Hs.246381	NM_001251:Homo sapiens CD68 antigen (CD6	2.51
	447026	BE313144	Hs.324844	Hs.324844:hypothetical protein IMAGE3455	2.51
	439223	AW238299	Hs.250618	Hs.250618:UL16 binding protein 2	2.50
25	435151	AA348482	Hs.4788	Hs.4788:nicastrin	2.50
	448202	AB002292	Hs.20695	NM_014629:Homo sapiens Rho guanine nucle	2.50
	449943	AF104266	Hs.24212	Hs.24212:latrophilin	2.50
	425743	BE396495	Hs.159428	Hs.159428:BCL2-associated X protein	2.50
	444681	AJ243937	Hs.288316	Hs.288316:chromosome 6 open reading fram	2.50
30	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.50
	425865	D63476	Hs.172813	NM_003899:Homo sapiens Rho guanine nucle	2.50
	432306	Y18207	Hs.303090	NM_005398:Homo sapiens protein phosphata	2.49
	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kise C su	2.49
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	2.49
35	419493	AF001212	Hs.90744	NM_002815:Homo sapiens proteasome (proso	2.49
	422530	AW972300	Hs.118110	NM_004335:Homo sapiens bone marrow strom	2.48
	442821	BE391929	Hs.8752	NM_014255:Homo sapiens transmembrane pro	2.48
	416919	T97839	Hs.80464	NM_006402:Homo sapiens hepatitis B virus	2.48
	443105	X96753	Hs.9004	NM_001897:Homo sapiens chondroitin sulfa	2.48
40	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
	428028	U52112	Hs.182018	NM_001569:Homo sapiens interleukin-1 rec	2.47
	424307	AW293399	Hs.356377	Hs.356377:Homo sapiens, clone IMAGE.3633	2.46
	434511	R28982	Hs.18106	Hs.18106:ESTs, Weakly similar to T06291	2.46
	454390	AB020713	Hs.56966	Hs.56966:KIAA0906 protein	2.46
45	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.46
	424673	AA345051	Hs.294092	Hs.294092:Homo sapiens mR full length in	2.46
	422003	AA361760	Hs.296326	Hs.296326:ESTs, Weakly similar to A33533	2.46
	432126	AA865239	Hs.37196	Hs.37196:putative G protein coupled rece	2.46
	445937	AI452943	Hs.321231	NM_003779:Homo sapiens UDP-Gal:betaGlc	2.46
	409354	N68188	Hs.159472	Hs.159472:Homo sapiens cD: FLJ22224 fis,	2.46
50	401179				2.46
	418151	AA854238.comp	Hs.83583	NM_005731:Homo sapiens actin related pro	2.45
	422648	D86983	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (pref	2.45
55	431222	X56777	Hs.273790	NM_007155:Homo sapiens zo pellucida glyc	2.45
	411529	AA430348	Hs.317596	Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45
	426825	AL133415	Hs.297753	NM_003380:Homo sapiens vimentin (VIM), m	2.45
	422242	AJ251760	Hs.273385	NM_016592:Homo sapiens GS complex locus	2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44
60	426410	BE298446	Hs.305890	Hs.305890:BCL2-like 1	2.44
	421064	AI245432	Hs.101382	NM_006291:Homo sapiens tumor necrosis fa	2.44
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokise 2 (HK2),	2.44
	424398	BE397787	Hs.146393	NM_014685:Homo sapiens homocysteine-indu	2.44
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	2.44
65	426031	AA295251	Hs.166066	Hs.166066:cisplatin resistance associate	2.43
	409817	BE295464	Hs.56607	Hs.56607:Williams-Beuren syndrome chromo	2.43
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.43
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	2.43
	429332	AF030403	Hs.199263	NM_013233:Homo sapiens serine threonine	2.43
70	425923	NM_005026	Hs.162808	NM_005026:Homo sapiens phosphoinositide-	2.43
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.43
	433339	AF019226	Hs.8036	Hs.8036:RAB3D, member RAS oncogene famil	2.42
	420539	AA282735	Hs.44004	Hs.44004:AD031 protein	2.42
	413243	AA769266	Hs.193657	Hs.193657:ESTs	2.42
75	435029	AF167706	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
	422374	AW732869	Hs.1519	Hs.1519:protein kise, cAMP-dependent, re	2.42
	444501	AW247624	Hs.11342	NM_004148:Homo sapiens ninjurin 1 (NINJ1	2.42
	414919	AW087337	Hs.194461	Hs.194461:ESTs	2.42
	419355	AA428520	Hs.90061	NM_006667:Homo sapiens progesterone rece	2.42
80	436042	AF284422	Hs.119178	Hs.119178:cation-chloride cotransporter-	2.42
	418245	AA088767	Hs.83883	Hs.83883:transmembrane, prostate androge	2.42
	444215	AB033075	Hs.10669	Hs.10669:development and differentiation	2.41
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.41
	423701	AA329856	Hs.143022	Hs.143022:ESTs	2.41

5	441783	BE313412	Hs.7961	Hs.7961:Homo sapiens clone 25012 mR sequ	2.41
	428072	BE258602	Hs.182366	NM_015292:Homo sapiens heat shock protei	2.41
	434599	AB002313	Hs.3989	Hs.3989:plexin B2	2.40
	442351	W52642	Hs.8261	Hs.8261:SPRY domain-containing SOCS box	2.40
	407894	AJ278313	Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449	W16752	Hs.32981	Hs.32981:sema domain, immunoglobulin dom	2.40
	408688	AI634522	Hs.152925	Hs.152925:KIAA1268 protein	2.40
	422448	AW372922	Hs.116774	Hs.116774:integrin, alpha 1	2.40
10	416269	AA177138	Hs.161671	Hs.161671:ESTs	2.39
	452679	Z42387	Hs.83883	Hs.83883:transmembrane, prostate androge	2.39
	432981	NM_002733	Hs.3136	NM_002733:Homo sapiens protein kise, AMP	2.38
	419846	NM_015977	Hs.285681	Hs.285681:Williams Beuren syndrome chrom	2.38
	422110	AJ376736	Hs.111779	Hs.111779:secreted protein, acidic, cyst	2.38
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.38
15	433969	AW207279	Hs.271786	Hs.271786:ESTs, Weakly similar to PC4395	2.37
	451267	AI033894	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.37
	447526	AL048753	Hs.303649	NM_002982:Homo sapiens small inducible c	2.37
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	2.37
20	420255	NM_007289	Hs.1298	NM_007289:Homo sapiens membrane metallo-	2.37
	409274	NM_003930	Hs.52644	NM_003930:Homo sapiens src family associ	2.36
	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.36
	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) protease i	2.36
	408212	AA297567	Hs.43728	NM_015696:Homo sapiens weakly similar to	2.36
25	430478	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L,	2.36
	405102				2.35
	423583	AL122055	Hs.129836	Hs.129836:KIAA1028 protein	2.35
	426125	X87241	Hs.166994	NM_005245:Homo sapiens FAT tumor suppres	2.35
30	425204	NM_002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete	2.35
	421079	AW404994	Hs.101695	Hs.101695:NCK adaptor protein 2	2.35
	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
	412958	BE391579	Hs.75087	NM_006712:Homo sapiens FAST kise (FASTK)	2.34
	430363	M28713	Hs.274464	NM_000398:Homo sapiens diaphorase (DH) (2.34
35	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (D)	2.34
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso)	2.34
	449027	AJ271216	Hs.22880	Hs.22880:dipeptidylpeptidase III	2.34
	429457	BE243065	Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	417709	D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
40	412805	AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.34
	430702	U56979	Hs.278568	NM_000186:Homo sapiens H factor 1 (compl	2.33
	456804	AI421645	Hs.139851	NM_001233:Homo sapiens caveolin 2 (CAV2)	2.33
	453648	W21493	Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33
45	450812	AB002360	Hs.25515	Hs.25515:MCF-2 cell line derived transfo	2.33
	402575				2.33
	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32
	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine	2.32
50	442968	AK000606	Hs.8868	NM_004871:Homo sapiens golgi SP receptor	2.32
	410639	BE269047	Hs.65234	Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32
	450160	BE048099	Hs.183738	Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32
	407223	H96850		H96850:yo03b12.s1 Soares melanocyte 2N6H	2.32
55	426780	BE242284	Hs.172199	NM_001114:Homo sapiens adenylate cyclase	2.32
	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
	453107	NM_016113	Hs.279746	NM_016113:Homo sapiens transient recepto	2.31
	422963	M79141	Hs.13234	Hs.13234:ESTs, Weakly similar to hypothe	2.31
	433618	AA602639	Hs.345494	Hs.345494:ESTs, Moderately similar to ZN	2.31
60	438584	AA811347		AA811347:ob81h06.s1 NCI_CGAP_GC81 Homo s	2.31
	446126	AW085909	Hs.356618	Hs.356618:ESTs, Weakly similar to PC4259	2.31
	408716	AI567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30
	433230	AW136134	Hs.220277	Hs.220277:ESTs, Weakly similar to expres	2.30
	410168	AW834050	Hs.351432	Hs.351432:tensin	2.30
65	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mR; cD DKFZp564D01	2.30
	418452	BE379749	Hs.85201	NM_005127:Homo sapiens C-type (calcium d	2.30
	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.29
	452848	AI417193	Hs.288912	Hs.288912:BBP-like protein 2	2.29
70	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
	422562	AI962060	Hs.118397	NM_001128:Homo sapiens AE binding protei	2.28
	432828	AB042326	Hs.287402	Hs.287402:chondroitin 4-sulfotransferase	2.28
	412948	BE243313	Hs.334851	NM_006148:Homo sapiens LIM and SH3 prote	2.28
	426068	AF029778	Hs.166154	NM_002226:Homo sapiens jagged 2 (JAG2)	2.28
75	456919	NM_003900	Hs.182248	NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.28
	453983	H94997	Hs.16450	Hs.16450:ESTs	2.28
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cD FLJ30677 fis,	2.28
80	413211	AW967107	Hs.109274	Hs.109274:hypothetical protein MGCA365	2.27
	422051	AW327546	Hs.111024	Hs.111024:solute carrier family 25 (mito	2.27
	438438	AA257992	Hs.50651	Hs.50651:Janus kise 1 (a protein tyrosin	2.27
	436278	BE396290	Hs.5097	NM_004710:Homo sapiens syntrophin 2 (SYN	2.27
	454080	AI199711	Hs.576	NM_000147:Homo sapiens fucosidase, alpha	2.27
	426542	AF190746	Hs.170310	NM_017424:Homo sapiens cat eye syndrome	2.27

	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27
	402901				2.26
	412898	AI129903	Hs.74669	NM_006634:Homo sapiens vesicle-associate	2.26
	413020	R98736		R98736.yr31h09.r1 Soares fetal liver spl	2.26
5	413939	AL047051	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.26
	408681	AW953853	Hs.281462	Hs.281462:hypothetical protein FLJ14251	2.25
	412330	NM_005100	Hs.788	NM_005100:Homo sapiens A kise (PRKA) anc	2.25
	442083	R50192	Hs.165062	Hs.165062:ESTs	2.25
	418271	NM_000919	Hs.83920	NM_000919:Homo sapiens peptidylglycine a	2.25
10	433376	AI249361	Hs.74122	NM_001225:Homo sapiens caspase 4, apopto	2.25
	438562	AI566826	Hs.25890	Hs.25890:ESTs, Weakly similar to transdu	2.25
	443883	AA114212	Hs.9930	NM_001235:Homo sapiens serine (or cystei	2.25
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.24
	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
15	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24
	407904	W44735	Hs.107260	Hs.107260:putative UDP-Galc:polypeptide	2.24
	429690	AW956329	Hs.23721	Hs.23721:ESTs	2.24
	443813	AA876372	Hs.93961	Hs.93961:Homo sapiens mR: cD DKFZp667D09	2.24
	427458	BE208364	Hs.29283	Hs.29283:ESTs, Weakly similar to UKHU pr	2.24
20	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24
	407192	AA609200	Hs.366318	Hs.366318:ESTs	2.23
	425751	T19239	Hs.1940	NM_001885:Homo sapiens crystallin, alpha	2.23
	456437	AI924228	Hs.115185	Hs.115185:ESTs	2.23
	413019	BE281604	Hs.75140	NM_002337:Homo sapiens low density lipop	2.23
25	418862	BE550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23
	435284	AA879470	Hs.96849	Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
	429630	M85289	Hs.211573	NM_005529:Homo sapiens heparan sulfate p	2.23
	427609	AK000436	Hs.179791	Hs.179791:RAB20, member RAS oncogene fam	2.23
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.23
30	446616	R55964	Hs.334873	Hs.334873:carboxypeptidase M	2.23
	407232	X04526		X04526:Human liver mR for beta-subunit s	2.23
	423798	AF047033	Hs.132904	Hs.132904:solute carrier family 4, sodiu	2.23
	446755	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	2.22
35	431393	AW971493	Hs.134269	Hs.134269:ESTs, Weakly similar to 200439	2.22
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.22
	428782	X12830	Hs.193400	NM_000565:Homo sapiens interleukin 6 rec	2.22
	446006	NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
	436418	AJ245874	Hs.4245	Hs.4245:chromosome 11 hypothetical prote	2.22
40	423869	BE409301	Hs.134012	NM_006688:Homo sapiens C1q-related facto	2.21
	437730	AW071087	Hs.239176	Hs.239176:insulin-like growth factor 1 r	2.21
	444020	R92962	Hs.35052	Hs.35052:ESTs	2.21
	413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR: cD DKFZp667B0	2.21
	412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
45	448988	Y09763	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21
	426841	AI052358	Hs.131741	Hs.131741:ESTs	2.21
	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.21
	451711	AK000461	Hs.26890	Hs.26890:cat eye syndrome chromosome reg	2.20
	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
50	424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20
	448883	BE614989	Hs.7503	Hs.7503:hypothetical protein FLJ14153	2.20
	411296	BE207307	Hs.10114	Hs.10114:growth suppressor 1	2.20
	452268	NM_003512	Hs.28777	NM_003512:Homo sapiens H2A histone famil	2.20
	416810	AF035606	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
55	441415	H21497	Hs.7471	Hs.7471:BBP-like protein 1	2.20
	444212	AW503976	Hs.10649	NM_004848:Homo sapiens basement membrane	2.19
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens R binding motif p	2.19
	430017	AA263172	Hs.35	NM_002832:Homo sapiens protein tyrosine	2.19
	424490	AJ278016	Hs.55565	Hs.55565:ankyrin repeat domain 3	2.19
60	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.19
	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19
	448262	AW880830	Hs.186273	Hs.186273:ESTs	2.19
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	2.19
	442045	C05768	Hs.8078	Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19
65	423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimul	2.19
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19
	424503	NM_002205	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.19
	437696	Z83844	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18
	405204				2.18
70	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.18
	417418	NM_002468	Hs.82116	NM_002468:Homo sapiens myeloid different	2.18
	412773	H15785	Hs.74573	NM_012268:Homo sapiens similar to vaccin	2.18
	409402	AF208234	Hs.695	NM_000100:Homo sapiens cystatin B (stefi	2.18
75	443791	N64458	Hs.143345	Hs.143345:ESTs	2.18
	435049	AL122067	Hs.4746	Hs.4746:hypothetical protein FLJ21324	2.18
	418389	AA830613	Hs.293849	Hs.293849:ESTs	2.18
	450712	AI732130	Hs.270496	Hs.270496:ESTs, Weakly similar to ALUB_H	2.18
	422007	AI739435	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.18
	453676	AW853745	Hs.286035	Hs.286035:hypothetical protein FLJ22686	2.18
80	415718	F30631	Hs.200237	Hs.200237:ESTs	2.18
	452688	AA721140	Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18
	415988	BE407713	Hs.78943	NM_000386:Homo sapiens bleomycin hydrola	2.18
	409453	AI885516	Hs.95612	Hs.95612:ESTs	2.17

	417512	X76534	Hs.82226	NM_002510:Homo sapiens glycoprotein (tra	2.17
	427202	BE272922	Hs.173936	NM_000628:Homo sapiens interleukin 10 re	2.17
	440983	M20581	Hs.7594	NM_006931:Homo sapiens solute carrier fa	2.17
5	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.17
	429642	X68264	Hs.211579	NM_006500:Homo sapiens melanoma adhesion	2.17
	427213	AW007211	Hs.348389	Hs.348389:hypothetical protein FLJ12876	2.17
	437763	AA469369	Hs.5831	NM_003254:Homo sapiens tissue inhibitor	2.17
	454000	AA040620	Hs.5672	Hs.5672:golgi membrane protein S8140	2.17
10	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (rel amy	2.16
	403857				2.16
	406648	AA563730	Hs.277477	Hs.277477:major histocompatibility compl	2.16
	400265				2.16
	442379	NM_004613	Hs.8265	NM_004613:Homo sapiens transglutaminase 2	2.16
15	441892	AB028981	Hs.8021	Hs.8021:KIAA1058 protein	2.16
	417446	AL118671	Hs.82163	NM_000898:Homo sapiens monoamine oxidase	2.16
	418386	AA361739	Hs.84549	NM_002494:Homo sapiens DH dehydrogenase (u	2.16
	414053	BE391635	Hs.75725	NM_003564:Homo sapiens transgelin 2 (TAG	2.16
	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
20	447660	AW160386	Hs.163667	Hs.163667:ESTs, Weakly similar to CA1H_H	2.16
	408279	AF216965	Hs.44095	Hs.44095:cyclin M3	2.16
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.16
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.16
	415661	AF057307	Hs.78575	Hs.78575:prosaposin (variant Gaucher dis	2.15
25	425302	U79115	Hs.155566	NM_003805:Homo sapiens CASP2 and RIPK1 d	2.15
	425996	W67330	Hs.374451	Hs.374451:ESTs	2.15
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.15
	422070	AF149785	Hs.111126	Hs.111126:pituitary tumor-transforming 1	2.15
	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
30	430035	NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	2.15
	435551	AF212365	Hs.5470	Hs.5470:interleukin 17B receptor	2.15
	437741	BE561610	Hs.5809	Hs.5809:putative transmembrane protein;	2.15
	441192	AA526626	Hs.7736	NM_016504:Homo sapiens mitochondrial rib	2.15
35	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.15
	411165	NM_000169	Hs.89089	NM_000169:Homo sapiens galactosidase, al	2.15
	425252	AW391162	Hs.349306	Hs.349306:hypothetical protein FLJ31951	2.14
	427600	AW630918	Hs.179774	NM_002818:Homo sapiens proteasome (proso	2.14
	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
40	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.14
	407797	AK000524	Hs.39850	Hs.39850:uridine kise-like 1	2.14
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolite phospho	2.14
	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cD FLJ32174 fis	2.14
45	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	2.14
	458097	AW341135	Hs.58104	Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
	411925	AW014588	Hs.72925	NM_003475:Homo sapiens chromosome 11 ope	2.14
	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transi	2.14
50	428586	M36712	Hs.2299	Hs.2299:CD8 antigen, beta polypeptide 1	2.14
	429379	NM_014840	Hs.200598	NM_014840:Homo sapiens KIAA0537 gene pro	2.13
	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	2.13
	443695	AW979048	Hs.292566	Hs.292566:YEA4 protein	2.13
	428145	BE243327	Hs.182626	NM_012264:Homo sapiens chromosome 22 ope	2.13
55	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cD: FLJ21933 fis	2.13
	456534	X91195	Hs.100623	Hs.100623:protein phosphatase 1, regulat	2.13
	419972	AL041465	Hs.182982	Hs.182982:golgin-57	2.13
	424950	AA602917	Hs.156974	Hs.156974:ESTs	2.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	2.13
60	431449	M55994	Hs.256278	NM_001066:Homo sapiens tumor necrosis fa	2.13
	418758	AW959311	Hs.172012	Hs.172012:hypothetical protein DKFZp434J	2.13
	434202	BE382411	Hs.3764	NM_000858:Homo sapiens guanylate kise 1	2.13
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.12
	452700	AI859390	Hs.288940	Hs.288940:transmembrane protein 8 (five	2.12
65	438033	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing fi	2.12
	400847				2.12
	447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12
	417052	NM_000712	Hs.81029	NM_000712:Homo sapiens biliverdin reduct	2.12
	413284	AU077055	Hs.289107	NM_001166:Homo sapiens baculoviral IAP r	2.11
70	434558	AW264102	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.11
	404030				2.11
	410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	2.11
	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kise	2.11
	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.11
75	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical prot	2.11
	426433	L38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3	2.11
	442439	U09759	Hs.246857	NM_002752:Homo sapiens mitogen-activated	2.11
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.11
	400208				2.11
80	455705	AW161061	Hs.356580	Hs.356580:ESTs, Weakly similar to zinc f	2.11
	417599	AA204688	Hs.62954	Hs.62954:lemün, heavy polypeptide 1	2.10
	416728	AB024597	Hs.79658	NM_001894:Homo sapiens casein kise 1, ep	2.10
	439920	H05430	Hs.288433	Hs.288433:neurotrophin	2.10
	422309	U79745	Hs.114924	NM_004694:Homo sapiens solute carrier fa	2.10

	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517				2.10
	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kise, rec	2.10
5	431214	AA294921	Hs.348024	NM_002881:Homo sapiens v-ra simian leuk	2.10
	412856	BE386745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442054	AI422867	Hs.88594	Hs.88594:Homo sapiens, clone IMAGE:43329	2.10
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.10
	426728	NM_007118	Hs.367689	NM_007118:Homo sapiens triple functioi d	2.10
10	419596	BE379320	Hs.91448	NM_007026:Homo sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxynucleotidase	2.09
	424658	NM_002406	Hs.151513	NM_002406:Homo sapiens mannosyl (alpha-1	2.09
15	432805	X94630	Hs.3107	Hs.3107:CD97 antigen	2.09
	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09
	445584	AF217518	Hs.8360	Hs.8360:PTD012 protein	2.09
	402559				2.09
20	418043	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kise	2.09
	448888	AW196663	Hs.200242	Hs.200242:caspase recruitment domain fam	2.09
	436910	AA926944	Hs.261587	Hs.261587:GCN2 eIF2alpha kise	2.09
	422573	AW297985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin	2.08
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.08
25	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08
	410301	AW502935	Hs.740	Hs.740:PTK2 protein tyrosine kise 2	2.08
	449538	AI559444	Hs.104679	Hs.104679:Homo sapiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541:netrin 4	2.08
	411779	AA292811	Hs.72050	NM_003551:Homo sapiens non-metastatic ce	2.08
30	427704	AW971063	Hs.292882	Hs.292882:ESTs	2.07
	413518	BE149455	Hs.75415	NM_004048:Homo sapiens beta-2-microglu	2.07
	447345	BE247767	Hs.18166	Hs.18166:KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613061	Hs.337772	Hs.337772:hypothetical protein BC009331	2.07
35	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.07
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
	403966				2.07
	409115	AI223335	Hs.50651	NM_002227:Homo sapiens Janus kise 1 (a p	2.07
40	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	2.07
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.06
	413980	NM_002437	Hs.75659	NM_002437:Homo sapiens MpV17 transgene,	2.06
	439414	NM_001183	Hs.6551	NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06
45	429849	U33053	Hs.2499	NM_002741:Homo sapiens protein kise C-li	2.06
	402424				2.06
	406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, lysoso	2.05
	426086	T94907	Hs.188572	Hs.188572:ESTs	2.05
50	419726	U50330	Hs.1274	NM_006129:Homo sapiens bone morphogeneti	2.05
	452344	AI264357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
	442498	U54617	Hs.8364	NM_002612:Homo sapiens pyruvate dehydrog	2.05
	422114	AW194851	Hs.111801	NM_015908:Homo sapiens arsete resistance	2.05
	413420	AW410235	Hs.75348	NM_006263:Homo sapiens proteasome (proso	2.05
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	2.05
55	409932	AI376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
	434848	BE256304	Hs.32148	Hs.32148:AD-015 protein	2.04
	453852	AW961818	Hs.374424	Hs.374424:ESTs	2.04
	427637	AK000816	Hs.179986	NM_005803:Homo sapiens flotillin 1 (FLOT	2.04
	400264				2.04
60	430016	NM_004736	Hs.227656	NM_004736:Homo sapiens xenotropic and po	2.04
	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like	2.04
	440975	AW499914	Hs.7579	Hs.7579:importin 9	2.04
	432280	BE440142	Hs.2943	NM_003135:Homo sapiens sigl recognition	2.04
65	409504	AA304961	Hs.699	NM_000942:Homo sapiens peptidylprolyl is	2.04
	412146	M92444	Hs.73722	NM_001641:Homo sapiens APEX nuclease (mu	2.04
	434203	BE262677	Hs.283558	Hs.283558:hypothetical protein PRO1855	2.04
	422754	AA316476	Hs.171811	Hs.171811:adenylate kise 2	2.04
	406729	AA069711		AA069711:zm52b11.s1 Stratagene fibroblas	2.04
70	413086	AA126841	Hs.183834	Hs.183834:ESTs	2.03
	424340	AA339036	Hs.7033	Hs.7033:ESTs	2.03
	450440	AB024334	Hs.25001	NM_012479:Homo sapiens tyrosine 3-monoox	2.03
	424662	NM_002870	Hs.151536	NM_002870:Homo sapiens RAB13, member RAS	2.03
	415740	N80486	Hs.39911	Hs.39911:Homo sapiens mR for FLJ00089 pr	2.03
75	412749	AA378417	Hs.74564	NM_003145:Homo sapiens sigl sequence rec	2.03
	408393	AW015318	Hs.23165	Hs.23165:ESTs	2.03
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.03
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cD FLJ10196 fis, c	2.03
	414883	AA926960	Hs.348669	NM_001826:Homo sapiens CDC28 protein kis	2.03
80	447298	BE617527	Hs.239818	Hs.239818:phosphoinositide-3-kise, catal	2.02
	459580	AA022888	Hs.176065	Hs.176065:ESTs	2.02
	422785	AI824114	Hs.289088	Hs.289088:heat shock 90kD protein 1, atp	2.02
	452696	AI826645	Hs.211534	Hs.211534:Homo sapiens cD FLJ31665 fis,	2.02
	452056	AW955065	Hs.101150	Hs.101150:KIAA1949 protein	2.02

5	450690	AA296696	Hs.333418	NM_014164:Homo sapiens FXRD domain-conta	2.02	
	423527	A1206965	Hs.105861	Hs.105861:engulfment and cell motility 3	2.01	
	429545	A1824164	Hs.356130	Hs.356130:ESTs	2.01	
	439180	A1393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukemia	2.01	
	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.01	
	436014	AF281134	Hs.283741	Hs.283741:exosome component Rrp46	2.01	
	453329	T97205	Hs.193400	Hs.193400:interleukin 6 receptor	2.01	
	407347	AA829847		TZ3514:seq3329 1-NIB Homo sapiens cD cl	2.01	
	435370	A964074	Hs.225838	Hs.225838:ESTs	2.01	
	10	430657	AA482910	Hs.370602	Hs.370602:ESTs, Weakly similar to hypoth	2.01
15	427157	U51166	Hs.173824	NM_003211:Homo sapiens thymine-D glycosy	2.01	
	424833	NM_003894	Hs.153405	NM_003894:Homo sapiens period homolog 2	2.01	
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	2.01	
	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.01	
	417426	NM_002291	Hs.82124	NM_002291:Homo sapiens laminin, beta 1 (2.01	
	412790	NM_014767	Hs.74583	NM_014767:Homo sapiens KIAA0275 gene pro	2.01	
	445892	AV655500	Hs.93961	Hs.93961:Homo sapiens mR: cD DKFZp667D09	2.01	
	TABLE 39B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
Accession:	Genbank accession numbers					
25	Pkey	CAT Number	Accession			
	409745	MH1944_5	B1030997 AA921874 AW188822 B1027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625			
			B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377			
			AA150780 B1033518 B1027818 BG015789 B1033807 AA341445			
			AA229762 AA230035			
	418869	12789_14	BG171436 BE079601 BE079534 AA299964 BE392717 BE883402 BE079532 BE018148 BF889427 W00396.			
	421902	276321_1	BC013310 AF261085 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459			
	400231	MH494_5	BG926429 BG389312 BG477333 A1031799 B1763443 B1260432 AA989106 AV728576 B1091380 AA402499 A1200513 A1284734 A1223995 A1289749			
			BG283291 BM013814 AW438544 BM450203 F35435 F33262 BE890952 AA401181 BG939668 F35525 B1088182 F34674 F33506 BM471326 F34677			
			AW276712 AA187508 F34866 AA114245 AA522581 N23835 A1076923 A1018505 BE879774 BM465637 A1753078 BG222159 AA595947 BF970917			
35			B1094125 AA719841 BE893087 BG775178 BE793983 BE797071 BF339134 BE409272 BE266456 BE796770 BE745957 BG755835 BE266758			
			BE259342 BM450181 BG748174 BE299322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743			
			BM459094 BM455306 BM472001 BM478247 BM478771 BM480379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359			
			BM462924 BM455329 BM471815 B1862301 BG331736 H04903 AA374894 BE902964			
	438584	1241536_1	AW977949 AA811347 D79715			
	413020	1485885_1	BE048113 R98736 Z42904			
	400265	1145_1	X58141 NM_001119 A1246786 BE645243 A1685698 A1208590 BE222576 A1191715 A1423108 BF064068 BG057819 A1208589 A1880535 A1262890			
			A1246261 BF939926 A1282848 A1802409 BE301053 A1884624 A1160385 A1335983 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739			
			A1871126 AW080375 A1350160 A1300855 A1818598 A1085263 A1306653 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105			
			A1131474 AW316548 AW128942 AW571682 A1583962 AW300674 BF509394 A1891077 BF221538 A1651874 F25731 AW881176 A1685962 D44936			
45			A1753874 BF593905 BE832830 A1637970 BE834103 BE464301 A1908017 A1378261 AA975416 R16732 H47612 H45402 AA668719 AA722441			
			AA991443 T51951 AW514058 A1277763 AA421907 A1083831 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806			
			B1195013 BE219292 BF055534 T95785 BE833037 AV648052 AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 A1292151			
			H26003 R62487 BG766512 BE815124 AW136122 H96767 R39407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180			
			R92185 H18680 R43192 AA401390 AA977941 A1091944 AA993369 AA617840 H14351 A1866242 A1915028 AA780787 AA506995 AA827496 AA634305			
			AA019060 AA814222 AA693469 N99931 N67840 R26834 BF342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 AA180888			
			AA149218 AA565201 B1001597 BE676565 AW169797 AW190994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414			
		400208	16640_1	AA180973 AA766800 W96432 B1550308 H52236 AA491029 BG420468 BG827522		
				X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 A1910663 BF905778 BG251264 AL562106 A1890538 AW769258 A1590391		
				A1913055 AW083235 A1078474 A1925022 AW504628 AW129725 BE466589 AW002786 AW591760 A1968816 AW006268 AW593787 BG236814		
55			AW769893 AW407608 AW075982 A1248207 A1762509 A1812070 A1249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245			
			B1014177 AL519126 BE675314 AW806520 B1870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893			
		400264	1145_1	BE798121 R09703 B1013066		
			X58141 NM_001119 A1246786 BE645243 A1685698 A1208590 BE222576 A1191715 A1423108 BF064068 BG057819 A1208589 A1880535 A1262890			
			A1246261 BF939926 A1282848 A1802409 BE301053 A1884624 A1160385 A1335983 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739			
			A1871126 AW080375 A1350160 A1300855 A1818598 A1085263 A1306653 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105			
			A1131474 AW316548 AW128942 AW571682 A1583962 AW300674 BF509394 A1891077 BF221538 A1651874 F25731 AW881176 A1685962 D44936			
			A1753874 BF593905 BE832830 A1637970 BE834103 BE464301 A1908017 A1378261 AA975416 R16732 H47612 H45402 AA668719 AA722441			
			AA991443 T51951 AW514058 A1277763 AA421907 A1083831 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806			
			B1195013 BE219292 BF055534 T95785 BE833037 AV648052 AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 A1292151			
65			H26003 R62487 BG766512 BE815124 AW136122 H96767 R39407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180			
			R92185 H18680 R43192 AA401390 AA977941 A1091944 AA993369 AA617840 H14351 A1866242 A1915028 AA780787 AA506995 AA827496 AA634305			
			AA846358 AA470463 AA618163 AA601963 W74212 AA021520 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793			
			AA019060 AA814222 AA693469 N99931 N67840 R26834 BF342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 AA180888			
			AA149218 AA565201 B1001597 BE676565 AW169797 AW190994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414			
		406729	0_0	AA180973 AA766800 W96432 B1550308 H52236 AA491029 BG420468 BG827522		
		407347	810943_1	AA069711		
				TZ3514 A1655785		
	75	TABLE 39C:				
		Pkey:	Unique number corresponding to an Eos probeset			
Ref:		Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA				
Strand:		sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.				
Nt_position:		Indicates DNA strand from which exons were predicted.				
		Indicates nucleotide positions of predicted exons.				
80		Pkey	Ref	Strand	Nt_position	
		404240	5002624	Minus	116132-116407,116653-116922	
		404277	1834458	Minus	91665-91946	

5	401179	9438647	Plus	113477-113893
	405102	8076881	Minus	120922-121296
	402575	9884830	Minus	109742-109883
	402901	8894222	Minus	175426-175667
	405204	7230116	Plus	126569-126754
10	403857	7708910	Minus	2524-3408
	400847	9188605	Plus	44643-44835
	404030	7671252	Plus	149362-151749
	405517	9454624	Plus	114757-114877
	402559	9864273	Plus	33539-33715
15	403966	8568881	Plus	158193-158277, 160116-160290
	402424	9796344	Minus	64925-65073

TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER

Table 40A lists about 977 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.0. The "average" stomach cancer level was set to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
411243	AB039886	Hs.69319	CA11	30.66
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.94
444325	AW152618	Hs.16757	ESTs	13.51
445891	AW391342	Hs.199460	ESTs	11.92
448811	A1590371	Hs.174759	ESTs	11.08
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.84
409757	NM_001898	Hs.123114	cystatin SN	10.38
421110	AJ250717	Hs.1355	cathepsin E	9.11
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.66
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	8.50
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.11
428651	AF196478	Hs.188401	annexin A10	6.86
425211	M18667	Hs.1867	progastricin (pepsinogen C)	6.51
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.49
409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.39
422260	AA315993	Hs.105484	ESTs, Weakly similar to UTB_HUMAN LITHO	6.31
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	6.25
409041	AB033025	Hs.50081	KIAA1199 protein	5.72
408380	AF123050	Hs.44532	diubiquitin	5.72
428953	AA306610	Hs.194676	DKFZP434C013 protein	5.46
450685	L15533	Hs.423	pancreatitis-associated protein	5.40
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.34
434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	5.16
421346	Z34277	Hs.103707	apomucin	5.14
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.06
425679	X05997	Hs.159177	lipase, gastric	4.94
421582	A1910275	Hs.1406	trefoil factor 1 (breast cancer, estroge	4.93
434414	A1798376	Hs.122579	gb.tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.92
422956	BE545072	Hs.170675	hypothetical protein FLJ10461	4.89
448105	AW591433	Hs.163443	ESTs, Weakly similar to TMS2_HUMAN TRANS	4.84
423575	C18863	Hs.840	Homo sapiens cDNA FLJ11576 fis, clone HE	4.72
413385	M34455	Hs.82772	indoleamine-pyrrole 2,3 dioxygenase	4.72
417866	AW067903	Hs.228320	collagen, type XI, alpha 1	4.68
448693	AW004854	Hs.202656	Homo sapiens cDNA: FLJ23537 fis, clone L	4.53
441377	BE218239	Hs.1247	ESTs	4.51
419278	AU076799	Hs.40098	apolipoprotein A-IV	4.48
407811	AW190902		cysteine knot superfamily 1, BMP antagon	4.47
403422				4.38
403776				4.32
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.32
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.30
421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	4.30
451181	A1796330	Hs.207461	ESTs	4.26
432168	AK000563	Hs.272805	hypothetical protein FLJ20556	4.23
454464	AW811606	Hs.271819	Homo sapiens cDNA: FLJ22751 fis, clone K	4.20
448844	A1581519	Hs.177164	ESTs	4.14
428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	4.13
452461	N78223	Hs.108106	transcription factor	4.08
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), klatini	4.04
431611	U58766	Hs.264428	tissue specific transplantation antigen	4.04
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	4.03
430044	AA464510	Hs.152812	ESTs	4.02
409956	AW103364	Hs.1524	inhibin, beta A (activin A, activin AB a	4.01
422420	U03398	Hs.99785	tumor necrosis factor (ligand) superfam	4.00
420159	A1572490		Homo sapiens cDNA: FLJ21245 fis, clone C	3.98
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.91

5	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.87
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.84
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab6ines	3.82
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.81
	419833	AA251131	Hs.220697	ESTs	3.81
	446232	AI281848	Hs.165547	ESTs	3.74
	432398	AA307808	Hs.2979	trefol factor 2 (spasmodic protein 1)	3.70
	451105	AI761324		gb:wi60b11.x1 NC1_CGAP_Co16 Homo sapiens	3.67
10	413281	AA861271	Hs.34396	ESTs	3.66
	432867	AW016936	Hs.233364	ESTs	3.66
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	3.65
	457465	AW301344	Hs.195969	ESTs	3.65
	414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fis, clone PL	3.61
15	418738	AW388633	Hs.6682	ESTs	3.60
	427778	AA412323	Hs.105323	ESTs	3.60
	454293	H49739	Hs.134013	ESTs, Moderately similar to NK homeobox	3.59
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 (H.sapi	3.57
	442577	AA292998	Hs.163900	ESTs	3.57
20	426174	AA547959	Hs.115838	ESTs	3.53
	452862	AW378065	Hs.8687	ESTs	3.51
	418869	AW516565	Hs.258279	ESTs	3.48
	430178	AW449612	Hs.152475	ESTs	3.48
	430397	AI924533	Hs.105607	ESTs	3.46
25	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	3.45
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.44
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	3.44
	431764	AA515212	Hs.271819	Homo sapiens cDNA: FLJ22751 fis, clone K	3.43
	421948	L42583	Hs.111758	keratin 6A	3.43
30	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	3.41
	442896	R37725	Hs.261108	ESTs	3.41
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.39
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.39
	408832	AW085690	Hs.63428	ESTs	3.39
35	406585	M18728		gb:Human nonspecific crossreacting antig	3.37
	437527	AI241019	Hs.145644	ESTs	3.37
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	3.37
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.36
	441318	AI078234	Hs.176130	ESTs	3.35
40	458897	U85642	Hs.138506	ESTs	3.33
	413808	J00287	Hs.182183	caldesmon 1	3.33
	411274	NM_002776	Hs.69423	kalikrein 10	3.32
	418406	X73501	Hs.84905	cytokeratin 20	3.32
	419559	Y07828	Hs.91096	ring finger protein	3.32
45	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.31
	423271	W47225	Hs.126256	interleukin 1, beta	3.31
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.30
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	3.30
	422310	AA316622	Hs.98370	cytochrome P540 family member predicted	3.29
50	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo	3.29
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.29
	443211	AI128388	Hs.143655	ESTs	3.29
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.28
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.28
55	452121	NM_004081	Hs.70936	deleted in azoospermia	3.27
	408633	AW963372	Hs.46677	PRO2000 protein	3.27
	447342	AI199268	Hs.19322	ESTs	3.25
	419229	AI827237	Hs.282884	ESTs	3.24
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	3.23
60	452699	AW295390	Hs.213062	ESTs	3.23
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.23
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.21
	408524	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	3.20
65	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	3.20
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.19
	453160	AI263307	Hs.146228	ESTs	3.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.19
	430187	AI799909	Hs.158989	ESTs	3.18
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.16
70	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	3.14
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.14
	425465	L18964	Hs.1904	protein kinase C, iota	3.13
	425826	U97698	Hs.159593	mucin 6, gastric	3.13
	431662	AA513406	Hs.152307	ESTs	3.13
75	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.13
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.12
	417315	AI080042	Hs.180450	ribosomal protein S24	3.11
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.11
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	3.11
80	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	3.10
	434370	AF130988	Hs.58346	downless (mouse) homolog	3.10
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	3.10
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.10
	420380	AA640891	Hs.102406	ESTs	3.10

	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.10
	415989	A1267700	Hs.111128	ESTs	3.09
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.09
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.09
5	420297	A1628272	Hs.88323	ESTs	3.08
	447519	U46258	Hs.23448	ESTs	3.08
	448045	AJ297436	Hs.20166	prostate stem cell antigen	3.07
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	3.06
10	410286	A1739159	Hs.61898	DKFZP586N2124 protein	3.05
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	3.05
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3	3.05
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.05
	430573	AA744550	Hs.136345	ESTs	3.05
15	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3, m	3.04
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	3.04
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.03
	415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	3.03
	411789	AF245505	Hs.72157	Homo sapiens adican mRNA, complete cds	3.02
20	417956	AA210704	Hs.190465	ESTs	3.02
	408908	BE296227	Hs.48915	serine/threonine kinase 15	3.01
	422330	D30783	Hs.115263	epiregulin	3.01
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.00
	425761	AW664214	Hs.196729	ESTs	2.99
25	432978	AF126743	Hs.279884	DNAJ domain-containing	2.99
	418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.99
	425371	D49441	Hs.155981	mesothelin	2.99
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	2.98
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.98
30	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.97
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.95
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	2.95
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	2.94
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	2.94
35	432917	NM_014125	Hs.279812	PRO0327 protein	2.94
	433384	AJ021992	Hs.124244	ESTs	2.93
	432731	R31178	Hs.287820	fibronectin 1	2.93
	420552	AK000492	Hs.98806	hypothetical protein	2.92
40	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.92
	409687	T51125	Hs.8493	ESTs	2.91
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fascin)	2.89
	417791	AW965339	Hs.111471	ESTs	2.89
	457288	AA521458	Hs.192738	ESTs	2.89
	456181	L36463	Hs.1030	ras inhibitor	2.89
45	450190	T51387		gb:yb20e08.r1 Stratagene fetal spleen (9	2.88
	411573	AB029000	Hs.70823	KIAA1077 protein	2.88
	430204	AA618335	Hs.146137	ESTs, Weakly similar to putative [C.eleg	2.88
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 antige	2.87
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.87
50	418670	AA601036	Hs.285083	ESTs	2.87
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	2.87
	409723	AW885757	Hs.257862	ESTs	2.87
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.86
	408660	AA525775	Hs.292523	ESTs	2.86
55	434032	AW009951	Hs.206892	ESTs	2.85
	418216	AA662240	Hs.283099	AF15q14 protein	2.85
	453331	AJ240665	Hs.8895	ESTs	2.85
	450221	AA328102	Hs.24541	cytoskeleton associated protein 2	2.84
	402075				2.84
60	410145	AW886300		gb:RC5-OT0078-100400-023-C11 OT0078 Homo	2.83
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	2.83
	439867	AA847510	Hs.161292	ESTs	2.83
	443715	AI583187	Hs.9700	cyclin E1	2.83
	420005	AW271106	Hs.133294	ESTs	2.83
65	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.83
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.82
	404567				2.82
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.82
	449224	AW995911	Hs.299883	hypothetical protein FLJ23399	2.81
70	407584	W25945	Hs.18745	ESTs	2.81
	453884	AA355925	Hs.36232	KIAA0186 gene product	2.81
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	2.80
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.79
	449722	BE280074	Hs.23960	cyclin B1	2.79
	445676	AI247763	Hs.16928	ESTs	2.79
75	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.78
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.78
	421777	BE562088	Hs.108196	HSPC037 protein	2.78
	452571	W31518	Hs.34665	ESTs	2.77
	420759	T11832	Hs.127797	ESTs	2.77
80	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	2.77
	412723	AA648459	Hs.179912	ESTs	2.76
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	2.76
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	2.76

	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.76
	449378	AW664026	Hs.59892	ESTs	2.75
	423903	M57765	Hs.1721	interleukin 11	2.75
5	412059	AA317962	Hs.249721	ESTs	2.75
	431104	AW970859	Hs.269109	ESTs	2.75
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	2.75
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.75
	452940	AA029722	Hs.20279	ESTs	2.74
10	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.74
	407777	AA161071	Hs.71465	squalene epoxidase	2.73
	432201	AJ538613	Hs.135657	ESTs	2.73
	414416	AW409985	Hs.76084	lamin B2	2.73
	414617	AJ339520	Hs.20524	ESTs, Moderately similar to hexokinase I	2.73
15	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	2.73
	444301	AK000136	Hs.10760	hypothetical protein FLJ20129	2.72
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	2.72
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	2.72
	408298	AJ745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.72
20	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.71
	429432	AJ678059	Hs.202676	synaptonemal complex protein 2	2.71
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.71
	418801	AA228366	Hs.115122	ESTs	2.71
25	440283	AJ732892	Hs.190489	ESTs	2.71
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.71
	408366	AW511255	Hs.258082	ESTs	2.70
	406399				2.69
	434217	AW014795	Hs.23349	ESTs	2.68
30	449785	AJ225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	2.68
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.68
	443349	AJ052572	Hs.269864	ESTs	2.68
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.67
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.67
35	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	2.67
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.66
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.65
	424408	AJ754813	Hs.146428	collagen, type V, alpha 1	2.65
	430832	AJ073913	Hs.100686	ESTs, Weakly similar to secreted cement	2.65
40	427217	AA399272	Hs.144341	ESTs	2.65
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	2.64
	450400	AJ694722	Hs.279744	ESTs	2.64
	435380	AA679001	Hs.192221	ESTs	2.64
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	2.63
45	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	2.63
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.63
	453134	AA032211	Hs.118493	ESTs	2.63
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.62
	408868	AW292286	Hs.255058	ESTs	2.62
50	414972	BE263782	Hs.77695	KIAA0008 gene product	2.62
	440255	AJ932285	Hs.160569	ESTs	2.62
	403055				2.62
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	2.62
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	2.61
55	413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	2.61
	445114	AW991959	Hs.254664	ESTs	2.61
	422397	AJ223366	Hs.116051	myeloma overexpressed gene(in a subset o	2.60
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.60
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	2.60
60	440249	AJ246590	Hs.125325	ESTs	2.60
	433220	AJ076192	Hs.131933	ESTs	2.60
	438533	AJ440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	2.60
	436251	BE515065	Hs.5092	nucleolar protein (KKE/D repeat)	2.60
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	2.60
65	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	2.60
	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	2.60
	435370	AJ964074	Hs.225838	ESTs	2.59
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.59
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	2.59
70	443919	AJ091284	Hs.135224	ESTs	2.58
	413268	AL039079	Hs.75256	regulator of G-protein signaling 1	2.58
	404519				2.58
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.57
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.57
75	426841	AJ052358	Hs.193726	ESTs	2.57
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.57
	417933	X02308	Hs.82962	thymidylate synthetase	2.56
	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	2.56
	441384	AA447849	Hs.288660	protease, serine, 23	2.56
80	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	2.56
	418867	D31771	Hs.89404	rsh (Drosophila) homeo box homolog 2	2.55
	449042	AW294985	Hs.301148	potassium voltage-gated channel, Isk-rel	2.55
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.55
	414132	AJ801235	Hs.48480	ESTs	2.55

	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.55
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.55
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamin	2.54
5	415250	F02614	Hs.27319	ESTs	2.54
	435647	AI653240	Hs.49823	ESTs	2.54
	459306	AW578452	Hs.232988	ESTs, Weakly similar to mucin [H.sapiens	2.54
	414361	AI086138	Hs.204044	ESTs	2.54
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	2.53
10	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	2.53
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.53
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.53
	456743	AI630124	Hs.7434	ESTs	2.53
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.52
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	2.52
15	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cos	2.52
	432657	AA831815	Hs.270940	ESTs	2.51
	434080	AI820719	Hs.154662	hypothetical protein PRO1472	2.51
	438190	AA780020	Hs.136798	ESTs	2.51
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	2.51
20	446405	AW451259	Hs.57851	ESTs	2.51
	450002	AI679524	Hs.201629	ESTs, Moderately similar to ALU8_HUMAN A	2.51
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	2.51
	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	2.50
25	447634	AW967902	Hs.5152	Homo sapiens cDNA: FLJ22618 fis, clone H	2.50
	436393	AW022213	Hs.143617	ESTs	2.50
	453751	R36762	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	2.49
	445669	AI570830	Hs.174870	ESTs	2.49
	445865	AI262584	Hs.145575	ESTs	2.49
30	448437	AW470125		gb:wx60c04.x1 NCI_CGAP_Pan1 Homo sapiens	2.49
	414883	AA926960	Hs.77550	CDC28 protein kinase 1	2.49
	406747	AI925153	Hs.217493	annexin A2	2.49
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.49
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.48
35	412903	BE007967	Hs.155795	ESTs	2.48
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.48
	447030	AW444659	Hs.232184	ESTs	2.48
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.48
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.48
40	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.48
	409640	U78722	Hs.55481	zinc finger protein 165	2.48
	424639	AI917494	Hs.131329	ESTs	2.48
	404171				2.47
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	2.47
45	407839	AA045144	Hs.161566	ESTs	2.47
	410406	AI969703	Hs.301842	ESTs	2.47
	452220	BE158006	Hs.212296	ESTs	2.46
	427691	AW194426	Hs.20726	ESTs	2.46
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.46
50	444838	AV651680	Hs.208558	ESTs	2.46
	413816	AW958181	Hs.189998	ESTs	2.46
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.46
	436613	AA972691	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	2.45
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	2.45
55	432874	W94322	Hs.279651	melanoma inhibitory activity	2.45
	425268	AI807883	Hs.156932	ESTs	2.45
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.45
	427961	AW293165	Hs.143134	ESTs	2.45
60	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.45
	433083	AL042759	Hs.191762	ESTs	2.45
	439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	2.44
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.44
	431457	NM_012211	Hs.256297	integrin, alpha 11	2.44
65	443949	AW827419	Hs.235070	ESTs	2.44
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.44
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.43
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.43
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.43
70	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.43
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	2.43
	424273	W40460	Hs.144442	phospholipase A2, group X	2.42
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	2.42
	453966	BE148734	Hs.252833	ESTs	2.42
75	427043	AA397679	Hs.298460	ESTs	2.42
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.42
	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 112 PRO	2.42
	433159	AB035898	Hs.150587	kinesin-like protein 2	2.42
	439396	BE562958	Hs.74346	ESTs, Weakly similar to /prediction	2.42
80	426427	M86699	Hs.169840	TTK protein kinase	2.41
	434725	AK000796	Hs.4104	hypothetical protein	2.41
	427719	AI393122	Hs.134726	ESTs	2.41
	433312	AI241331	Hs.131765	ESTs	2.41
	432615	AA557191	Hs.55028	ESTs	2.41

	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	2.41
	419220	AA811938	Hs.291759	ESTs	2.40
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	2.40
5	435219	AA676349	Hs.190331	ESTs	2.40
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	2.40
	416713	T70174		gb:yc18b03.s1 Stratagene tung (937210) H	2.40
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.40
	409802	AI337658	Hs.156351	ESTs	2.40
10	443597	AI078418		gb:oz05e03.x1 Soares_fetal_liver_spleen_	2.40
	404253				2.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	2.40
	443462	AI064690	Hs.171176	ESTs	2.39
	418693	AI750878	Hs.87409	thrombospondin 1	2.39
15	451237	AW600293		gb:EST00049 pGEM-T library Homo sapiens	2.39
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.39
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	2.39
	445625	BE246743	Hs.288529	Homo sapiens cDNA: FLJ22635 fis, clone H	2.39
	435937	AA830893	Hs.119769	ESTs	2.39
20	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	2.38
	422082	AA016188	Hs.111244	hypothetical protein	2.38
	435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUD	2.38
	407242	M18728		gb:Human nonspecific crossreacting antig	2.38
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	2.38
25	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble	2.38
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	2.38
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	2.38
	450737	AW007152	Hs.203330	ESTs	2.38
	428070	T63918	Hs.182313	retinol-binding protein 2, cellular	2.38
30	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.37
	433345	AI681545	Hs.152982	Homo sapiens cDNA FLJ13117 fis, clone NT	2.37
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.37
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.37
	453204	R10799	Hs.191990	ESTs	2.37
35	453876	AW021748	Hs.110406	ESTs	2.36
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.36
	434682	AA827165	Hs.191958	ESTs	2.36
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.36
	414108	AI267592	Hs.75761	SFRS protein kinase 1	2.36
40	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.36
	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	2.36
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	2.36
	441020	W79283	Hs.35962	ESTs	2.36
	448019	AW947164	Hs.195641	ESTs	2.36
45	431753	X76029	Hs.2841	neuromedin U	2.36
	441703	AW390054	Hs.192843	ESTs	2.36
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.36
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.36
	444478	W07318	Hs.240	M-phase phosphoprotein 1	2.36
50	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	2.35
	428388	AA729827	Hs.101265	Homo sapiens cDNA: FLJ22593 fis, clone H	2.35
	436961	AW375974	Hs.156704	ESTs	2.35
	408194	AA601038	Hs.191797	ESTs	2.35
	438578	AA811244	Hs.164168	ESTs	2.35
55	429183	AB014604	Hs.197955	KIAA0704 protein	2.35
	435663	AI023707	Hs.134273	ESTs	2.35
	430290	AI734110	Hs.136355	ESTs	2.34
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.34
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.33
60	450378	AW249181	Hs.19954	ESTs, Weakly similar to cDNA EST yk386e1	2.33
	432877	AW974111	Hs.292477	ESTs	2.33
	451928	AI823801	Hs.30315	ESTs	2.33
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	2.33
65	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.33
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.33
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	2.33
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	2.33
	458531	AA367718	Hs.159083	ESTs	2.33
	449532	W74653	Hs.271593	ESTs	2.33
70	446354	AW449650	Hs.202249	ESTs	2.33
	409703	NM_006187	Hs.56009	Z'-oligoadenylate synthetase 3	2.33
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	435607	W73428	Hs.8750	uncharacterized bone marrow protein BM04	2.32
	405818				2.32
75	423132	AF070647	Hs.124126	Homo sapiens clone 24438 mRNA sequence	2.32
	444371	BE540274	Hs.239	forkhead box M1	2.32
	432675	AI791855	Hs.105884	ESTs	2.32
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.31
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.31
80	434775	AA648983	Hs.212911	ESTs	2.31
	407378	AA299264		gb:EST11752 Uterus Homo sapiens cDNA S	2.31
	442353	BE379694	Hs.49136	ESTs	2.31
	422611	AA158177	Hs.118722	fucosyltransferase B (alpha (1,6) fucosy	2.31
	409965	AA079229		gb:zm95f04.r1 Stratagene colon HT29 (937	2.31

	421677	H64092	Hs.38282	ESTs	2.31
	419493	AF001212	Hs.90744	proteasome (prosome, macropain) 26S subu	2.31
	424435	AB011167	Hs.146957	KIAA0595 protein	2.30
5	446880	AJ811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT	2.30
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	2.30
	452834	AI638627	Hs.105685	ESTs	2.30
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.30
	428125	AA393071	Hs.182579	leucine aminopeptidase	2.30
10	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	2.29
	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.29
	428923	BE047698	Hs.188785	ESTs	2.29
	452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/	2.29
	409402	AF208234	Hs.695	cystatin B (stefin B)	2.29
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.29
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.29
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	2.29
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.28
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	2.28
20	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.28
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.28
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.28
	438170	AI916685	Hs.194601	ESTs	2.28
	445378	AV653564	Hs.226946	ESTs	2.28
25	428048	AA705745	Hs.185070	ESTs	2.28
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.27
	446665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypotheti	2.27
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.27
	422128	AW881145		gb:OVD-OT0033-010400-182-a07 OT0033 Homo	2.27
30	433535	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni	2.27
	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	2.27
	421155	H87879	Hs.102267	lysyl oxidase	2.27
	405545				2.27
	449467	AW205006	Hs.197042	ESTs	2.27
35	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.27
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.26
	423634	AW959908	Hs.16590	heparin-binding growth factor binding pr	2.26
	443868	W88483	Hs.293650	ESTs	2.26
	407742	AF186252	Hs.38084	sulfotransferase family, cytosolic, 1C,	2.26
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.26
	432655	AA832195	Hs.292266	ESTs	2.26
	429731	AK001592	Hs.212172	beta,beta-carotene 15,15'-dioxygenase ho	2.26
	400514				2.26
	431846	BE019924	Hs.271580	uroplakin 1B	2.26
45	439521	AI808955	Hs.58248	ESTs	2.26
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	2.26
	437641	AA811452	Hs.291911	ESTs	2.26
	418982	AI348838	Hs.13073	ESTs	2.26
	411393	AW797437	Hs.69771	B-factor, properdin	2.26
50	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	2.25
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	2.25
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	2.25
	449962	AA004879	Hs.187820	ESTs	2.25
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	2.25
55	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.25
	414368	W70171	Hs.75939	uridine monophosphate kinase	2.25
	408353	BE439838	Hs.44298	hypothetical protein	2.25
	439223	AW238299	Hs.23945	ESTs	2.25
	448753	AL048858	Hs.224355	ESTs, Weakly similar to A39650 protein k	2.25
60	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.24
	432403	AA550815	Hs.124840	ESTs	2.24
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	2.24
	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	2.24
	446887	AJ346656	Hs.156652	Homo sapiens cDNA: FLJ22800 fis, clone K	2.24
65	452833	BE559681	Hs.30736	KIAA0124 protein	2.24
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.24
	422039	BE567832	Hs.82148	hypothetical protein	2.24
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	2.24
	445413	AA151342	Hs.12677	CGI-147 protein	2.23
70	423645	AJ215632	Hs.147487	ESTs	2.23
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.23
	423515	AA327017	Hs.162204	ESTs	2.23
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.23
	434518	H56995	Hs.37372	Homo sapiens DNA binding peptide mRNA, p	2.23
75	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.23
	449974	AW970948	Hs.269403	ESTs	2.23
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.23
	457982	AW856093	Hs.183617	ESTs	2.23
	414420	AA043424	Hs.76095	immediate early response 3	2.23
80	449019	AI949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.23
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	2.23
	452930	AW195285	Hs.194097	ESTs	2.23
	436391	AJ227892	Hs.146274	ESTs	2.23
	439186	AI697274	Hs.6487	Xq28, 2000bp sequence contig. ORF	2.23

	427254	AL121523	Hs.97774	ESTs	2.22
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	2.22
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.22
5	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	2.22
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.22
	438223	AA781171		gb:aj24405.s1 Soares_testis_NHT Homo sap	2.22
	434504	AI887341	Hs.121590	Homo sapiens cDNA FLJ12827 fis, clone NT	2.22
	450149	AW969781	Hs.293440	ESTs, Moderately similar to ZIC2 protein	2.22
10	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.22
	401519				2.22
	441794	AW197794	Hs.253338	ESTs	2.22
	412108	AA100293	Hs.185043	ESTs	2.22
	431849	AI670823	Hs.85573	Homo sapiens mRNA; cDNA DKFZp566N034 (fr	2.22
15	444969	AI203334	Hs.160628	ESTs	2.21
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	2.21
	434423	NM_006769	Hs.3844	LIM domain only 4	2.21
	438328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	2.21
	400021			AFFX control: STAT1	2.21
20	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.21
	434170	AA626509	Hs.122329	ESTs	2.21
	423453	AW450737	Hs.128791	CGI-09 protein	2.21
	428438	NM_001955	Hs.2271	endothelin 1	2.21
	433102	AI343966	Hs.158528	ESTs	2.21
25	421470	R27496	Hs.1378	annexin A3	2.21
	425499	T62489		gb:yc0309.r1 Stratagene lung (S37210) H	2.21
	438280	AW015534	Hs.217493	annexin A2	2.21
	440381	AA917808	Hs.190495	ESTs	2.20
	453779	N35187	Hs.43388	ESTs	2.20
30	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	2.20
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	2.20
	452299	AW206330	Hs.73239	hypothetical protein FLJ10901	2.20
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	2.20
	448457	H65629	Hs.245997	ESTs	2.20
35	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.20
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	2.20
	430603	AA148164	Hs.247280	HBV associated factor	2.20
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.20
	452679	Z42387	Hs.4299	Homo sapiens cDNA: FLJ20965 fis, clone A	2.20
40	410619	BE512730	Hs.65114	keratin 18	2.20
	424332	AA338919	Hs.101615	ESTs	2.20
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.20
	418661	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	2.20
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.20
45	427920	Z11502	Hs.181107	annexin A13	2.19
	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fis, clone H	2.19
	419752	AA249573	Hs.152618	ESTs	2.19
	441436	AW137772	Hs.185980	ESTs	2.19
	413095	AA494359	Hs.30715	ESTs	2.19
50	403208				2.19
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	2.19
	444261	AA298958	Hs.10724	MDSO23 protein	2.19
	419474	AW968619	Hs.155849	ESTs	2.19
	453883	AI638516	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamm	2.18
55	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.18
	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	2.18
	440250	AA876179	Hs.134650	ESTs	2.18
	444334	BE296785	Hs.10848	KIAA0187 gene product	2.18
	437616	AI797163	Hs.207954	ESTs	2.18
60	451807	W52854	Hs.27099	DKFZP564J0863 protein	2.18
	430441	BE398091	Hs.6880	DKFZP434D156 protein	2.18
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	2.18
	411678	AI907114	Hs.71465	squalene epoxidase	2.18
	453735	AI066629	Hs.125073	ESTs	2.18
65	450499	AA235207	Hs.250456	hypothetical protein DKFZp762F2011	2.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.18
	421532	AW138207	Hs.146170	hypothetical protein FLJ22969	2.18
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	2.18
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.18
70	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl) protease	2.18
	425873	NM_013390	Hs.160417	transmembrane protein 2	2.17
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.17
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	2.17
	446995	AI355012		gb:qu16d10.x1 NCI_CGAP_Ov23 Homo sapiens	2.17
75	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT	2.17
	411127	AA668995	Hs.218329	hypothetical protein	2.17
	439961	AA857451	Hs.269696	ESTs	2.17
	429125	AA446854	Hs.271004	ESTs	2.17
	407103	AA424881	Hs.256301	ESTs	2.17
80	435990	AI015862	Hs.131793	ESTs	2.17
	415116	AA160363	Hs.269956	ESTs	2.17
	440052	AI633744	Hs.195648	ESTs	2.17
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascidin	2.17
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.16

	443599	AI079559	Hs.134125	ESTs	2.16
	423623	AB011117	Hs.129943	KIAA0545 protein	2.16
	427258	AA400091	Hs.39421	ESTs	2.16
5	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.16
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	2.16
	428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypotheti	2.16
	421408	AI688223	Hs.104114	Hs.sapiens HCG 1 mRNA	2.16
	449057	AB037784	Hs.22941	KIAA1363 protein	2.16
10	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	2.16
	443552	NG5982	Hs.109434	ESTs	2.16
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.16
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	2.16
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	2.16
15	452865	AI924046	Hs.119567	ESTs	2.16
	432789	D26361	Hs.3104	KIAA0042 gene product	2.16
	438580	AA811262	Hs.299202	ESTs	2.16
	422192	AA305159	Hs.113019	fts485	2.15
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	2.15
20	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	2.15
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.15
	441021	AW578716	Hs.7644	H1 histone family, member 2	2.15
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.15
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.15
25	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	2.15
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.15
	447033	AI357412	Hs.157601	ESTs	2.15
	410407	X66839	Hs.63287	carbonic anhydrase IX	2.15
	446077	BE251048	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	2.15
30	420900	AL045633	Hs.44269	ESTs	2.15
	411975	AI916058	Hs.144583	ESTs, Weakly similar to gag [H.sapiens]	2.15
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.15
	449571	AW016812	Hs.200266	ESTs	2.15
	452721	AJ269529	Hs.30377	Homo sapiens EST from clone 470080, full	2.15
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.14
	410664	NM_006033	Hs.65370	lipase, endothelial	2.14
	435730	AB020635	Hs.4984	KIAA0828 protein	2.14
	452835	AK001269	Hs.30738	hypothetical protein FLJ10407	2.14
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.14
40	401708				2.14
	411400	AA311919	Hs.69851	GAR1 protein	2.14
	448526	AB028946	Hs.21361	KIAA1023 protein	2.14
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.14
	412338	AA151527	Hs.69485	Homo sapiens cDNA FLJ12436 fis, clone NT	2.14
45	420894	AA744597	Hs.88854	ESTs	2.14
	409235	AA188827	Hs.7988	ESTs, Weakly similar to endo-alpha-D-man	2.14
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	2.14
	447760	AI431328	Hs.291179	ESTs, Weakly similar to topoisomerase I	2.14
	413511	AI627178	Hs.75412	Arginine-rich protein	2.13
50	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	2.13
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.13
	441790	AW294909	Hs.132208	ESTs	2.13
	425298	AK000209	Hs.155556	hypothetical protein FLJ20202	2.13
	450956	AW193531	Hs.205647	ESTs, Moderately similar to ALU1_HUMAN A	2.13
55	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	2.13
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.13
	453975	AW009808	Hs.270829	ESTs	2.13
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.13
60	422783	AA598956	Hs.120439	ethanolamine kinase	2.13
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.13
	410418	D31382	Hs.63325	transmembrane protease, serine 4	2.13
	419791	AI579909	Hs.105104	ESTs	2.13
	414860	BE255593	Hs.77502	methionine adenosyltransferase II, alpha	2.13
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	2.13
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	2.13
	437050	AA766420	Hs.291606	ESTs	2.13
	430217	N47863	Hs.180450	ribosomal protein S24	2.13
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.12
	409012	AL117435	Hs.49725	DKFZP434I216 protein	2.12
70	450645	AL117441	Hs.25264	DKFZP434N126 protein	2.12
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	2.12
	451356	AA748418	Hs.164577	ESTs	2.12
	429534	AW976987	Hs.163327	ESTs	2.12
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	2.12
75	441495	AW294603	Hs.127039	ESTs	2.12
	443564	AI921685	Hs.199713	ESTs	2.12
	410839	NM_006849	Hs.66581	protein disulfide isomerase	2.12
	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	2.12
	442947	R40800	Hs.21303	ESTs	2.12
80	414987	AA524394	Hs.165544	ESTs	2.12
	450510	AA010056	Hs.242998	ESTs	2.12
	427475	AA403151	Hs.191605	ESTs	2.12
	444670	H58373	Hs.37494	ESTs	2.12
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.12

	433748	R12244		gb:yf33c12.r1 Soares fetal liver spleen	2.12
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	2.11
	438138	R98299	Hs.177502	ESTs	2.11
5	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-like) 10	2.11
	415474	NM_014252	Hs.78457	solute carrier family 25 (mitochondrial	2.11
	416472	AA180756	Hs.193094	ESTs, Moderately similar to ALU4_HUMAN A	2.11
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	2.11
	410718	AI920783	Hs.191435	ESTs	2.11
10	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.11
	433344	AI741506	Hs.186753	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.11
	431621	AW292329	Hs.163481	ESTs	2.11
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	2.11
15	433849	BE465884	Hs.280728	ESTs	2.11
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.11
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.11
	409717	AW452871	Hs.56043	CGI-115 protein	2.11
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.11
20	445837	AI261700	Hs.145544	ESTs	2.11
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.11
	436326	BE085236	Hs.181244	major histocompatibility complex, class	2.10
	423880	BE278111	Hs.134200	DKFZP564C186 protein	2.10
	421574	AJ000152	Hs.105924	defensin, beta 2	2.10
25	437103	AW139408	Hs.152940	ESTs	2.10
	435550	AI224456	Hs.4934	H.sapiens polyA site DNA	2.10
	450747	AI064821	Hs.48306	ESTs, Highly similar to EWS_HUMAN RNA-BI	2.10
	437033	AW248364	Hs.5409	RNA polymerase I subunit	2.10
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.10
30	431120	AA492588		gb:mg99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.10
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	2.10
	429669	BE185499	Hs.2471	KIAA0020 gene product	2.10
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.10
	436124	AA705012	Hs.269584	ESTs	2.10
35	436415	BE265254	Hs.5181	proliferation-associated 2C4, 38kD	2.10
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	2.10
	453968	AA847843	Hs.62711	ESTs	2.10
	437549	AA759149		gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.10
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.10
40	447720	AL038765	Hs.161304	ESTs	2.09
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	2.09
	429743	AA804398	Hs.288995	hypothetical protein FLJ20813	2.09
	447815	AI432199	Hs.247084	ESTs	2.09
	441675	AI914329	Hs.5461	ESTs	2.09
45	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.09
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.09
	442525	AF150282	Hs.145945	ESTs	2.09
	423750	AF165883	Hs.132415	prefoldin 2	2.09
	449199	AI990122	Hs.196988	ESTs	2.09
50	415363	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas	2.09
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	2.09
	418462	BE001596	Hs.85266	integrin, beta 4	2.09
	432093	H28383		gb:yf52c03.r1 Soares breast 3NbHBst Homo	2.09
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV	2.09
55	434442	AA737415	Hs.152826	ESTs	2.09
	442671	AI005668	Hs.134779	EST	2.09
	428771	AB028992	Hs.193143	KIAA1069 protein	2.09
	430335	D80007	Hs.239499	KIAA0185 protein	2.08
	425087	R52424	Hs.126059	ESTs	2.08
60	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	2.08
	443450	N66045	Hs.133529	ESTs	2.08
	418753	BE217818	Hs.87016	Homo sapiens cDNA: FLJ22938 fis, clone K	2.08
	432204	AI916132	Hs.121593	Homo sapiens cDNA FLJ13123 fis, clone NT	2.08
	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.08
65	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.08
	431628	AF146277	Hs.265561	CD2-associated protein	2.08
	446528	ALU076640	Hs.15243	nucleolar protein 1 (120kD)	2.08
	432284	AA532807	Hs.105822	ESTs	2.08
	411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	2.08
70	459319	NM_000059		gb:Homo sapiens breast cancer 2, early o	2.08
	408730	AV660717	Hs.47144	DKFZP585N0819 protein	2.08
	443607	AI452512	Hs.134069	ESTs	2.08
	422058	AA862231		gb:oe13g03.s1 NCL_CGAP_Ov2 Homo sapiens	2.08
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.08
75	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.08
	409686	AK000002	Hs.55879	Homo sapiens mRNA for FLJ00036 protein,	2.08
	438394	BE379623	Hs.27693	CGI-124 protein	2.08
	413092	AA126856	Hs.118665	ESTs	2.08
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	2.08
80	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.07
	438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	2.07
	453379	AA035261	Hs.61753	ESTs	2.07
	432125	AW972667	Hs.287510	Homo sapiens cDNA FLJ12300 fis, clone MA	2.07
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	2.07

	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.07
	450096	AI682088	Hs.223368	ESTs	2.07
	454011	M31008	Hs.37009	alkaline phosphatase, intestinal	2.07
5	427876	AI494291	Hs.111977	ESTs	2.07
	422901	R81936	Hs.121576	aspartate beta-hydroxylase	2.07
	419235	AW470411	Hs.288433	neurotrophin	2.07
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.07
	408243	Y00787	Hs.624	interleukin 8	2.07
10	415652	T79213	Hs.272073	ESTs	2.07
	446546	BE167687	Hs.156628	ESTs	2.07
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	2.07
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.07
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	2.07
15	456157	AW979153		gb:EST391263 MAGE resequences, MAGP Homo	2.06
	407143	C14076	Hs.248968	EST	2.06
	454269	AV61060	Hs.296411	ESTs, Moderately similar to KF1A_HUMAN K	2.06
	432440	X63597	Hs.2996	sucrase-isomaltase	2.06
	410668	BE379794	Hs.65403	hypothetical protein	2.06
20	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.06
	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	2.06
	439832	T81829	Hs.14870	ESTs	2.06
	456264	AW974175	Hs.105251	ESTs	2.06
	431201	AA678405	Hs.8854	Human transcription unit PVT gene, exons	2.06
25	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone PL	2.06
	438714	AA814859	Hs.294112	ESTs	2.06
	445318	AW500652	Hs.200885	ESTs	2.06
	439951	AI347067	Hs.124636	ESTs	2.06
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.06
30	428307	W27393	Hs.183648	protein tyrosine phosphatase, receptor t	2.06
	426874	N67325	Hs.247132	ESTs	2.06
	451295	AI557212	Hs.17132	ESTs	2.06
	432584	AA928829	Hs.47099	Homo sapiens cDNA: FLJ21212 fis, clone C	2.06
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.06
35	433716	AA608808	Hs.225118	ESTs	2.06
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.06
	426235	AI631964	Hs.34447	ESTs	2.06
	449026	BE500946	Hs.209105	ESTs	2.06
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.06
40	400019			AFFX control: STAT1	2.06
	408873	AL046017	Hs.23247	ESTs	2.06
	442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	2.06
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.06
	439975	AW328081	Hs.6817	Homo sapiens putative oncogene protein m	2.06
45	433037	NM_014158	Hs.279938	HSPC067 protein	2.06
	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	2.06
	436414	BE264633	Hs.143638	WD repeat domain 4	2.05
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.05
	407293	AA602234	Hs.270551	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
50	409459	D86407	Hs.54481	low density lipoprotein receptor-related	2.05
	436238	AK002163	Hs.301724	ESTs, Highly similar to unnamed protein	2.05
	400517	AF242388	Hs.149585	lengsin	2.05
	439943	AW083789	Hs.124620	ESTs	2.05
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	2.05
55	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kD)	2.05
	417491	AW376842	Hs.1085	guanylate cyclase 2C (heat stable entero	2.05
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.05
	435525	AI831297	Hs.123310	ESTs	2.05
	412627	BE391959	Hs.74276	chloride intracellular channel 1	2.05
60	439702	AW085525	Hs.134182	ESTs	2.05
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.05
	432979	AA573263	Hs.120860	ESTs	2.05
	417308	H50720	Hs.81892	KIAA0101 gene product	2.05
	432925	AA878324	Hs.192734	ESTs	2.05
65	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
	427871	AW992405	Hs.59622	ESTs, Weakly similar to unknown [H.sapie	2.05
	453804	AA300204	Hs.35276	KIAA0852 protein	2.05
	449939	T86420	Hs.272139	ESTs	2.05
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo	2.05
70	417819	AI253112	Hs.133540	ESTs	2.04
	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.04
	415009	C75253	Hs.220950	ESTs	2.04
	437829	AI358522	Hs.270188	ESTs	2.04
	435381	AW136397	Hs.247572	ESTs	2.04
75	439778	AL109729	Hs.18948	ESTs, Highly similar to HPS1_HUMAN PROTE	2.04
	428753	AW939252	Hs.192927	hypothetical protein FLJ20251	2.04
	446475	AI908188	Hs.209245	ESTs	2.04
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	2.04
	423701	AA329856	Hs.143022	ESTs	2.04
80	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.04
	422369	AF005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinas	2.04
	432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis, clone HE	2.04
	443746	AW861379	Hs.160602	ESTs	2.04
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (I	2.04

5	432393	AW205863	Hs.133988	ESTs, Weakly similar to I52825 gene MAC2	2.04
	430785	Z30201		gb:HHEA22G Atrium cDNA library Human hea	2.04
	428343	AL043021	Hs.12705	ESTs, Weakly similar to plakophilin 2b	2.04
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	2.04
	452488	N74921	Hs.184389	ESTs	2.04
	403485				2.04
	413313	NM_002047	Hs.75280	glycyl-tRNA synthetase	2.04
	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 intra	2.04
10	433326	AI379486	Hs.159430	ESTs	2.04
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	2.03
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	2.03
	422963	M79141	Hs.13234	ESTs	2.03
	418684	U82987	Hs.87246	Bcl-2 binding component 3	2.03
15	407824	AA147884	Hs.9812	ESTs	2.03
	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	2.03
	440246	W52010	Hs.191379	ESTs	2.03
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.03
	431301	AA502384	Hs.151529	ESTs	2.03
20	452705	H49805	Hs.246005	ESTs	2.03
	421724	AB037832	Hs.107287	KIAA1411 protein	2.03
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	2.03
	450200	AW975625	Hs.173088	ESTs	2.03
	447474	AW614220	Hs.189402	ESTs	2.03
25	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	2.03
	445019	AI205540	Hs.281295	ESTs	2.03
	435202	AI971313	Hs.170204	KIAA0551 protein	2.03
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	2.03
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.03
30	440773	AA352702	Hs.37747	hypothetical protein FLJ12484	2.03
	443425	AI056776	Hs.133397	ESTs	2.03
	454166	AW993356	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	2.03
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	2.03
	428299	AL038004	Hs.29419	ESTs	2.03
35	418735	N48769	Hs.44609	ESTs	2.03
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.03
	415757	AA830854	Hs.187810	ESTs	2.03
	432559	AW452948	Hs.257631	ESTs	2.03
40	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	2.02
	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	2.02
	417576	AA339449	Hs.82285	phosphoribosylglycylamide formyltransfer	2.02
	418559	AA225048	Hs.104207	ESTs	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.02
	433906	AI167816	Hs.43355	ESTs	2.02
45	422072	AB018255	Hs.111138	KIAA0712 gene product	2.02
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	2.02
	446229	AI744864	Hs.14449	KIAA1609 protein	2.02
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	2.02
	431721	AB032996	Hs.268044	KIAA1170 protein	2.02
50	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	2.02
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.02
	401866				2.02
	443129	R16075	Hs.21668	ESTs	2.02
55	426991	AK001536	Hs.285803	Homo sapiens cDNA FLJ12852 fis, clone NT	2.01
	414731	AI890434	Hs.77135	Homo sapiens mRNA; cDNA DKFZp586A191 (fr	2.01
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associate	2.01
	413293	AL047483	Hs.75270	GTP-binding protein homologous to Saccha	2.01
	435787	AW162767	Hs.100914	hypothetical protein FLJ10352	2.01
60	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.01
	442660	AW138174	Hs.130651	ESTs	2.01
	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated g	2.01
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	2.01
	431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.01
65	443180	R15875	Hs.70945	ESTs	2.01
	450914	AI743761	Hs.142528	ESTs	2.01
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	2.01
	405484				2.01
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	2.01
70	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.01
	439696	W95298	Hs.171882	ESTs	2.01
	432378	AI493046	Hs.146133	ESTs	2.01
	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone L	2.01
	453665	AA626250	Hs.181165	eukaryotic translation elongation factor	2.01
75	419981	AA897581	Hs.128773	ESTs	2.01
	445808	AV655234	Hs.298083	ESTs	2.01
	435767	H73505	Hs.117874	ESTs	2.01
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.01
	452747	BE153855	Hs.61460	ESTs	2.01
80	422790	AA809875	Hs.25933	ESTs	2.01
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.01
	433929	AI375499	Hs.27379	ESTs	2.01
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	2.01
	448954	AB014564	Hs.22616	KIAA0664 protein	2.00
	440774	AI420611	Hs.127832	ESTs	2.00

5	451351	AW058261	Hs.168213	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.00
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	2.00
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.00
	407154	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.00
	410240	AL157424	Hs.61289	synaptojanin 2	2.00
	426830	AA385751	Hs.160392	ESTs	2.00
	435014	BE560898	Hs.10026	ribosomal protein L17 isolog	2.00
	408620	AI918693	Hs.81848	RAD21 (S. pombe) homolog	2.00
	432829	W60377	Hs.57772	ESTs	2.00
	406752	AI285598	Hs.217493	annexin A2	2.00

15	TABLE 40A:		
	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	

20	Pkey	CAT number	Accession
	408690	107490_1	AW864542 AA056567 AW882724
	409965	116301_1	AA079229 AA079201 AA078874
	410008	116812_1	AA079552 BE142525 BE142527
	410145	1178960_1	AW886300 AW887902 AW887893 AW886291 AW592641
	411765	125700_1	H43346 AA248302 AA095182
	416713	1610889_1	T70174 H79244 T69850 H79151
	418546	176677_1	AA224827 T59708 T59843 BE156903
	419546	185766_1	AA244199 AA244272 H57440
	419807	188252_1	R77402 AA262462 AA250988 R06794
25	420637	195241_1	AW976153 AA278945 AA747691
	422058	210815_1	AA862231 AA659033 AA302799 AA302798
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
	422689	219896_1	AW856665 AA315006 AW954733
	425499	252539_1	T62489 T62634 AA828581 AA358569
	430704	322217_1	AW813091 AW206655 AA484440
	430785	323486_1	Z30201 AA486132 T72025
	431120	328264_1	AA492588 AA492498 AA492571
	431300	331217_1	AA502346 BE159863
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
30	432009	34025_1	AL137424 BE007148 T52277
	432093	341283_1	H28383 AW972670 H28359 AA525808
	433748	37385_1	R12244 H71290 AI110858 AF090916 AF075357 AA011531
	434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
			AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531 H59570
			AA759149 AW751066 AW844938
35	437549	438403_1	AA781171 AI202139 AI202098
	438223	452646_1	AA828995 AA834879 AI926361
	438993	467651_1	AW979249 D63277 AA846968
	439848	477806_1	AI078418 W80626 AW387769
	443597	574739_1	AI355012 AW812856
	446995	702707_1	R36075 AI366546 R36167
	447197	711623_1	AW470125 AI734872 AI749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236
	448437	763310_1	T51387 AW191595 T51271 AI686285
	450190	827655_1	AI761324 AW880941 AW880937
	451105	859083_1	BE072881 BE072946 AI762181
40	451129	859870_1	AW600293 AI767468
	451237	863269_1	BE065813 BE065788 BE065889 BE065832
	455666	1349545_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
	455778	1364506_1	AW979153 AA176967 AA826015
	456157	158261_1	

65	TABLE 40C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
70	NI_position:	Indicates nucleotide positions of predicted exons.	

75	Pkey	Ref	Strand	NI_position
	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
	401519	6649315	Plus	157315-157950
	401708	2951946	Plus	154511-155298
	401866	8018106	Plus	73126-73623
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	403055	8748904	Minus	109532-110225
	403208	7630829	Minus	147706-147903,148667-148804
	403422	9665041	Minus	151169-151561
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
80	403776	7770611	Minus	1414-1513,1624-1756
	404171	9930793	Plus	173667-173783,176876-177055
	404253	9367202	Minus	55675-56055

5	404519	8152000	Plus	12817-13000
	404567	7249169	Minus	101320-101501
	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405818	4071056	Plus	29055-29196
	406399	9256288	Minus	63448-63554

TABLE 41A: ABOUT 634 SEQUENCES UP-REGULATED IN STOMACH CANCER

Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 40A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

15	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	PSDomain:	Protein Structural Domain			
20	R1:	Ratio of tumor to normal adult tissues			
	Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain
	411243	AB039886	Hs.69319	CA11	SS
	418007	M13509	Hs.83169	matrix metallo	hemopexin,Peptidase_M10,SS
	448811	AI590371	Hs.174759	ESTs	TM
25	409757	NM_001898	Hs.123114	cystatin SN	cystatin,SS
	421110	AJ250717	Hs.1355	cathepsin E	asp,SS
	428368	BE440042	Hs.83326	matrix metallo	hemopexin,Peptidase_M10,SS
	406687	M31126	Hs.272620	pregnancy speci	hemopexin, TM,
	428651	AF196478	Hs.188401	annexin A10	annexin, TM,
30	425211	M18667	Hs.1867	progastricin (asp, TM,SS
	423673	BE003054	Hs.1695	matrix metallo	hemopexin,Peptidase_M10,SS
	409683	U33317	Hs.711	defensin, alpha	defensins,Defensin_propep,SS
	428664	AK001666	Hs.189095	similar to SALL	zf-C2H2,TM,SS
	408380	AF123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,
35	428953	AA306610	Hs.194676	DKFZP434C013 pr	art,TNFR_c6,DEAD,Stathmin,TM,SS
	450685	L15533	Hs.423	pancreatitis-as	lectin_c,TM,SS
	409187	AF154830	Hs.50966	carbamoyl-phosp	GATase,CPSase_L_chain,CPSase_sm_chain,MGS,TM,
	434206	AW136973	Hs.288516	ESTs, Weakly si	PH,TM,
	421346	Z34277	Hs.103707	apomucin	Cys_knot,vwd,
40	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS
	425679	X05997	Hs.159177	lipase, gastric	abhydrolase,SS
	421582	AI910275	Hs.1406	trefoil factor	trefoil,trypsin,TM,SS
	422956	BE545072	Hs.122579	hypothetical pr	TM
	448105	AW591433	Hs.170675	ESTs, Weakly si	trypsin,TM,
45	413385	M34455	Hs.840	indoleamine-pyr	IDO,TM,
	417866	AW067903	Hs.82772	collagen, type	TSPN,Collagen,COLFI,SS
	419278	AU076799	Hs.1247	apolipoprotein	Apolipoprotein,SS
	407811	AW190902	Hs.40098	cysteine knot s	SS
	403422				SS
50	403776				IL8,TM,SS
	418478	U38945	Hs.1174	cyclin-dependen	ank,TM,SS
	428242	H55709	Hs.2250	leukemia inhibi	LJF_OSM,SS
	421341	AJ243212	Hs.279611	deleted in mali	SS
	428434	AW363590	Hs.65551	ESTs, Weakly si	SS
55	409420	Z15008	Hs.54451	laminin, gamma	laminin_EGF,laminin_B,SS
	431611	U58766	Hs.264428	tissue specific	Epimerase,TM,SS
	413719	BE439580	Hs.75498	small inducible	IL8,SS
	409956	AW103364	Hs.727	inhibin, beta A	TGF-beta,TGFb_propeptide,SS
	422420	U03398	Hs.1524	tumor necrosis	TNF,TM,
60	428227	AA321649	Hs.2248	small inducible	IL8,TM,SS
	422168	AA586894	Hs.112408	S100 calcium-bi	efhand,TM,
	412140	AA219691	Hs.73625	RAB5 interactin	kinesin,TM,SS
	414812	X72755	Hs.77367	monokine induce	IL8,SS
	419833	AA251131	Hs.220697	ESTs	WHEP-TRS,TM,
65	446232	AI281848	Hs.165547	ESTs	7tm_3,TM,
	432398	AA307808	Hs.2979	trefoil factor	trefoil,TM,SS
	432867	AW016936	Hs.233364	ESTs	GSHPx,TM,SS
	424046	AF027866	Hs.138202	serine (or cyst	serpin,TM,
	414918	AI219207	Hs.72222	Homo sapiens cD	TM
70	454293	H49739	Hs.134013	ESTs, Moderate	TM
	442577	AA292998	Hs.163900	ESTs	TM
	426174	AA547959	Hs.115838	ESTs	SS
	418869	AW516565	Hs.258279	ESTs	Sema,TM,
	418054	NM_002318	Hs.83354	lysyl oxidase-I	Lysyl_oxidase,SRCR,SS
75	442295	AI827248	Hs.224398	Homo sapiens cD	Collagen,COLFI,vwc,TM,SS
	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,
	421948	L42583	Hs.111758	keratin 5A	filamenLTM,
	444783	AK001468	Hs.62180	anillin (Drosop	PH,TM,
	437527	AI241019	Hs.145644	ESTs	PIPSK,TM,SS
80	433084	M18079	Hs.282265	fatty acid bind	lipocatin,SS
	452401	NM_007115	Hs.29352	tumor necrosis	Xlink,CUB,TM,SS
	458897	U85642	Hs.138506	ESTs	TM
	413808	J00287	Hs.182183	caldesmon 1	asp,TM,SS
	411274	NM_002776	Hs.69423	kallikrein 10	trypsin,TM,

5	418406	X73501	Hs.84905	cytokeratin 20	filament, TM,	3.32
	419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4, zf-B_box, TM,	3.32
	423217	NM_000094	Hs.1640	collagen, type	fn3, Collagen, Kunitz_BPT1, vwa, SS	3.31
	411558	AA102670	Hs.70725	gamma-aminobuty	neur_chan, TM, SS	3.30
	427722	AK000123	Hs.180479	hypothetical pr	PH, SS	3.30
	422310	AA316622	Hs.98370	cytochrome P540	p450, SS	3.30
	411263	BE297802	Hs.69360	kinesin-like 6	kinesin, TM,	3.29
	443426	AF098158	Hs.9329	chromosome 20 o	TM	3.28
10	452121	NM_004081	Hs.70936	deleted in azoo	TM	3.27
	447342	AI199268	Hs.19322	ESTs	TM, SS	3.25
	452699	AW295390	Hs.213062	ESTs	TM	3.23
	425188	AK002052	Hs.155071	hypothetical pr	TM	3.23
	400289	X07820	Hs.2258	matrix metallo	hemopexin, SS	3.21
15	408524	D87942	Hs.46328	fucosyltransfer	Glyco_transf_11, TM, SS	3.20
	437897	AA770561	Hs.145170	hypothetical pr	TM	3.20
	453922	AF053306	Hs.36708	budding uninhib	TM	3.19
	406690	M29540	Hs.220529	carcinoembryoni	ig, TM, SS	3.19
	416209	AA236776	Hs.79078	MAD2 (mitotic a	HORMA, SS	3.16
20	408113	T82427	Hs.194101	Homo sapiens cD	7tm_3, TM,	3.14
	425465	L18964	Hs.1904	protein kinase	Slk_Sno, DAG_PE-bind, OPR, pkise, pkise_C, TM, SS	3.13
	419216	AU076718	Hs.164021	small inducible	IL8, TM, SS	3.13
	418203	X54942	Hs.83758	CDC28 protein k	CKS, TM,	3.12
	417315	AI080042	Hs.180450	ribosomal prote	TM, SS	3.11
25	433001	AF217513	Hs.279905	clone HQ0310 PR	TM, SS	3.11
	459587	AA031956		gb:zkl5e04.s1 S	UM, TM,	3.11
	421379	Y15221	Hs.103982	small inducible	IL8, TM, SS	3.10
	414774	X02419	Hs.77274	plasminogen act	kringle, trypsin, SS	3.10
	407289	AA135159	Hs.203349	Homo sapiens cD	TM	3.09
30	447519	U46258	Hs.23448	ESTs	histone, Ribosomal_L22e, TM,	3.08
	448045	AJ297436	Hs.20166	prostate stem c	TM, SS	3.07
	431956	AK002032	Hs.272245	Homo sapiens cD	RA, SS	3.06
	409632	W74001	Hs.55279	serine (or cyst	serpin, TM,	3.05
35	454034	NM_000691	Hs.575	aldehyde dehydr	aldedh, TM,	3.05
	436481	AA379597	Hs.5199	HSPC150 protein	UQ_con, TM,	3.05
	428987	NM_004751	Hs.194710	glucosaminyl (N	Branch, TM, SS	3.04
	424252	AK000520	Hs.143811	hypothetical pr	casein_kappa, SS	3.04
	436291	BE568452	Hs.5101	protein regulat	TM	3.03
	411789	AF245505	Hs.72157	Homo sapiens ad	ig, LRRCT, SS	3.02
40	417956	AA210704	Hs.190465	ESTs	sushi, SS	3.02
	408908	BE296227	Hs.48915	serine/threonin	pkise, TM, SS	3.01
	422330	D30783	Hs.115263	epiregulin	EGF, TM, SS	3.01
	425071	NM_013989	Hs.154424	deiodinase, iod	T4_deiodise, TM, SS	3.00
	425761	AW664214	Hs.196729	ESTs	SH3, TM,	2.99
45	432978	AF126743	Hs.279884	DNAJ domain-con	DJ, TM,	2.99
	418546	AA224827		gb:nc32g04.s1 N	vwa, integrin_A, FG-GAP, TM, SS	2.99
	425371	D49441	Hs.155981	mesothelin	TM, SS	2.99
	422440	NM_004812	Hs.116724	aldo-keto reduc	aldo_ket_red, TM,	2.98
	439453	BE264974	Hs.6566	thyroid hormone	AAA, TM,	2.98
50	413278	BE563085	Hs.833	interferon-stim	ubiquitin, TM,	2.97
	428450	NM_014791	Hs.184339	KIAA0175 gene p	pkise, KA1, TM,	2.95
	424345	AK001380	Hs.145479	Homo sapiens cD	TM, SS	2.95
	433133	AB027249	Hs.104741	PDZ-binding kin	pkise, TM,	2.94
	432269	NM_002447	Hs.2942	macrophage stim	pkise, Sema, Plexin_repeat, TIG, TM, SS	2.94
55	432917	NM_014125	Hs.279812	PRO0327 protein	TM	2.94
	432731	R31178	Hs.287820	fibronectin 1	SS	2.93
	420552	AK000492	Hs.98806	hypothetical pr	SS	2.92
	428303	AW974476	Hs.183601	regulator of G-	RGS, TM,	2.92
	409687	T51125	Hs.8493	ESTs	Ets, SAM_PNT, TM,	2.91
60	457288	AA521458	Hs.192738	ESTs	TM	2.89
	456181	L36463	Hs.1030	ras inhibitor	RA, VPS9, TM, SS	2.89
	450190	T51387		gb:yb20e08.r1 S	SH3, TM,	2.88
	430204	AA618335	Hs.146137	ESTs, Weakly si	TM	2.88
	434808	AF155108	Hs.256150	ESTs, Highly si	TM	2.87
65	450983	AA305384	Hs.25740	ERO1 (S. cerevi	SS	2.87
	418670	AA601036	Hs.285083	ESTs	TM	2.87
	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain, TM,	2.87
	435099	AC004770	Hs.4756	flap structure-	XPG_I, XPG_N, TM,	2.86
	402075				serpin, TM,	2.84
70	410681	AW246890	Hs.65425	calbindin 1, (2	efhand, FHA, BRCT, adh_short, adh_short_C2, TM,	2.83
	439867	AA847510	Hs.161292	ESTs	TM	2.83
	443715	AI583187	Hs.9700	cyclin E1	cyclin, TM, SS	2.83
	417366	BE185289	Hs.1076	small protine-r	Cornifin, TM,	2.83
	422283	AW411307	Hs.114311	CDC45 (cell div	CDC45, TM, SS	2.82
75	404567				HECT, zf-UBR1, TM,	2.82
	422158	L10343	Hs.112341	protease inhibi	wap, SS	2.82
	449224	AW995911	Hs.299883	hypothetical pr	fn3, TM,	2.81
	407584	W25945	Hs.18745	ESTs	PK, SS	2.81
	453884	AA355925	Hs.36232	KIAA0186 gene p	TM	2.81
80	449032	AA045573	Hs.22900	nuclear factor	bZIP, Chromo_shadow, TM, SS	2.80
	422809	AK001379	Hs.121028	hypothetical pr	IQ, TM,	2.79
	449722	BE280074	Hs.23960	cyclin B1	cyclin, TM,	2.79
	453028	AB006532	Hs.31442	RecQ protein-li	DEAD, helicase_C, TM,	2.78
	421777	BE562088	Hs.108196	HSPC037 protein	TM	2.78

	452571	W31518	Hs.34665	ESTs	TM	
	422675	BE018517	Hs.119140	eukaryotic tran	eIF-5a, TM,	2.77
	400298	AA032279	Hs.61635	six transmembra	TM	2.77
5	414569	AF109298	Hs.118258	prostate cancer	TM	2.76
	449378	AW664026	Hs.59892	ESTs	TM	2.76
	423903	M57765	Hs.1721	interleukin 11	TM, SS	2.75
	431104	AW970859	Hs.269109	ESTs	Sema, TM, SS	2.75
	452940	AA029722	Hs.20279	ESTs	7tm_1, TM, SS	2.75
10	432201	AI538613	Hs.135657	ESTs	trypsin, TM,	2.74
	414617	AI339520	Hs.20524	ESTs, Moderatel	hexokise, TM,	2.73
	444301	AK000136	Hs.10760	hypothetical pr	LRR, TM,	2.73
	426711	AA383471	Hs.180689	conserved gene	TM	2.72
	429432	AI678059	Hs.202676	synaptonemal co	TM	2.71
15	450506	NM_004460	Hs.418	fibroblast aci	Peptidase_S9, DPPIV_N_term, SS	2.71
	427528	AU077143	Hs.179565	minichromosome	MCM, TM, SS	2.71
	418801	AA228366	Hs.115122	ESTs	integrin_A, FGF-GAP, TM, SS	2.71
	429486	AF155827	Hs.203963	hypothetical pr	SNF2_N, helicase_C, TM,	2.71
	408366	AW511255	Hs.258082	ESTs	SS	2.71
20	406399				kazal, TM, SS	2.70
	446269	AW263155	Hs.14559	hypothetical pr	TM	2.69
	426514	BE616633	Hs.301122	bone morphogene	TGF-beta, TGFb_propeptide, TM, SS	2.68
	417079	U65590	Hs.81134	interleukin 1 r	IL1, SS	2.67
	444754	T83911	Hs.11881	transmembrane 4	TM, SS	2.67
25	424687	J05070	Hs.151738	matrix metallo	fn2, hemopexin, Peptidase_M10, SS	2.67
	439979	AW600291	Hs.6823	hypothetical pr	TM	2.66
	430832	AI073913	Hs.100686	ESTs, Weakly si	TM, SS	2.65
	429170	NM_001394	Hs.2359	dual specificit	DSPc, Rhodanese, TM,	2.65
	450400	AI694722	Hs.279744	ESTs	TM	2.64
30	435380	AA679001	Hs.192221	ESTs	Occludin, TM, SS	2.64
	432375	BE536069	Hs.2962	S100 calcium-bi	S_100, ethand, TM, SS	2.64
	453700	AB009426	Hs.560	apolipoprotein	dCMP_cyt_deam, sugar_tr, TM, SS	2.63
	422938	NM_001809	Hs.1594	centromere prot	histone, TM,	2.63
	453134	AA032211	Hs.118493	ESTs	adh_short, TM, SS	2.63
35	420727	H75701	Hs.99886	complement comp	sushi,	2.63
	408868	AW292286	Hs.255058	ESTs	TM	2.62
	414972	BE263782	Hs.77695	KIAA0008 gene p	TM	2.62
	403055				filament, TM, SS	2.62
40	447400	AK000322	Hs.18457	hypothetical pr	zf-C3HC4, TM,	2.62
	413753	U17760	Hs.301103	Human DNA seque	laminin_EGF, laminin_Nterm, SS	2.61
	433220	AI076192	Hs.131933	ESTs	TM	2.61
	436251	BE515065	Hs.5092	nucleolar prote	Nop, TM, SS	2.60
	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan, TM, SS	2.60
	425463	AK000740	Hs.157986	hypothetical pr	TM	2.60
45	435370	AI964074	Hs.225838	ESTs	EGF, fn3, fibrinogen_C, TM, SS	2.59
	432215	AU076609	Hs.2934	ribonucleotide	ribonucleo_red, ribonuc_red Ig, TM,	2.59
	409142	AL136877	Hs.50758	chromosome-asso	SMC_N, TM, SS	2.59
	443919	AI091284	Hs.135224	ESTs	adh_short, TM, SS	2.58
	413268	AL039079	Hs.75256	regulator of G-	RGS, TM,	2.58
50	404519				defensins, SS	2.58
	414998	NM_002543	Hs.77729	oxidised low de	TM	2.57
	429597	NM_003816	Hs.2442	a disintegrin a	TM, SS	2.57
	426841	AI052358	Hs.193726	ESTs	asp, TM, SS	2.57
55	416768	AA363733	Hs.1032	regenerating is	lectin_c, SS	2.57
	417933	X02308	Hs.82962	thymidylate syn	thymidylat_synt, SS	2.56
	441384	AA447849	Hs.288660	protease, serin	TM	2.56
	451939	U80456	Hs.27311	single-minded (PAC, PAS, BPL, BPL_C, TM,	2.56
	418867	D31771	Hs.89404	msh (Drosophila	homeobox, TM,	2.55
	416065	BE267931	Hs.78996	proliferating c	TM	2.55
60	431890	X17033	Hs.271986	integrin, alpha	vwa, integrin_A, FGF-GAP, TM, SS	2.55
	407830	NM_001086	Hs.587	arylacetamide d	COesterase, 7tm_1, TM, SS	2.55
	434815	AF155582	Hs.46744	core 1 UDP-galac	SS	2.54
	435647	AI653240	Hs.49823	ESTs	TM	2.54
65	459306	AW578452	Hs.232988	ESTs, Weakly si	TM, SS	2.54
	414361	AI086138	Hs.204044	ESTs	TM	2.54
	425782	U66468	Hs.159525	cell growth reg	SS	2.54
	416984	H38765	Hs.80706	diaphorase (NAD	TM	2.53
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-G	ER_lumen_recept, IRK, DEAD, helicase_C, TM, SS	2.53
	456743	AI630124	Hs.7434	ESTs	TM	2.53
70	410268	AA316181	Hs.61635	six transmembra	TM	2.52
	424905	NM_002497	Hs.153704	NIMA (never in	pkuse, TM,	2.52
	432657	AA831815	Hs.270940	ESTs	TM	2.51
	434080	AI820719	Hs.154662	hypothetical pr	DJ_CXXCXGXG, TM, SS	2.51
	418969	W33191	Hs.28907	hypothetical pr	SH3, TM,	2.51
75	431808	M30703	Hs.270833	amphiregulin (s	EGF, TM, SS	2.51
	429093	NM_000253	Hs.195799	microsomal trig	Vitellogenin_N, TM, SS	2.51
	447634	AW967902	Hs.5152	Homo sapiens cD	TM	2.50
	436393	AW022213	Hs.143617	ESTs	Galactosyl_T_2, TM, SS	2.50
	453751	R36762	Hs.101282	Homo sapiens mR	TM	2.50
80	445865	AI262584	Hs.145575	ESTs	SS	2.49
	414883	AA926960	Hs.77550	CDC28 protein k	CKS, TM,	2.49
	406747	AI925153	Hs.217493	annexin A2	TM	2.49
	446921	AB012113	Hs.16530	small inducible	IL8, SS	2.49
	426322	J05068	Hs.2012	transcobalamin	Cobalamin_bind, TM, SS	2.48

5	422515	AW500470	Hs.117950	multifunctional	AIRC,SAICAR_synth,TM,	2.48
	447030	AW444659	Hs.232184	ESTs	TM	2.48
	448454	NM_005879	Hs.21254	TRAF interactin	zf-C3HC4,TM,	2.48
	419092	J05581	Hs.89603	mucin 1, trans	SEA,TM,SS	2.48
	409640	U78722	Hs.55481	zinc finger pro	zf-C2H2,SCAN,TM,	2.48
10	404171				sodfe,TM,	2.47
	414747	U30872	Hs.77204	centromere prot	SS	2.47
	410406	AI969703	Hs.301842	ESTs	FGGY,TM,	2.47
	452220	BE158006	Hs.212296	ESTs	FG-GAP,TM,SS	2.46
	421493	BE300341	Hs.104925	ectodermal-neur	BTB,Kelch,TM,	2.46
15	444838	AV651680	Hs.208558	ESTs	integrin_A,FG-GAP,TM,SS	2.46
	413816	AW958181	Hs.189998	ESTs	AMP-binding,G_glu_transpept,TM,	2.46
	436613	AA972691	Hs.192974	Homo sapiens cD	TM,SS	2.45
	432874	W94322	Hs.279651	melanoma inhibi	SH3,SS	2.45
	425397	J04088	Hs.156346	topoisomerase (HATPase_c,SS	2.45
20	422363	T55979	Hs.115474	replication fac	TM	2.45
	431924	AK000850	Hs.272203	Homo sapiens cD	SH3,TM,	2.44
	431457	NM_012211	Hs.256297	integrin, alpha	FG-GAP,vwa,TM,SS	2.44
	416498	U33632	Hs.79351	potassium chann	TM	2.44
	428484	AF104032	Hs.184601	solute carrier	aa_permeases,TM,	2.43
25	431958	X63629	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM,SS	2.43
	413833	Z15005	Hs.75573	centromere prol	kinesin,TM,	2.43
	407243	AA058357	Hs.74466	carcinoembryoni	TM,SS	2.43
	410044	BE566742	Hs.58169	highly expresse	TM,SS	2.43
	424273	W40460	Hs.144442	phospholipase A	phoslip,TM,SS	2.42
30	409533	AW969543	Hs.21291	mitogen-activat	TM,SS	2.42
	419741	NM_007019	Hs.93002	ubiquitin carri	UQ_con,efhand,TM,SS	2.42
	449987	AW079749	Hs.184719	ESTs, Weakly si	ABC_tran,ABC_membrane,TM,	2.42
	433159	AB035898	Hs.150587	kinesin-like pr	kinesin,Myosin_tail,TM,SS	2.42
	439396	BE562958	Hs.74346	ESTs, Weakly si	SS	2.42
35	426427	M86699	Hs.169840	TTK protein kin	pkise,TM,	2.41
	434725	AK000796	Hs.4104	hypothetical pr	TM	2.41
	433312	AJ241331	Hs.131765	ESTs	zf-C2H2,SS	2.41
	407047	X65965		gb:H.sapiens SO	sodfe,TM,	2.41
	419220	AA811938	Hs.291759	ESTs	TM,SS	2.40
40	416530	U62801	Hs.79361	kallikrein 6 (n	trypsin_pro_isomerase,TM,SS	2.40
	435219	AA676349	Hs.190331	ESTs	TM	2.40
	418322	AA284166	Hs.84113	cyclin-dependen	SS	2.40
	404253				histone,TM,SS	2.40
	428970	BE276891	Hs.194691	retinoic acid i	7tm_3,TM,	2.40
45	418693	AI750878	Hs.87409	thrombospondin	EGF,TSPN,tsp_1,tsp_3,vwc,SS	2.39
	451237	AW600293		gb:EST00049 pGE	TM	2.39
	407756	AA116021	Hs.38260	ubiquitin speci	UCH-1,UCH-2,SS	2.39
	437935	AW939591	Hs.5940	hypothetical pr	TM,SS	2.39
	445625	BE246743	Hs.288529	Homo sapiens cD	TM	2.39
50	435937	AA830893	Hs.119769	ESTs	TM	2.39
	438993	AA828995		gb:od77b08.s1 N	integrin_B,TM,SS	2.38
	422082	AA016188	Hs.111244	hypothetical pr	TM	2.38
	450396	AU077002	Hs.24950	regulator of G-	RGS,TM,	2.38
	422578	AF239666	Hs.1545	caudal type hom	homeobox,SS	2.38
55	428070	T63918	Hs.182313	retinol-binding	lipocalin,TM,	2.38
	416111	AA033813	Hs.79018	chromatin assem	TM,SS	2.37
	433345	AI681545	Hs.152982	Homo sapiens cD	TM	2.37
	427557	NM_002659	Hs.179657	plasminogen act	UPAR_LY6,SS	2.37
	423554	M90516	Hs.1674	glutamine-fruct	GATase_2,Sis,TM,SS	2.37
60	453204	R10799	Hs.191990	ESTs	TM	2.37
	425081	X74794	Hs.154443	minichromosome	MCM,TM,	2.36
	434682	AA827165	Hs.191958	ESTs	TM	2.36
	414108	AI267592	Hs.75761	SFRS protein ki	pkise,TM,	2.36
	417900	BE250127	Hs.82906	CDC20 (cell div	WD40,TM,	2.36
65	428046	AW812795	Hs.155381	ESTs, Moderatel	ank,SS	2.36
	448019	AW947164	Hs.195641	ESTs	TM	2.36
	431753	X76029	Hs.2841	neuromedin U	NMU,TM,SS	2.36
	410361	BE391804	Hs.62661	guanylate bindi	GBP,TM,SS	2.36
	418526	BE019020	Hs.85838	solute carrier	MCT,TM,SS	2.36
70	444478	W07318	Hs.240	M-phase phospho	kinesin,SS	2.36
	436961	AW375974	Hs.156704	ESTs	TM	2.35
	408194	AA601038	Hs.191797	ESTs	TM	2.35
	438578	AA811244	Hs.164168	ESTs	formyl_transf,AIRS,GARS,TM,	2.35
	429183	AB014604	Hs.197955	KIAA0704 protei	TM	2.35
75	453900	AW003582	Hs.226414	ESTs, Weakly si	TM	2.33
	432877	AW974111	Hs.292477	ESTs	Ets,SAM_PNT,TM,	2.33
	451928	AI823801	Hs.30315	ESTs	TM	2.33
	418245	AA088767	Hs.83883	transmembrane,	ldl_recept_a,TM,SS	2.33
	435106	AA100847	Hs.193380	ESTs, Highly si	TM	2.33
80	432193	AA372264	Hs.273193	hypothetical pr	TM,SS	2.33
	449532	W74653	Hs.271593	ESTs	TM	2.33
	409703	NM_006187	Hs.56009	Z'-5'oligoadeny	NTP_transf_2,TM,SS	2.33
	419373	NM_003244	Hs.90077	TG-interacting	homeobox,SS	2.32
	435607	W73428	Hs.8750	uncharacterized	SS	2.32
	405818				TM,SS	2.32
	444371	BE540274	Hs.239	forkhead box M1	Fork_head,SS	2.32
	432675	AI791855	Hs.105884	ESTs	PDEase,TM,	2.32

	411773	NM_006799	Hs.72026	protease, serin	trypsin,SS	2.31
	434775	AA648983	Hs.212911	ESTs	TM,SS	2.31
	422611	AA158177	Hs.118722	lucosyltransfer	SS	2.31
5	419493	AF001212	Hs.90744	proteasome (pro	SS	2.31
	424435	AB011167	Hs.146957	KIAA0595 protei	TM	2.30
	409262	AK000631	Hs.52256	hypothetical pr	WD40,TM,SS	2.30
	428125	AA393071	Hs.182579	leucine aminope	Peptidase_M17,TM,SS	2.30
	417655	AA780791	Hs.14014	ESTs, Weakly si	TM	2.29
10	407287	AI678812	Hs.201658	ESTs, Weakly si	ras,TM,SS	2.29
	428923	BE047698	Hs.188785	ESTs	TM,SS	2.29
	452203	X57522	Hs.158164	ATP-binding cas	ABC_tran,ABC_membrane,TM,	2.29
	409402	AF208234	Hs.695	cystatin 8 (ste	cystatin,SS	2.29
	419359	AL043202	Hs.90073	chromosome segr	TM,SS	2.29
15	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu	TM,SS	2.29
	400811	AF219139	Hs.87726	KIAA0154 protei	Cobalamin_bind,SS	2.29
	420931	AF044197	Hs.100431	small inducible	IL8,TM,SS	2.28
	425247	NM_005940	Hs.155324	matrix metallopro	hemopexin,Peptidase_M10,TM,SS	2.28
20	438170	AI918685	Hs.194601	ESTs	2-Hacid_DH,TM,	2.28
	445378	AV653564	Hs.226946	ESTs	TM	2.28
	428048	AA705745	Hs.185070	ESTs	AMP-binding,TM,	2.28
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS	2.27
	433535	AF111106	Hs.3382	protein phosphat	TM	2.27
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,SS	2.27
25	405545				ABC_tran,ABC_membrane,TM,SS	2.27
	445537	AJ245671	Hs.12844	EGF-like-domain	ECF,SS	2.27
	423634	AW959908	Hs.1690	heparin-binding	TM,SS	2.26
	407742	AF186252	Hs.38084	sulfotransferase	Sulfotransfer,SS	2.26
	428330	L22524	Hs.2256	matrix metallopro	Peptidase_M10,SS	2.26
30	429731	AK001592	Hs.212172	beta,beta-carot	TM	2.26
	400514				p450,TM,SS	2.26
	431846	BE019924	Hs.271580	uroplakin 1B	transmembrane4,TM,SS	2.26
	426010	AA136563	Hs.1975	Homo sapiens cD	TM	2.26
	437641	AA811452	Hs.291911	ESTs	TM	2.26
35	411393	AW797437	Hs.69771	B-factor, prope	sushi,trypsin,ywa,DEAD,rmn,EGF,fn3,fibrinogen_C,SS	2.26
	414809	AI434699	Hs.77356	transferrin rec	PA,Ribosomal_S2,TM,	2.25
	419488	AA316241	Hs.90691	nucleophosmin/h	SS	2.25
	434540	NM_016045	Hs.5184	TH1 drosophila	TM	2.25
	410196	AJ936442	Hs.59838	hypothetical pr	UBACT_repeat,TM,	2.25
40	456844	AI264155	Hs.152981	CDP-diacylglyce	Cydidyllyltrans,TM,	2.25
	408353	BE439838	Hs.44298	hypothetical pr	Ribosomal_S17,TM,	2.25
	448753	AL048858	Hs.224355	ESTs, Weakly si	TM	2.25
	428479	Y00272	Hs.184572	cell division c	pkise,TM,SS	2.24
	424971	AA479005	Hs.154036	tumor suppressi	ion_trans,PH,TM,	2.24
45	432673	AB028859	Hs.278605	ER-associated D	DJ,DJ_C,TM,SS	2.24
	409432	D49372	Hs.54460	small inducible	IL8,TM,SS	2.24
	429925	NM_000786	Hs.226213	cytochrome P450	p450,TM,SS	2.24
	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099,TM,SS	2.23
	447532	AK000614	Hs.18791	hypothetical pr	TM	2.23
50	423515	AA327017	Hs.162204	ESTs	SS	2.23
	444743	AA045648	Hs.11817	nudix (nucleosi	mutT,TM,	2.23
	434518	H56995	Hs.37372	Homo sapiens DN	TM	2.23
	435602	AF217515	Hs.283532	uncharacterized	TM,SS	2.23
	449974	AW970948	Hs.269403	ESTs	TM,SS	2.23
55	424927	AW973666	Hs.153850	hypothetical pr	TM	2.23
	414420	AA043424	Hs.76095	immediate early	TM	2.23
	431840	AA534908	Hs.2860	POU domain, cla	homeobox,pou,TM,SS	2.23
	452930	AW195285	Hs.194097	ESTs	SS	2.23
	436391	AJ227892	Hs.146274	ESTs	SS	2.23
60	439186	AK697274	Hs.6487	Xq28, 2000bp se	Epimerase,SS	2.23
	414732	AW410976	Hs.77152	minichromosome	MCM,TM,	2.22
	411835	U29343	Hs.72550	hyaluronan-medi	TM	2.22
	438223	AA781171		gb:aj24d05.s1 S	myosin_head,TM,	2.22
	450149	AW969781	Hs.293440	ESTs, Moderate	TM	2.22
65	401519				filament,TM,	2.22
	441794	AW197794	Hs.253338	ESTs	ank,TM,	2.22
	408901	AK001330	Hs.48855	hypothetical pr	TM	2.21
	434423	NM_006769	Hs.3844	LIM domain only	LIM,TM,	2.21
70	432140	AK000404	Hs.272688	hypothetical pr	SS	2.21
	423453	AW450737	Hs.128791	CGI-09 protein	Granin,CDP-OH_P_transf,TM,	2.21
	428438	NM_001955	Hs.2271	endothelin 1	endothelin,TM,SS	2.21
	421470	R27496	Hs.1378	annexin A3	annexin,TM,SS	2.21
	440381	AA917808	Hs.190495	ESTs	TM,SS	2.20
	453779	N35187	Hs.43388	ESTs	TM,SS	2.20
75	433627	AF078866	Hs.284296	Homo sapiens cD	SURF4,TM,	2.20
	417944	AL007719	Hs.82985	collagen, type	COLF1,Collagen,vwc,TM,SS	2.20
	422689	AW856655		gb:RC3-CT0297.2	SNF2_N,TM,	2.20
	448457	H65629	Hs.245997	ESTs	TM,SS	2.20
	426125	X87241	Hs.166994	FAT tumor suppr	EGF,cadherin,laminin_G,TM,SS	2.20
80	430603	AA148164	Hs.247280	HBV associated	zf-C3HC4,TM,	2.20
	425274	BE281191	Hs.155462	minichromosome	MCM,TM,	2.20
	452679	Z42387	Hs.4299	Homo sapiens cD	TM	2.20
	410619	BE512730	Hs.65114	keratin 18	filament,TM,	2.20
	424332	AA338919	Hs.101615	ESTs	SS	2.20

	418661	NM_001949	Hs.1189	Human mRNA for	E2F_TDP,TM,SS	2.20
	419341	N71463	Hs.118888	ESTs, Weakly si	UPF0016,TM,SS	2.20
	427920	Z11502	Hs.181107	annexin A13	annexin,TM,	2.19
5	403208				lectin_c,TM,SS	2.19
	422596	AF063611	Hs.118633	2'-5'oligoadeny	ubiquitin,SS	2.19
	444261	AA298958	Hs.10724	MDS023 protein	TM	2.19
	423401	NM_001992	Hs.128087	coagulation fac	7tm_1,TM,SS	2.18
	453450	AW797627	Hs.89474	ADP-ribosylatio	SS	2.18
10	444334	BE296785	Hs.10848	.KIAA0187 gene p	SS	2.18
	437616	AI797163	Hs.207954	ESTs	SMC_N,TM,SS	2.18
	451807	W52854	Hs.27099	DKFZP564J0863 p	TM	2.18
	430441	BE398091	Hs.6880	DKFZP434D156 pr	TM	2.18
	411678	AI907114	Hs.71465	squalene epoxid	Monooxygese,TM,	2.18
15	452291	AF015592	Hs.28853	CDC7 (cell divi	pkise,TM,	2.18
	444342	NM_014398	Hs.10887	similar to lyso	Lamp,TM,SS	2.18
	451099	RS2795	Hs.25954	interleukin 13	fn3,TM,SS	2.18
	425873	NM_013390	Hs.160417	transmembrane p	TM	2.17
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	2.17
20	446995	AI355012		gb:qu16d10.x1 N	TM	2.17
	439961	AA857451	Hs.269696	ESTs	TM	2.17
	429125	AA446854	Hs.271004	ESTs	TM	2.17
	407103	AA424881	Hs.256301	ESTs	TM	2.17
	415116	AA160363	Hs.269956	ESTs	ER_human_recept,TM,SS	2.17
25	440052	AI633744	Hs.195648	ESTs	PAC,TM,SS	2.17
	423961	D13666	Hs.136348	osteoblast spec	Fascidin,TM,SS	2.17
	431070	AW408164	Hs.249184	transcription f	FHA,SS	2.16
	443599	AI079559	Hs.134125	ESTs	TM	2.16
	427258	AA400091	Hs.39421	ESTs	TM	2.16
30	418113	AI272141	Hs.83484	SRY (sex determ	HMG_box,TM,	2.16
	450835	BE262773	Hs.25584	hypothetical pr	ArlGap,SS	2.16
	449057	AB037784	Hs.22941	KIAA1363 protei	TM	2.16
	448153	Y10805	Hs.20521	HMT1 (hnRNP met	TM,SS	2.16
	424653	AW977534	Hs.151469	calcium/calmodu	Guanylate_kin,PDZ,pkise,SH3,TM,	2.16
35	431341	AA307211	Hs.251531	proteasome (pro	proteasome,TM,	2.16
	452865	AI924046	Hs.119567	ESTs	PMP22_Claudin,TM,SS	2.16
	432789	D26361	Hs.3104	KIAA0042 gene p	TM	2.16
	438580	AA811262	Hs.299202	ESTs	pkise,TM,	2.16
	422192	AA305159	Hs.113019	fts485	SS	2.15
40	425607	U09860	Hs.158333	protease, serin	ldl_recept_a,trypsin,CUB,SrcR,MAM,SEA,TM,SS	2.15
	447289	AW247017	Hs.36978	melanoma antige	3Beta_HSD,Epimerase,MAGE,TM,	2.15
	447674	BE270640	Hs.19192	cyclin-dependen	pkise,TM,	2.15
	441021	AW578716	Hs.7644	H1 histone fami	linker_histone,TM,	2.15
	426471	M22440	Hs.170009	transforming gr	EGF,TM,SS	2.15
45	431941	AK000106	Hs.272227	Homo sapiens cD	pkise,Furin-like,TM,SS	2.15
	414761	AU077228	Hs.77256	enhancer of zes	SET,TM,	2.15
	410407	X66839	Hs.63287	carbonic anhydr	carb_anhydrase,TM,SS	2.15
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	2.15
	419239	AA468183	Hs.184598	Homo sapiens cD	TM	2.15
50	452721	AJ269529	Hs.30377	Homo sapiens ES	TM	2.15
	410664	NM_006033	Hs.65370	lipase, endothe	Ribosomal_L22,lipase,PLAT,TM,SS	2.14
	452835	AK001269	Hs.30738	hypothetical pr	TM	2.14
	452092	BE245374	Hs.27842	hypothetical pr	Acyltransferase,TM,SS	2.14
	401708				SS	2.14
55	411400	AA311919	Hs.69851	GAR1 protein	TM	2.14
	448526	AB028946	Hs.21361	KIAA1023 protei	TM	2.14
	421175	AI879099	Hs.102397	GIOT-3 for gona	zf-C2H2,KRAB,TM,SS	2.14
	413511	AI627178	Hs.75412	Arginine-rich p	TM	2.13
60	432945	AL043683	Hs.271357	ESTs, Weakly si	PK,SS	2.13
	418592	X99226	Hs.284153	Fanconi anemia,	TM	2.13
	425298	AK000209	Hs.155556	hypothetical pr	TM	2.13
	450956	AW193531	Hs.205647	ESTs, Moderatel	pkise,TM,SS	2.13
	419569	AI971651	Hs.91143	jagged 1 (Alagi	EGF_DSL,TM,SS	2.13
65	421508	NM_004833	Hs.105115	absent in melan	TM	2.13
	413670	AB000115	Hs.75470	hypothetical pr	TM	2.13
	422783	AA598956	Hs.120439	ethanolamine ki	Choline_kise,TM,	2.13
	410418	D31382	Hs.63325	transmembrane p	trypsin,ldl_recept_a,TM,SS	2.13
	414860	BE255593	Hs.77502	methionine aden	S-AdoMet_synt,SS	2.13
70	425860	L29339	Hs.1964	solute carrier	SSF,Ribosomal_S17e,TM,	2.13
	414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	2.13
	437050	AA766420	Hs.291606	ESTs	TM	2.13
	430217	N47863	Hs.180450	ribosomal prote	TM,SS	2.13
	409012	AL117435	Hs.49725	DKFZP434I216 pr	RhoGEF,TM,	2.12
	428365	AA295331	Hs.183861	Homo sapiens cD	TM	2.12
75	410839	NM_006849	Hs.66581	protein disulf	thiorel,TM,	2.12
	450510	AA010056	Hs.242998	ESTs	TM,SS	2.12
	427475	AA403151	Hs.191605	ESTs	SS	2.12
	433748	R12244		gb:yrf33c12.r1 S	AMP-binding,TM,	2.12
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPT1,G-gamma,TM,SS	2.11
80	414788	X78342	Hs.77313	cyclin-dependen	pkise,TM,SS	2.11
	415474	NM_014252	Hs.78457	solute carrier	mito_carr,TM,	2.11
	416472	AA180756	Hs.193094	ESTs, Moderatel	TM	2.11
	410718	AI920783	Hs.191435	ESTs	SQS_PSY,TM,SS	2.11
	425811	AL039104	Hs.159557	karyopherin alp	Armado seg_1BB,TM,SS	2.11

	447197	R36075		gb:yh88b01.s1 S		
	431621	AW292329	Hs.163481	ESTs	SDF,TM,	2.11
	433849	BE465884	Hs.280728	ESTs	PH_Band_41,TM,SS	2.11
5	438038	AI732629	Hs.194161	ESTs, Weakly si	SS	2.11
	422032	AA476966	Hs.110857	polymerase (RNA	Cytidylyltrans,TM,	2.11
	409717	AW452871	Hs.56043	CGI-115 protein	TFIIS,TM,SS	2.11
	445837	AI261700	Hs.145544	ESTs	TM	2.11
	423880	BE278111	Hs.134200	DKFZP564C186 pr	TM	2.11
10	421574	AJ000152	Hs.105924	defensin, beta	Defensin_beta,TM,SS	2.10
	437103	AW139408	Hs.152940	ESTs	Choline_kise,TM,	2.10
	450747	AI064821	Hs.48306	ESTs, Highly si	rm,TM,	2.10
	437033	AW248364	Hs.5409	RNA polymerase	TM	2.10
	417640	D30857	Hs.82353	protein C recep	TM,SS	2.10
15	431120	AA492588		gb:ng99c08.s1 N	TM,SS	2.10
	430510	AW162916	Hs.241576	hypothetical pr	TM	2.10
	429669	BE185499	Hs.2471	KIAA0020 gene p	TM	2.10
	407881	AW072003	Hs.40968	heparan sulfate	SS	2.10
	436415	BE265254	Hs.5181	proliferation-a	Peptidase_M24,TM,SS	2.10
20	407887	AA579668	Hs.41072	serine (or cyst	serpin,TM,	2.10
	447815	AI432199	Hs.247084	ESTs	LIM,TM,	2.10
	434274	AA628539	Hs.116252	ESTs, Moderatel	rm,TM,SS	2.09
	411571	AA122393	Hs.70811	hypothetical pr	SS	2.09
	442525	AF150282	Hs.145945	ESTs	pkise,TM,	2.09
25	423750	AF165883	Hs.132415	prefoldin 2	TM	2.09
	449199	AI990122	Hs.196988	ESTs	ras,TM,	2.09
	415363	AI670947	Hs.78406	phosphatidyino	PIP5K,pkise,TM,SS	2.09
	418462	BE001596	Hs.85266	integrin, beta	integrin_B,fn3,TM,SS	2.09
	430335	D80007	Hs.239499	KIAA0185 protei	S1,TM,	2.09
30	443450	N66045	Hs.133529	ESTs	TM	2.08
	418753	BE217818	Hs.87016	Homo sapiens cD	TM	2.08
	439018	AW300887	Hs.26638	ESTs, Weakly si	TM,SS	2.08
	431628	AF146277	Hs.265561	CD2-associated	SH3,SS	2.08
	446528	AU076640	Hs.15243	nucleolar prote	Nol1_Nop2_Sun,TM,	2.08
35	411372	AI147861	Hs.213289	low density lip	EGF_idl_recept_a,Idl_recept_b,TM,SS	2.08
	459319	NM_000059		gb:Homo sapiens	BRCA2_repeat,TM,	2.08
	408730	AV660717	Hs.47144	DKFZP586N0819 p	TM,SS	2.08
	409220	BE243323	Hs.51233	tumor necrosis	TNFR_c6,death,TM,	2.08
	429504	X99133	Hs.204238	lipocalin 2 (on	lipocalin,SS	2.08
40	409686	AK000002	Hs.55879	Homo sapiens mR	ABC_tran,ABC_membrane,TM,	2.08
	413092	AA126856	Hs.118665	ESTs	EGF,TM,SS	2.08
	413715	AW851121	Hs.75497	Homo sapiens cD	cyclin,TM,	2.08
	423020	AA383092	Hs.1608	replication pro	TM	2.07
	438378	AW970529	Hs.86434	Homo sapiens cD	TM,SS	2.07
45	432125	AW972667	Hs.287510	Homo sapiens cD	Band_41,TM,SS	2.07
	449370	AK002114	Hs.23495	hypothetical pr	TM,SS	2.07
	454011	M31008	Hs.37009	alkaline phosph	alk_phosphatase,TM,SS	2.07
	427876	AI494291	Hs.111977	ESTs	TM	2.07
	422901	R81936	Hs.121576	aspartate beta-	SS	2.07
50	449207	AL044222	Hs.23255	nucleoporin 155	TM,SS	2.07
	408243	Y00787	Hs.624	interleukin 8	IL8,TM,SS	2.07
	446546	BE167687	Hs.156628	ESTs	Sulfotransfer,TM,SS	2.07
	423472	AF041260	Hs.129057	breast carcinom	TM	2.07
	436211	AK001581	Hs.80961	polymerase (DNA	TM	2.07
55	456157	AW979153		gb:EST391263 MA	transmembrane4,TM,	2.07
	407143	C14076	Hs.248968	EST	TM	2.06
	432440	X63597	Hs.2996	sucrase-isomalt	Glyco_hydro_31,trefoil,TM,SS	2.06
	410668	BE379794	Hs.65403	hypothetical pr	TM	2.06
	422765	AW409701	Hs.1578	baculoviral IAP	BIR,TM,	2.06
60	439832	T81829	Hs.14870	ESTs	SS	2.06
	445318	AW500652	Hs.200885	ESTs	TM	2.06
	439951	AI347067	Hs.124636	ESTs	TM,SS	2.06
	428307	W27393	Hs.183648	protein tyrosin	TM	2.06
	432584	AA928829	Hs.47099	Homo sapiens cD	SS	2.06
65	433027	AF191018	Hs.279923	putative nucleo	MMR_HSR1,TM,	2.06
	433716	AA608808	Hs.225118	ESTs	TM	2.06
	429412	NM_006235	Hs.2407	POU domain, cla	TM	2.06
	449026	BE500946	Hs.209105	ESTs	TM	2.06
	437016	AU076916	Hs.5398	guanine monphos	GATase,GMP_synt_C,TM,	2.06
70	442547	AA306997	Hs.268362	ESTs, Weakly si	SS	2.06
	455778	BE088746		gb:CM2-BT0693-2	TM	2.06
	439975	AW328081	Hs.5817	Homo sapiens pu	TM,SS	2.06
	433037	NM_014158	Hs.279938	HSPC067 protein	TM	2.06
	440086	NM_005402	Hs.288757	v-rat simian le	ras,TM,	2.06
75	436414	BE264633	Hs.143638	WD repeat domai	WD40,TM,	2.05
	411770	NM_014278	Hs.71992	heat shock prot	HSP70,TM,	2.05
	409459	D86407	Hs.54481	low density lip	EGF_idl_recept_a,Idl_recept_b,TM,SS	2.05
	436238	AK002163	Hs.301724	ESTs, Highly si	MMR_HSR1,TM,	2.05
	400517	AF242388	Hs.149585	tensin	TM	2.05
80	421904	BE143533	Hs.109309	hypothetical pr	SS	2.05
	417850	AA215724	Hs.82741	primase, polype	SS	2.05
	417491	AW376842	Hs.1085	guanylate cycla	pkise,guanylate_cyc,ANF_receptor,TM,SS	2.05
	453775	NM_002916	Hs.35120	replication fac	AAA,TM,SS	2.05
	435525	AI831297	Hs.123310	ESTs	TM	2.05

5	412627	BE391959	Hs.74276	chloride intrac	G-patch,jg,MuTS_C,TM,	2.05
	439702	AW085525	Hs.134182	ESTs	A2M,SS	2.05
	440006	AK000517	Hs.6844	hypothetical pr	TM	2.05
	417308	H60720	Hs.81892	KIAA0101 gene p	TM	2.05
	446311	AW007294	Hs.149795	ESTs, Weakly si	pkise,TM,	2.05
	427871	AW992405	Hs.59622	ESTs, Weakly si	SS	2.05
	453804	AA300204	Hs.35276	KIAA0852 protei	TM,SS	2.05
	449939	T86420	Hs.272139	ESTs	DIL,myosin_head,TM,SS	2.05
10	417819	AI253112	Hs.133540	ESTs	TM	2.04
	427747	AW411425	Hs.180655	serine/threonin	pkise,TM,	2.04
	415009	C75253	Hs.220950	ESTs	TM	2.04
	437829	AI358522	Hs.270188	ESTs	TM	2.04
	428753	AW939252	Hs.192927	hypothetical pr	TM	2.04
15	446475	AI908188	Hs.209245	ESTs	OPR,TM,	2.04
	431394	AK000692	Hs.252351	HERV-H LTR-asso	ig,TM,SS	2.04
	423701	AA329856	Hs.143022	ESTs	TM	2.04
	422359	AF005216	Hs.115541	Janus kinase 2	SH2,pkise,TM,	2.04
	432481	AW451645	Hs.151504	Homo sapiens cD	TSPN,Collagen,TM,SS	2.04
20	443746	AW861379	Hs.160602	ESTs	TM	2.04
	400792	AA635062	Hs.50094	Homo sapiens mR	zf-C3HC4,CARD,BIR,TM,	2.04
	428343	AL043021	Hs.12705	ESTs, Weakly si	TM	2.04
	419329	AY007220	Hs.288998	S100-type calci	TM	2.04
	403485				filament,TM,	2.04
25	413313	NM_002047	Hs.75280	glycyl-tRNA syn	WHEP-TRS,7tm_2,TM,SS	2.04
	433326	AI379486	Hs.159430	ESTs	TM	2.03
	440246	W52010	Hs.191379	ESTs	serpin,TM,	2.03
	444006	BE395085	Hs.10086	type I transmem	TM,SS	2.03
	452705	H49805	Hs.246005	ESTs	TM	2.03
30	421724	AB037832	Hs.107287	KIAA1411 protei	TM	2.03
	447474	AW614220	Hs.189402	ESTs	SS	2.03
	418852	BE537037	Hs.273294	hypothetical pr	TM	2.03
	431842	NM_005764	Hs.271473	epithelial prot	TM,SS	2.03
	440773	AA352702	Hs.37747	hypothetical pr	TM	2.03
35	443425	AI056776	Hs.133397	ESTs	TM,SS	2.03
	407975	X89426	Hs.41716	endothelial cel	IGFBP,SS	2.03
	428299	AL038004	Hs.29419	ESTs	TM,SS	2.03
	415757	AA830854	Hs.187810	ESTs	TM	2.03
	432559	AW452948	Hs.257631	ESTs	PAC,TM,SS	2.03
40	425912	AL137629	Hs.162189	serine/threonin	fn3,ig,PH,RhoGEF,TM,SS	2.02
	419395	BE268326	Hs.90280	5-aminimidazol	AICARFT_IMPCHas,MGS,TM,	2.02
	417576	AA339449	Hs.82285	phosphoribosylg	AIRS,formyl_transf,GARS,TM,	2.02
	418559	AA225048	Hs.104207	ESTs	TM	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevi	SNF2_N,helicase_C,TM,	2.02
45	422072	AB018255	Hs.111138	KIAA0712 gene p	TM	2.02
	419546	AA244199		gb:nc06c05.s1 N	Y_phosphatase,TM,	2.02
	450516	AA902656	Hs.21943	NIF3 (Ngg1 inte	DUF34,TM,	2.02
	419807	R77402		gb:yi75f11.s1 S	TM	2.02
	438192	AI859065	Hs.16808	ESTs, Weakly si	TM,SS	2.02
50	401866				filament,TM,SS	2.02
	443129	R16075	Hs.21668	ESTs	TM,SS	2.02
	424783	AA913909	Hs.153088	TATA box bindin	TM	2.01
	413293	AL047483	Hs.75270	GTP-binding pro	ras,TM,SS	2.01
	435787	AW162767	Hs.100914	hypothetical pr	SS	2.01
55	422599	BE387202	Hs.118638	non-metastatic	NDK,SS	2.01
	431630	NM_002204	Hs.265829	integrin, alpha	FG-GAP,integrin_A,TM,SS	2.01
	448275	BE514434	Hs.20830	synaptic Ras GT	kinesin,PHD,abhydrolase_2,TM,SS	2.01
	405484				filament,SS	2.01
60	436469	AK001455	Hs.5198	Down syndrome c	TM	2.01
	451273	NM_014811	Hs.26163	KIAA0649 gene p	TM	2.01
	432378	AI493046	Hs.146133	ESTs	TM	2.01
	419981	AA897581	Hs.128773	ESTs	Ski_Sno,SS	2.01
	445808	AV655234	Hs.298083	ESTs	sushi,TM,SS	2.01
	435767	H73505	Hs.117874	ESTs	Peptidase_S8,P,TM,	2.01
65	430466	AF052573	Hs.241517	polymerase (DNA	TM	2.01
	422790	AA809875	Hs.25933	ESTs	TM	2.01
	443303	U67319	Hs.9216	caspase 7, apop	ICE_p10,ICE_p20,TM,	2.01
	410008	AA079552		gb:zm20h12.s1 S	FG-GAP,TM,SS	2.01
	440774	AI420611	Hs.127832	ESTs	zf-MYND,TM,SS	2.00
70	442961	BE614474	Hs.289074	Homo sapiens cD	TM	2.00
	424420	BE614743	Hs.146688	prostaglandin E	MAPEG,TM,SS	2.00
	410240	AL157424	Hs.61289	synaplojanin 2	TM	2.00
	435014	BE560898	Hs.10026	ribosomal prote	Ribosomal_L17,TM,	2.00
	406752	AI285598	Hs.217493	annexin A2	TM	2.00
75	TABLE 41B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
80	Pkey	CAT number	Accession			
	410008	116812_1	AA079552 BE142525 BE142527			
	418546	176677_1	AA224827 T59708 T59843 BE156903			
	419546	185766_1	AA244199 AA244272 H57440			

5	419807	188252_1	R77402 AA262462 AA250988 R06794
	422689	219896_1	AW856665 AA315006 AW954733
	431120	328264_1	AA492588 AA492498 AA492571
	433748	37385_1	R12244 H71290 A110858 AF090916 AF075357 AA011531
	438223	452646_1	AA781171 A1202139 A1202098
	438993	467651_1	AA828995 AA834879 A1926361
	446995	702707_1	A1355012 AW812856
	447197	711623_1	R36075 A1366546 R36167
10	450190	827655_1	T51387 AW191595 T51271 A1686285
	451237	863269_1	AW600293 A1767468
	455778	1364506_1	BE088746 BE088802 BE088756 BE088876 BE088947 BE088881 BE088952
	456157	158261_1	AW979153 AA176967 AA826015

15	TABLE 41C:		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
20	NL_position:	Indicates nucleotide positions of predicted exons.	

Pkey	Ref	Strand	NL_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
401519	6649315	Plus	157315-157950
401708	2951946	Plus	154511-155298
401866	8018106	Plus	73126-73623
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
403055	8748904	Minus	109532-110225
403208	7630829	Minus	147706-147903,148667-148804
403422	9665041	Minus	151169-151561
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403776	7770611	Minus	1414-1513,1624-1756
404171	9930793	Plus	173667-173783,176876-177055
404253	9367202	Minus	55675-56055
404519	8152000	Plus	12817-13000
404567	7249169	Minus	101320-101501
405484	5922025	Plus	199214-199579,199672-199920,200262-200495
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405818	4071056	Plus	29055-29196
406399	9256288	Minus	63448-63554

TABLE 42A: ABOUT 561 GENES UP-REGULATED IN STOMACH CANCER

Table 42A lists about 561 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 40A except using various non-malignant stomach specimens in determining the denominator value.

45	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
50	R1:	Ratio of tumor to normal tissue		
	Pkey	ExAccn	UnigeneID	Unigene Title
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin)
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L
55	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like
	422330	D30783	Hs.115263	epiregulin
	415989	A1267700	Hs.111128	ESTs
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2
60	403776			17.1
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k
	414132	A1801235	Hs.48480	ESTs
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
65	436032	AA150797	Hs.109276	latexin protein
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	414972	BE263782	Hs.77695	KIAA0008 gene product
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence
70	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	441377	BE218239	Hs.202656	ESTs
	419423	D26488	Hs.90315	KIAA0007 protein
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2
	424639	A1917494	Hs.131329	ESTs
75	412472	AW975398	Hs.293836	ESTs
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L
	418379	AA218940	Hs.137516	fidgetin-like 1
	423020	AA383092	Hs.1608	replication protein A3 (14kD)
	408908	BE296227	Hs.48915	serine/threonine kinase 15
80	419948	AB041035	Hs.93847	NADPH oxidase 4
	411750	BE562298	Hs.71827	KIAA0112 protein: homolog of yeast ribos
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo
	420900	AL045633	Hs.44269	ESTs
	449347	AV649748	Hs.295901	ESTs

	409041	AB033025	Hs.50081	KIAA1199 protein	8.0
	450480	X82125	Hs.25040	zinc finger protein 239	7.6
	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	7.6
	453878	AW964440	Hs.19025	ESTs	7.6
5	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	7.5
	427961	AW293165	Hs.143134	ESTs	7.4
	428330	L25224	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.3
	426235	AI631964	Hs.34447	ESTs	7.1
	452291	AF015592	Hs.28853	CDK7 (cell division cycle 7, S. cerevisi	7.0
10	418205	L21715	Hs.83760	troponin I, skeletal, fast	7.0
	409757	NM_001898	Hs.123114	cystatin SN	6.9
	430044	AA464510	Hs.152812	ESTs	6.6
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.5
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.5
15	449020	AI621170	Hs.192699	ESTs	6.3
	431958	X53629	Hs.2877	cadherin 3, type 1; P-cadherin (placenta	5.8
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	5.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.6
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.4
20	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	5.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.0
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	4.9
	400268				4.8
	408427	AW194270	Hs.177236	ESTs	4.7
25	453785	AI368236	Hs.283732	ESTs	4.7
	411274	NM_002776	Hs.69423	kallikrein 10	4.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.7
	415752	BE314524	Hs.78776	putative transmembrane protein	4.6
	434370	AF130988	Hs.58346	downless (mouse) homolog	4.6
30	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	4.6
	400205				4.6
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.5
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.4
	453160	AI263307	Hs.146228	ESTs	4.4
35	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.4
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	4.4
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	4.3
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.3
	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo	4.1
40	433159	AB035898	Hs.150587	kinesin-like protein 2	4.1
	446142	AI754693	Hs.145968	ESTs	4.1
	414727	BE466904		gb:hz28f03.x1 NC1_CGAP_G06 Homo sapiens	4.1
	422285	AI803103		gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi	4.1
	451807	W52854	Hs.27099	DKFZP564J0863 protein	4.1
45	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.0
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.0
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	3.9
	452909	NM_015368	Hs.30985	pannexin 1	3.9
	443211	AI128388	Hs.143655	ESTs	3.9
50	442896	R37725	Hs.261108	ESTs	3.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	3.8
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.8
	421155	H87879	Hs.102267	lysyl oxidase	3.8
	420552	AK000492	Hs.98806	hypothetical protein	3.8
55	420727	H75701	Hs.99886	complement component 4-binding protein,	3.7
	422665	AJ011812	Hs.119018	transcription factor NRF	3.7
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.7
	417715	AW969587	Hs.86366	ESTs	3.7
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	3.6
60	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ111041 fis, clone PL	3.6
	412723	AA648459	Hs.179912	ESTs	3.6
	452461	J78223	Hs.108106	transcription factor	3.6
	453331	AI240665	Hs.8895	ESTs	3.6
	406434				3.6
65	417956	AA210704	Hs.190465	ESTs	3.6
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.6
	426471	M22440	Hs.170009	transforming growth factor, alpha	3.5
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.5
70	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	3.5
	426957	AA393676	Hs.97459	ESTs, Weakly similar to KIAA0819 protein	3.5
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANS	3.5
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.5
	442942	AW167087	Hs.131562	ESTs	3.4
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.4
75	420230	AL034344	Hs.298020	Homo sapiens cDNA FLJ11796 fis, clone HE	3.4
	408243	Y00787	Hs.624	interleukin 8	3.4
	412978	AI431708	Hs.820	homeo box C6	3.4
	412851	AI826502	Hs.106149	ESTs	3.4
	417720	AA205625	Hs.208067	ESTs	3.4
80	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.4
	453884	AA355925	Hs.36232	KIAA0186 gene product	3.4
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	3.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	3.4

	420092	AA814043	Hs.88045	ESTs	3.3
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.3
	421787	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m	3.3
5	447342	AI199268	Hs.19322	ESTs	3.3
	430178	AW449612	Hs.152475	ESTs	3.3
	452826	BE245286	Hs.301636	ESTs, Moderately similar to PEX6_HUMAN P	3.3
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.3
	413339	AI818080	Hs.194290	ESTs	3.3
10	448756	AI739241	Hs.171480	ESTs	3.3
	421948	L42583	Hs.111758	keratin 6A	3.3
	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	3.3
	438538	AA832203	Hs.291955	ESTs	3.3
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	3.3
15	431721	AB032996	Hs.268044	KIAA1170 protein	3.3
	436391	AJ227892	Hs.146274	ESTs	3.3
	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans	3.3
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.2
	411678	AJ907114	Hs.71465	squalene epoxidase	3.2
20	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	3.2
	450400	AI694722	Hs.279744	ESTs	3.2
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.2
	423528	AB011137	Hs.129740	KIAA0565 gene product	3.2
	440659	AF134160	Hs.7327	claudin 1	3.2
25	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.2
	412022	AI005043	Hs.24143	ESTs	3.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.1
	408633	AW963372	Hs.46677	PRO2000 protein	3.1
30	445808	AV655234	Hs.298083	ESTs	3.1
	414618	AI204600	Hs.96978	ESTs	3.1
	421340	F07783	Hs.1369	decay accelerating factor for complement	3.1
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	3.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.1
35	420759	T11832	Hs.127797	ESTs	3.1
	452637	AW971231	Hs.291020	ESTs	3.1
	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	3.1
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	3.1
	424051	AL110203	Hs.138411	Homo sapiens mRNA: cDNA DKFZp586J1922 (f	3.1
40	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	3.1
	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	3.0
	429125	AA446854	Hs.271004	ESTs	3.0
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.0
	438394	BE379623	Hs.27693	CGI-124 protein	3.0
45	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.0
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.0
	422746	NM_004484	Hs.119651	glypican 3	3.0
	424947	R77952	Hs.239625	integral membrane protein 2B	3.0
50	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.0
	449386	AA001308	Hs.193213	ESTs	3.0
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	2.9
	401747				2.9
55	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.9
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	2.9
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.9
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	2.9
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	2.9
60	454798	AW821295		gb:PM3-ST0307-241299-002-g03 ST0307 Homo	2.9
	421650	AA781795	Hs.122587	ESTs	2.9
	434398	AA121098	Hs.3838	serum-inducible kinase	2.9
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	2.9
	435706	W31254	Hs.7045	GL004 protein	2.9
65	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.9
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	2.8
	423493	AI815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.8
	430242	U66569	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase	2.8
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	2.8
70	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.8
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	2.8
	400440	X83957	Hs.83870	nebulin	2.8
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.8
	428725	AI565937	Hs.98692	ESTs	2.8
75	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	2.8
	449420	AI654852	Hs.196562	ESTs, Highly similar to TS24 MOUSE PROTE	2.8
	433929	AI375499	Hs.27379	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	2.8
	423346	AI267677	Hs.127416	synaptotagmin 1	2.8
80	407824	AA147884	Hs.9812	ESTs	2.8
	408482	NM_000676	Hs.45743	adenosine A2b receptor	2.8
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.8
	456999	AA319798	Hs.172247	eukaryotic translation elongation factor	2.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.8

	407839	AA045144	Hs.161566	ESTs	2.7
	409012	AL117435	Hs.49725	DKFZP434I216 protein	2.7
	410762	AF226053	Hs.66170	HSKM-B protein	2.7
5	426925	NM_001196	Hs.172894	BH3 interacting domain death agonist	2.7
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	2.7
	428398	AI249368	Hs.98558	ESTs	2.7
	400048			AFFX control: YEL002c/WBP1	2.7
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.7
10	435664	AI032087	Hs.269819	ESTs	2.7
	405695				2.7
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	2.7
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	2.7
	422576	BE548555	Hs.118554	CGI-83 protein	2.7
15	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	2.7
	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.7
	426874	N67325	Hs.247132	ESTs	2.7
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.7
	409902	AI337658	Hs.156351	ESTs	2.7
20	422336	AI761322	Hs.115285	dihydrolypoamide S-acetyltransferase (E2	2.7
	408434	AW195317	Hs.107716	Homo sapiens cDNA: FLJ22344 fis, clone H	2.7
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	2.7
	407633	NM_007069	Hs.37189	similar to rat HREV107	2.6
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.6
25	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.6
	445564	AB028957	Hs.12896	KIAA1034 protein	2.6
	401644				2.6
	417479	AI057052	Hs.133554	ESTs	2.6
	434217	AW014795	Hs.23349	ESTs	2.6
30	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.6
	414800	BE538690		gb:601064676F1 NIH_MGC_10 Homo sapiens c	2.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.6
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-4	2.6
35	430397	AI924533	Hs.105607	ESTs	2.6
	428048	AA705745	Hs.185070	ESTs	2.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.6
	440052	AI633744	Hs.195648	ESTs	2.6
	433077	AA314262	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.6
40	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	2.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	2.6
	440100	BE382685	Hs.158549	ESTs	2.6
45	413746	AA133243	Hs.171553	ESTs	2.6
	414737	AI160386	Hs.125087	ESTs	2.6
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	2.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	2.6
	437641	AA811452	Hs.291911	ESTs	2.6
50	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.6
	452571	W31518	Hs.34665	ESTs	2.6
	452862	AW378065	Hs.8687	ESTs	2.6
	411984	NM_005419	Hs.72988	signal transducer and activator of trans	2.6
55	446440	AV658411	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT	2.6
	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	2.6
	426427	M86699	Hs.169840	TTK protein kinase	2.6
	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	2.6
	420022	AA256253	Hs.120817	ESTs	2.6
60	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	2.6
	428953	AA306610	Hs.194676	DKFZP434C013 protein	2.6
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	2.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.6
	414987	AA524394	Hs.165544	ESTs	2.6
	440249	AI246590	Hs.125325	ESTs	2.6
65	407966	AA295052	Hs.38516	ESTs	2.5
	406685	M18728		gb:Human nonspecific crossreacting antig	2.5
	403204				2.5
	436961	AW375974	Hs.156704	ESTs	2.5
70	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	2.5
	444471	AB020684	Hs.11217	KIAA0877 protein	2.5
	430290	AI734110	Hs.136355	ESTs	2.5
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.5
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	2.5
75	439580	AF086401	Hs.293847	ESTs	2.5
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.5
	457065	AI476318	Hs.192480	ESTs	2.5
	439521	AI808955	Hs.58248	ESTs	2.5
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.5
80	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	2.5
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.5
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.5
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	2.5
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	2.5

	424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ10967 fis, clone PL	2.5
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.5
	440594	AW445167	Hs.126036	ESTs	2.5
5	428264	AA424839	Hs.98484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	2.5
	451177	AI969716	Hs.13034	ESTs	2.5
	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.5
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.5
	400240				2.5
10	410519	AW612264	Hs.131705	ESTs	2.5
	440953	AI683036	Hs.124135	KIAA1618 protein	2.5
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	2.5
15	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.5
	420894	AA744597	Hs.88854	ESTs	2.5
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	2.4
	413998	AW103807	Hs.243933	ESTs	2.4
	412281	AI810054	Hs.14119	ESTs	2.4
	418105	AW937488	Hs.178000	ESTs	2.4
20	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhib	2.4
	446852	AW451643	Hs.257479	ESTs, Weakly similar to AF147747 1 BOG25	2.4
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	2.4
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.4
25	410193	AJ132592	Hs.59757	zinc finger protein 281	2.4
	410664	NM_006033	Hs.65370	lipase, endothelial	2.4
	449264	AI637649	Hs.196105	ESTs	2.4
	423453	AW450737	Hs.128791	CGI-09 protein	2.4
	433757	AI949974	Hs.152670	ESTs	2.4
30	411598	BE336654	Hs.70937	H3 histone family, member K	2.4
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	2.4
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.4
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.4
	419559	Y07828	Hs.91096	ring finger protein	2.4
35	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.4
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.4
	413281	AA861271	Hs.34396	ESTs	2.4
	402819				2.4
	431457	NM_012211	Hs.256297	integrin, alpha 11	2.4
40	422564	AI148006	Hs.222120	ESTs	2.4
	443683	BE241717	Hs.9676	uncharacterized hypothalamus protein HT0	2.4
	407242	M18728		gb:Human nonspecific crossreacting antig	2.4
	409235	AA188827	Hs.7988	ESTs, Weakly similar to endo-alpha-D-man	2.4
	408938	AA059013	Hs.22607	ESTs	2.4
45	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.4
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.4
	408321	AW405882	Hs.44205	coriastatin	2.4
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	2.4
	452945	AW978187	Hs.31086	Homo sapiens mRNA for cytochrome b5, par	2.4
50	452234	AW084176	Hs.223296	ESTs	2.4
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.4
	430399	AI916284	Hs.199671	ESTs	2.4
	450737	AW007152	Hs.203330	ESTs	2.4
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	2.4
	405454				2.4
55	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.3
	421462	AF016495	Hs.104624	aquaporin 9	2.3
	403416	AI744626	Hs.301506	ESTs, Highly similar to KIAA0564 protein	2.3
	422039	BE567832	Hs.82148	hypothetical protein	2.3
60	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	2.3
	429145	AI694923	Hs.49031	ESTs	2.3
	423198	M81933	Hs.1634	cell division cycle 25A	2.3
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y7	2.3
	449042	AW294985	Hs.301148	potassium voltage-gated channel, Isk-rel	2.3
65	421308	AA687322	Hs.192843	ESTs	2.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.3
	429992	AL050053	Hs.227397	Homo sapiens mRNA; cDNA DKFZp566E103 (fr	2.3
	440601	N62409	Hs.126688	ESTs	2.3
	445232	AI281848	Hs.165547	ESTs	2.3
70	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.3
	452110	T47667	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G2463 (f	2.3
	422493	AW474183	Hs.233816	ESTs	2.3
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	2.3
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	2.3
75	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.3
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	2.3
	446545	AI431798	Hs.164192	ESTs, Weakly similar to Y161_HUMAN HYPOT	2.3
	422094	AF129535	Hs.272027	F-box only protein 5	2.3
	421933	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	2.3
80	430001	AI580056	Hs.98992	ESTs	2.3
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.3
	402053				2.3
	415666	H72693		gb:yu03c11.r1 Soares fetal liver spleen	2.3
	432743	AI146966	Hs.101656	ESTs	2.3

	433409	AI278802	Hs.25661	ESTs	2.3
	408330	AW182602	Hs.249954	ESTs	2.3
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on	2.3
	436972	AA284679	Hs.25640	claudin 3	2.3
5	436747	AW977192	Hs.291343	ESTs	2.3
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	2.3
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	2.3
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.3
10	415339	NM_015156	Hs.78398	KIAA0071 protein	2.3
	449539	W80363	Hs.58446	ESTs	2.2
	412651	AA115333	Hs.107968	ESTs	2.2
	450956	AW193531	Hs.205647	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	430335	D80007	Hs.239499	KIAA0185 protein	2.2
15	417849	AW291587	Hs.82733	nidogen 2	2.2
	454946	AW846376	Hs.73817	gb:QV0-CT0179-090200-090-409 CT0179 Homo	2.2
	412326	R07566	Hs.44276	small inducible cytokine A3 (homologous	2.2
	408349	BE546947	Hs.152096	homeo box C10	2.2
	424704	AI263293	Hs.7395	cytochrome P450, subfamily 11J (arachido	2.2
20	419433	AA814807	Hs.55279	hypothetical protein FLJ23182	2.2
	409632	W74001	Hs.949	serine (or cysteine) proteinase inhibito	2.2
	415323	BE269352	Hs.1087	neutrophil cytosolic factor 2 (65kD, chr	2.2
	417531	NM_003157		serine/threonine kinase 2	2.2
	403137				2.2
25	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.2
	430200	BE613337	Hs.234896	geminin	2.2
	433745	AF075320	Hs.28980	Homo sapiens clone HQ0270	2.2
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-receptl	2.2
	408380	AF123050	Hs.44532	diubiquitin	2.2
30	422424	AI186431	Hs.9711	prostate differentiation factor	2.2
	431548	AI834273	Hs.61635	Homo sapiens cDNA FLJ13018 fis, clone NT	2.2
	400298	AA032279	Hs.193143	six transmembrane epithelial antigen of	2.2
	428771	AB028992	Hs.70811	KIAA1069 protein	2.2
	411571	AA122393	Hs.7567	hypothetical protein FLJ20516	2.2
35	442573	H93366	Hs.74602	Homo sapiens cDNA: FLJ21962 fis, clone H	2.2
	412802	U41518	Hs.266273	aquaporin 1 (channel-forming integral pr	2.2
	412530	AA766268	Hs.77256	Homo sapiens cDNA FLJ13346 fis, clone OV	2.2
	414761	AU077228		enhancer of zeste (Drosophila) homolog 2	2.2
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.2
40	440283	AI732892	Hs.208414	ESTs	2.2
	429568	AI088691	Hs.137506	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	2.2
	424003	BE274717	Hs.270259	Homo sapiens BAC clone RP11-120J2 from 7	2.2
	425300	AW601773	Hs.71947	ESTs	2.2
	448568	AA149121	Hs.282884	ESTs	2.2
45	419229	AI827237		ESTs	2.2
	420982	AW576160	Hs.100729	KIAA0692 protein	2.2
	403258				2.2
	439653	AW021103	Hs.172665	hypothetical protein FLJ20373	2.2
	426827	AW067805	Hs.270431	methylenetetrahydrofolate dehydrogenase	2.2
50	444514	AI682905	Hs.111583	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	426298	AW965058	Hs.155637	ESTs	2.2
	425322	U63630	Hs.106552	protein kinase, DNA-activated, catalytic	2.2
	421662	NM_014141	Hs.21734	cell recognition molecule Caspr2	2.2
	412505	AA974491		ESTs	2.2
55	438788	AA825716	Hs.194827	gb:od29e10.s1 NCI_CGAP_GCB1 Homo sapiens	2.2
	429058	AF138863	Hs.123647	hypothetical protein FLB6421	2.2
	423104	AJ005273	Hs.301842	antigenic determinant of recA protein (m	2.2
	410406	AI969703	Hs.70945	ESTs	2.2
	443180	R15875	Hs.288433	ESTs	2.2
60	419235	AW470411	Hs.103982	neurotrophin	2.2
	421379	Y15221	Hs.121028	small inducible cytokine subfamily B (Cy	2.2
	422809	AK001379	Hs.273829	hypothetical protein FLJ10549	2.2
	415058	AW902848	Hs.190488	ESTs	2.2
	418049	AA211467	Hs.254020	hypothetical protein FLJ10120	2.2
65	436209	AW850417	Hs.42244	ESTs, Moderately similar to unnamed prot	2.2
	408042	AL049233	Hs.155956	Homo sapiens mRNA: cDNA DKFZp564A023 (fr	2.2
	425692	D90041	Hs.55777	N-acetyltransferase 1 (arylamine N-acety	2.2
	409665	NM_006731	Hs.298668	Fukuyama type congenital muscular dystro	2.2
	428157	AJ738719	Hs.63984	ESTs	2.2
	410480	R97457	Hs.2488	cadherin 13, H-cadherin (heart)	2.2
70	429732	U20158	Hs.77204	lymphocyte cytosolic protein 2 (SH2 doma	2.2
	414747	U30872	Hs.159627	centromere protein F (350/400kD, mitotin	2.2
	425843	BE313280	Hs.118727	death associated protein 3	2.2
	445299	AI910382	Hs.5092	Homo sapiens cDNA FLJ13692 fis, clone PL	2.1
	436251	BE515065	Hs.237825	nucleolar protein (KKE/D repeat)	2.1
75	430066	AI929659	Hs.117950	signal recognition particle 72kD	2.1
	422516	BE258862	Hs.40719	multifunctional polypeptide similar to S	2.1
	407870	AB032990	Hs.126550	hypothetical protein KIAA1164	2.1
	416109	AI420311	Hs.179565	suppressor of K+ transport defect 1	2.1
80	427528	AU077143		minichromosome maintenance deficient (S.	2.1
	448089	AI467945		ESTs	2.1
	441790	AW294909	Hs.132208	ESTs	2.1
	400022			AFFX control: STAT1	2.1
	428728	NM_016625	Hs.191381	hypothetical protein	2.1

	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.1
	409929	R38772	Hs.172619	KIAA1106 protein	2.1
	405264				2.1
5	445625	BE246743	Hs.288529	Homo sapiens cDNA: FLJ22635 fis, clone H	2.1
	408949	AF189011	Hs.49163	putative ribonuclease III	2.1
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	2.1
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.1
	442952	AI743261	Hs.131860	ESTs	2.1
10	441020	W79283	Hs.35962	ESTs	2.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	2.1
	432378	AI493046	Hs.146133	ESTs	2.1
	447769	AW873704	Hs.48764	ESTs	2.1
	412654	AI093480	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	2.1
15	445669	AI570830	Hs.174870	ESTs	2.1
	417979	AU077284	Hs.83081	GTP cyclohydrolase I feedback regulatory	2.1
	433849	BE465884	Hs.280728	ESTs	2.1
	437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	2.1
	457341	BE181716		gb:QV1-HT0639-150500-198-e03 HT0639 Homo	2.1
20	452833	BE559681	Hs.30736	KIAA0124 protein	2.1
	403055				2.1
	414581	AA256213	Hs.72010	ESTs	2.1
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.1
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.1
25	440908	AI915225	Hs.126735	ESTs	2.1
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	2.1
	436895	AF037335	Hs.5338	carbonic anhydrase XII	2.1
	455716	BE070263			2.1
	408420	NM_006915	Hs.299481	gb:QV4-BT0407-280100-090-e07 BT0407 Homo	2.1
30	435849	BE305242	Hs.112442	Homo sapiens mRNA: cDNA DKFZp586B0118 (f	2.1
	424308	AW975531	Hs.154443	ESTs, Weakly similar to CLDE_HUMAN CLAU	2.1
	433644	AW342028	Hs.256112	minichromosome maintenance deficient (S,	2.1
	400020			ESTs	2.1
	434064	AL049045	Hs.180758	AFFX control: STAT1	2.1
35	410660	AI061118	Hs.65328	hypothetical protein PRO0082	2.1
	404076			Fanconi anemia, complementation group F	2.1
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	2.1
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.1
	444863	AW384082	Hs.301323	ESTs	2.1
40	445867	AF272663	Hs.13405	gephyrin	2.1
	441021	AW578716	Hs.7644	H1 histone family, member 2	2.1
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.1
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.1
	412429	AV650262	Hs.75765	GRO2 oncogene	2.1
45	449207	AL044222	Hs.23255	nucleoporin 155kD	2.1
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.1
	400861				2.1
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	2.1
	440591	AA431599	Hs.132799	Homo sapiens cDNA: FLJ23451 fis, clone H	2.1
50	426181	AA371422	Hs.69844	ESTs, Weakly similar to dJ191N21.1 [H.s	2.1
	452880	AA029332	Hs.87549	ESTs	2.1
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	2.1
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.1
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.1
55	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.1
	432487	AA550988	Hs.221472	ESTs	2.1
	429534	AW976987	Hs.163327	ESTs	2.1
	446051	BE048061	Hs.153315	ESTs	2.1
	447760	AI431328	Hs.291179	ESTs, Weakly similar to topoisomerase I	2.1
60	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	2.1
	415173	AW501735	Hs.253015	ESTs	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.1
	453751	R38762	Hs.101282	Homo sapiens mRNA: cDNA DKFZp434B102 (fr	2.1
65	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.1
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	2.1
	449555	AW450288	Hs.195390	ESTs	2.1
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	2.1
	424673	AA345051	Hs.294092	ESTs	2.1
70	407802	D84145	Hs.39913	novel RGD-containing protein	2.0
	452834	AI638627	Hs.105685	ESTs	2.0
	438895	AW007021	Hs.82894	ESTs	2.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.0
	406881	S71129	Hs.296844	Acetylcholinesterase (14-E5 domain) [huma	2.0
75	427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	439223	AW238299	Hs.23945	ESTs	2.0
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	414890	BE281095	Hs.77573	uridine phosphorylase	2.0
	423019	AI640185	Hs.225816	ESTs	2.0
80	435905	AW997484	Hs.5003	KIAA0456 protein	2.0
	422278	AF072873	Hs.114218	trizzled (Drosophila) homolog 6	2.0
	439608	AW864696	Hs.26198	Homo sapiens cDNA: FLJ23363 fis, clone H	2.0
	432114	AL036021	Hs.225597	ESTs	2.0
	405545				2.0

5	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	2.0
	442528	AF150317	Hs.134217	ESTs	2.0
	446237	AW270515	Hs.149596	ESTs	2.0
	428074	BE387770	Hs.182378	colony stimulating factor 2 receptor, al	2.0
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	2.0
	435767	H73505	Hs.117874	ESTs	2.0
	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	2.0
	428792	BE535955	Hs.193602	chromosome condensation protein G	2.0
10	404170				2.0
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.0
	434565	TS2172		gb:yb22d01.s1 Stratagene fetal spleen (9	2.0
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	2.0
	417933	X02308	Hs.82962	thymidylate synthetase	2.0
15	441384	AA447849	Hs.288660	protease, serine, 23	2.0
	437403	AI208149	Hs.121196	ESTs	2.0
	412673	AL042957	Hs.31845	ESTs	2.0
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.0
	438426	AA835936	Hs.269763	ESTs	2.0
20	413943	AW294416	Hs.144687	ESTs	2.0
	449001	AI619957	Hs.189854	ESTs	2.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.0
	435425	H16263	Hs.31416	ESTs	2.0
	433364	AI075407	Hs.296083	ESTs	2.0
25	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	2.0
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.0
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.0
	411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	2.0
	414266	BE267834		gb:601124428F1 NIH_MGC_8 Homo sapiens cD	2.0
30	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.0
	450534	AI570189	Hs.25132	KIAA0470 gene product	2.0
	446715	AI337735	Hs.173919	ESTs	2.0

TABLE 42B:

35	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

40	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
			AW848214
	411560	1249443_1	AW851186 AW996967 BE143456
	414266	1430984_1	BE267834 BE514180 BE514096
45	414366	1438636_1	BE549143 BE390613 BE277344
	414727	1481204_1	BE466904 W28721
	414800	1491863_1	BE538690 T40217
	415666	1543492_1	H72693 R08673 H72694 F20990 R08580
	422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839
50	422285	214669_1	AI803103 AI885143 AW470793 AW450703 AI090784 AW271587 AW236950 AW242783
	422689	219896_1	AW856665 AA315006 AW954733
	423871	232749_1	AA331906 AA332484
	429540	305828_1	M85776 AA454535 AA456208 H90189
	431453	333457_1	AW753917 BE152926 AA505333 BE155673
55	434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
			AA149776 AA699829 AW879188 AW813567 AW813538 AI267158 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531 H59570
60	434565	38898_1	TS2172 AF147324 TS2248
	436411	419334_1	AW674352 AA715374 Z25205
	437834	443674_1	AA769294 AW749299 AW749302 AW749295 AW749304 AW749293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749296
			AW749289 AW749287 BE535498
65	438788	465159_1	AA825716 AW978859 AA828841
	454456	1207088_1	AW850984 AW752836 M86124
	454678	1228915_1	AW813089 W28102
	454798	1235104_1	AW821295 AW821272 AW821282
	454946	1245753_1	AW846376 AW846375 AW846434 AW846287 AW846365 AW846554 AW846384 AW846290 AW846356 AW846474
70	455716	1352695_1	BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203
	457341	322221_1	BE181716 AW948314 AW801848 AW948320 AW983981 AA484444

TABLE 42C:

75	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

80	Pkey	Ref	Strand	Nt_position
	400861	9757506	Plus	163855-164016
	401644	8576138	Plus	82655-83959
	401747	9789672	Minus	118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130468-130593, 131097-131258, 131866-31932, 132451-132575, 133580-134011

5	402053	8083229	Plus	62703-63179
	402819	6729581	Plus	29217-29422
	403055	8748904	Minus	109532-110225
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403204	7622392	Plus	16214-16439
10	403258	7770439	Minus	156251-156619
	403776	7770611	Minus	1414-1513,1624-1756
	404076	9931752	Minus	3848-3967
	404170	9930793	Plus	168836-169248
	405264	7329374	Plus	28556-28684
15	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405695	4309958	Plus	51860-52162
	406434	9256651	Minus	17803-17931

TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER

Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. These were selected as for Table 42A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, ln3, egr, 7tm domains). Predicted protein domains are noted.

20	Pkey: Unique Eos probeset identifier number					
	ExAccn: Exemplar Accession number, Genbank accession number					
	UnigenelD: Unigenes number					
	Unigenes Title: Unigenes gene title					
	PSDomain: Protein Structural Domain					
25	R1: Ratio of tumor to normal tissue					
30	Pkey	ExAccn	UnigenelD	Unigenes Title	PSDomain	R1
	428368	BE440042	Hs.83326	matrix metallo	hemopexin,Peptidase_M10,SS	60.4
	428664	AK001666	Hs.189095	similar to SALL	zf-C2H2,TM,SS	26.8
	422330	D30783	Hs.115263	epiregulin	EGF,TM,SS	22.0
	439979	AW600291	Hs.6823	hypothetical pr	TM	19.0
35	451099	RS2795	Hs.25954	interleukin 13	ln3,TM,SS	17.1
	403776				IL8,TM,SS	14.9
	424905	NM_002497	Hs.153704	NIMA (never in	kinase,TM,	14.8
	453922	AF053306	Hs.36708	budding uninhib	TM	13.8
	436032	AA150797	Hs.109276	latexin protein	TM	13.1
40	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS	12.5
	416661	AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain,TM,	12.2
	414972	BE263782	Hs.77695	KIAA0008 gene p	TM	10.6
	446619	AU076643	Hs.313	secreted phosph	Osteopontin,TM,SS	10.5
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma,TM,SS	9.6
45	423020	AA383092	Hs.1608	replication pro	TM	8.6
	408908	BE296227	Hs.48915	serine/threonin	kinase,TM,SS	8.5
	419948	AB041035	Hs.93847	NADPH oxidase 4	Ferric_reduct,TM,SS	8.3
	411750	BE562298	Hs.71827	KIAA0112 protei	SS	8.3
	420900	AL045633	Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	8.0
50	450480	X82125	Hs.25040	zinc finger pro	zf-C2H2,TM,SS	7.6
	417655	AA780791	Hs.14014	ESTs, Weakly si	TM	7.6
	430403	AF039390	Hs.241382	tumor necrosis	TM,SS	7.5
	428330	L22524	Hs.2256	matrix metallo	Peptidase_M10,SS	7.3
	452291	AF015592	Hs.28853	CDC7 (cell divi	kinase,TM,	7.0
55	418205	L21715	Hs.83760	troponin I, ske	Troponin,SS	7.0
	409757	NM_001898	Hs.123114	cystatin SN	cystatin,SS	6.9
	444783	AK001468	Hs.62180	anilin (Drosop	PH,TM,	6.5
	416209	AA236776	Hs.79078	MAD2 (mitotic a	HORMA,SS	6.5
	431958	X63629	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM,SS	5.8
60	424345	AK001380	Hs.145479	Homo sapiens cD	TM,SS	5.6
	428227	AA321649	Hs.2248	small inducible	IL8,TM,SS	5.4
	424960	BE245380	Hs.153952	5' nucleotidase	5_nucleotidase,TM,SS	4.9
	400268				Myosin_tail,SS	4.8
	411274	NM_002776	Hs.69423	kallikrein 10	trypsin,TM,	4.7
65	415752	BE314524	Hs.78776	putative transm	TM	4.6
	431806	AF186114	Hs.270737	tumor necrosis	TM,SS	4.6
	400205				SS	4.6
	422938	NM_001809	Hs.1594	centromere prot	histone,TM,	4.5
	406687	M31126	Hs.272620	pregnancy speci	hemopexin,TM,	4.4
70	423871	AA331906		gb:EST35805 Emb	TM	4.4
	431211	M86849	Hs.5566	gap junction pr	connexin,TM,	4.4
	446638	AL133063	Hs.15783	Homo sapiens mR	TM	4.3
	406741	AA058357	Hs.74466	carcinoembryoni	ig,TM,SS	4.3
	411560	AW851186		gb:IL3-CT0220-1	TM	4.1
75	433159	AB035898	Hs.150587	kinesin-like pr	kinesin,Myosin_tail,TM,SS	4.1
	422285	AI803103		gb:tc14e06.x1 S	TM,SS	4.1
	451807	W52854	Hs.27099	DKFZP564J0863 p	TM	4.1
	411558	AA102670	Hs.70725	gamma-aminobuty	neur_chan,TM,SS	4.0
	415701	NM_003878	Hs.78619	gamma-glutamyl	TM,SS	4.0
80	409420	Z15008	Hs.54451	laminin, gamma	laminin_EGF,laminin_B,SS	3.9
	452909	NM_015368	Hs.30985	pannexin 1	TM	3.9
	407788	BE514982	Hs.38991	S100 calcium-bi	efhand,S_100,TM,SS	3.8
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,SS	3.8
	420552	AK000492	Hs.98806	hypothetical pr	SS	3.8
	420727	H175701	Hs.99886	complement comp	sushi,	3.7

	422665	AJ011812	Hs.119018	transcription f	R3H,G-patch,GTP,CDC,TM,SS	3.7
	447425	AI963747	Hs.18573	acylphosphatase	Acylphosphatase,TM,	3.7
	406076	AL390179	Hs.137011	Homo sapiens mR	TM	3.6
	406434				heme_1,TM,	3.6
5	417956	AA210704	Hs.190465	ESTs	sushi,SS	3.6
	410102	AW248508	Hs.279727	Homo sapiens cD	TM,SS	3.6
	426471	M22440	Hs.170009	transforming gr	EGF,TM,SS	3.5
	425782	U66468	Hs.159525	cell growth reg	SS	3.5
	426957	AA393676	Hs.97459	ESTs, Weakly si	SS	3.5
10	448105	AW591433	Hs.170675	ESTs, Weakly si	trypsin,TM,	3.5
	414998	NM_002543	Hs.77729	oxidised low de	TM	3.5
	442942	AW167087	Hs.131562	ESTs	pkinese,TM,SS	3.4
	416391	AI878927	Hs.79284	mesoderm specif	abhydrolase,TM,SS	3.4
	420230	AL034344	Hs.298020	Homo sapiens cD	Fork_head,TM,	3.4
15	408243	Y00787	Hs.624	interleukin 8	IL8,TM,SS	3.4
	412978	AA431708	Hs.820	homeo box C6	homeobox,TM,	3.4
	412851	AI826502	Hs.106149	ESTs	TM,SS	3.4
	414812	X72755	Hs.77367	monokine induce	IL8,SS	3.4
	453884	AA355925	Hs.36232	KIAA0186 gene p	TM	3.4
20	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,	3.4
	421787	AA227068	Hs.108301	nuclear recepto	TM	3.3
	447342	AI199268	Hs.19322	ESTs	TM,SS	3.3
	452826	BE245286	Hs.301636	ESTs, Moderatel	AAA,TM,	3.3
	414821	M63835	Hs.77424	Fc fragment of	ig,TM,SS	3.3
25	448756	AI739241	Hs.171480	ESTs	TM	3.3
	421948	L42583	Hs.111758	keratin 6A	filament,TM,	3.3
	438538	AA832203	Hs.291955	ESTs	TM	3.3
	436391	AJ227892	Hs.146274	ESTs	SS	3.3
30	418007	M13509	Hs.83169	matrix metallo	hemopexin,Peptidase_M10,SS	3.2
	411678	AI907114	Hs.71465	squalene epoxid	Monooxygenase,TM,	3.2
	422956	BE545072	Hs.122579	hypothetical pr	TM	3.2
	450400	AI694722	Hs.279744	ESTs	TM	3.2
	440659	AF134160	Hs.7327	claudin 1	PMP22,Claudin,TM,SS	3.2
	418203	X54942	Hs.83758	CDC28 protein k	CKS,TM,	3.1
35	416111	AA033813	Hs.79018	chromatin assem	TM,SS	3.1
	445808	AV655234	Hs.298083	ESTs	sushi,TM,SS	3.1
	421340	F07783	Hs.1369	decay accelerat	sushi,SS	3.1
	422689	AW856665		gb:RC3-CT0297-2	SNF2_N,TM,	3.1
40	439451	AF086270	Hs.278554	heterochromatin	chromo,Chromo_shadow,SS	3.1
	454456	AW850984		gb:IL3-CT0220-1	fn3,TM,SS	3.0
	429125	AA446854	Hs.271004	ESTs	TM	3.0
	409361	NM_005982	Hs.54416	sine oculis hom	homeobox,SS	3.0
	439453	BE264974	Hs.6566	thyroid hormone	AAA,TM,	3.0
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS	3.0
45	422746	NM_004484	Hs.119651	glypican 3	Glypican,TM,SS	3.0
	453775	NM_002916	Hs.35120	replication fac	AAA,TM,SS	3.0
	428862	NM_000346	Hs.2316	SRY (sex-determ	HMG_box,TM,	2.9
	401747				filament,TM,	2.9
50	429682	NM_006306	Hs.211602	SMC1 (structura	SMC_C,SMC_N,TM,	2.9
	413385	M34455	Hs.840	indoleamine-pyr	IDO,TM,	2.9
	442961	BE614474	Hs.289074	Homo sapiens cD	TM	2.9
	421650	AA781795	Hs.122587	ESTs	TM	2.9
	434398	AA121098	Hs.3838	serum-inducible	pkinese,POLO_box,TM,	2.9
55	435706	W31254	Hs.7045	GL004 protein	PDEase,TM,	2.9
	416065	BE267931	Hs.78996	proliferating c	TM	2.9
	423493	AI815965	Hs.129683	ubiquitin-conju	UQ_con,SS	2.8
	430242	U66669	Hs.236642	3-hydroxyisobut	TM	2.8
	411770	NM_014278	Hs.71992	heat shock prot	HSP70,TM,	2.8
60	400440	X83957	Hs.83870	nebulin	TM	2.8
	444743	AA045648	Hs.11817	nudix (nucleosi	nuIT,TM,	2.8
	417771	AA804698	Hs.82547	retinoic acid r	TM	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly si	TM,SS	2.8
	408482	NM_000676	Hs.45743	adenosine A2b r	7tm_1,TM,SS	2.8
	425188	AK002052	Hs.155071	hypothetical pr	TM	2.8
65	456999	AA319798	Hs.172247	eukaryotic tran	SS	2.8
	408875	NM_015434	Hs.48604	DKFZP434B168 pr	TM	2.8
	409012	AL117435	Hs.49725	DKFZP434I216 pr	RhoGEF,TM,	2.7
	410762	AF226053	Hs.66170	HSKM-B protein	zf-MYND,SS	2.7
70	426925	NM_001196	Hs.172894	BH3 interacting	TM	2.7
	410116	AW630671	Hs.58636	squamous cell c	TM,SS	2.7
	428398	AI249368	Hs.98558	ESTs	SS	2.7
	412140	AA219691	Hs.73625	RAB6 interactin	kinesin,TM,SS	2.7
	456655	AI376736	Hs.111779	secreted protei	kazal,SS	2.7
	408670	AF160967	Hs.46784	potassium large	TM,SS	2.7
75	422576	BE548555	Hs.118554	CGI-83 protein	lactamase_B,SS	2.7
	431379	AA504264	Hs.182937	peptidylprolyl	TM	2.7
	433183	AF231338	Hs.222024	transcription f	HLH,PAS,TM,SS	2.7
	432328	AI572739	Hs.195471	6-phosphofructo	PGAM,6PF2K,TM,	2.7
80	407633	NM_007069	Hs.37189	similar to rat	TM,SS	2.6
	419216	AU076718	Hs.164021	small inducible	IL8,TM,SS	2.6
	422363	T55979	Hs.115474	replication fac	TM	2.6
	401644				zf-C2H2,TM,	2.6
	417479	AI057052	Hs.133554	ESTs	CARD,TM,	2.6

5	426514	BE616633	Hs.301122	bone morphogene	TGF-beta,TGFb_propeptide,TM,SS	2.6
	400289	X07820	Hs.2258	matrix metallo	hemopexin,,SS	2.6
	418478	U38945	Hs.1174	cyclin-dependen	ank,TM,SS	2.6
	421246	AW582962	Hs.300961	ESTs, Highly si	PolyA_pol,TM,	2.6
	428048	AA705745	Hs.185070	ESTs	AMP-binding,TM,	2.6
	452092	BE245374	Hs.27842	hypothetical pr	Acyltransferase,TM,SS	2.6
	440052	AI633744	Hs.195648	ESTs	PAC,TM,SS	2.6
	452401	NM_007115	Hs.29352	tumor necrosis	Xlink,CUB,TM,SS	2.6
10	451813	NM_016117	Hs.27182	phospholipase A	WD40,,SS	2.6
	410889	X91662	Hs.66744	twist (Drosophi	HLH,TM,	2.6
	422063	BE156476		gb:OV0-HT0368-0	SS	2.6
	418250	U29926	Hs.83918	adenosine monop	A_deaminase,TM,	2.6
	437641	AA811452	Hs.291911	ESTs	TM	2.6
15	452571	W31518	Hs.34665	ESTs	TM	2.6
	411984	NM_005419	Hs.72988	signal transduc	SH2,STAT,,SS	2.6
	426427	M86699	Hs.169840	TTK protein kin	ptkinase,TM,	2.6
	445848	AA774824	Hs.13377	Homo sapiens cl	TM	2.6
	420022	AA256253	Hs.120817	ESTs	SS	2.6
20	451418	BE387790	Hs.26369	hypothetical pr	TM	2.6
	428953	AA306610	Hs.194676	DKFZP434C013 pr	arf,TNFR_c6,DEAD,Statmin,TM,SS	2.6
	424008	R02740	Hs.137555	putative chemok	7tm_1,TM,	2.6
	417863	AB000450	Hs.82771	vaccinia relate	ptkinase,TM,SS	2.6
	436961	AW375974	Hs.156704	ESTs	TM	2.6
25	413670	AB000115	Hs.75470	hypothetical pr	TM	2.5
	421928	AF013758	Hs.109643	polyadenylate b	SS	2.5
	439963	AW247529	Hs.6793	platelet-activa	PAF-AH,HMG_box,ptkinase,TM,	2.5
	426711	AA383471	Hs.180669	conserved gene	TM	2.5
	422631	BE218919	Hs.118793	hypothetical pr	TM	2.5
30	417866	AW067903	Hs.82772	collagen, type	TSPN,Collagen,COLFI,,SS	2.5
	416975	NM_004131	Hs.1051	granzyme B (gra	trypsin,,SS	2.5
	415947	U04045	Hs.78934	mutS (E. coli)	MutS_C,MutS_N,TM,	2.5
	454678	AW813089		gb:RC3-ST0186-2	TPR,Ribosomal_S5,TM,SS	2.5
35	426572	AB037783	Hs.170623	hypothetical pr	PH,FYVE,TM,	2.5
	428264	AA424839	Hs.98484	ESTs, Weakly si	TM	2.5
	444478	W07318	Hs.240	M-phase phospho	kinesin,,SS	2.5
	442295	AI827248	Hs.224398	Homo sapiens cD	Collagen,COLFI,vwc,TM,SS	2.5
	410094	BE147897	Hs.58593	general transcr	TFIIF_beta,TM,	2.5
	413998	AW103807	Hs.243933	ESTs	TPR,TM,SS	2.4
40	412281	AI810054	Hs.14119	ESTs	Ribosomal_S7e,TM,	2.4
	446852	AW451643	Hs.257479	ESTs, Weakly si	TM	2.4
	408915	NM_016651	Hs.48950	heptacellular c	TM,SS	2.4
	442991	BE281238	Hs.8886	hypothetical pr	TM	2.4
45	410193	AJ132592	Hs.59757	zinc finger pro	zf-C2H2,TM,	2.4
	410664	NM_006033	Hs.65370	lipase, endothe	Ribosomal_L22,lipase,PLAT,TM,SS	2.4
	423453	AW450737	Hs.128791	CGI-09 protein	Granin,CDP-OH_P_transf,TM,	2.4
	411598	BE336654	Hs.70937	H3 histone fami	histone,,SS	2.4
	429663	M68874	Hs.211587	phospholipase A	C2,PLA2_B,TM,	2.4
	428242	H55709	Hs.2250	leukemia inhibi	LIF_OSM,,SS	2.4
50	419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4,zf-B_box,TM,	2.4
	419839	U24577	Hs.93304	phospholipase A	SS	2.4
	402819				IBR,TM,	2.4
	431457	NM_012211	Hs.256297	integrin, alpha	FG-GAP,vwa,TM,SS	2.4
55	443683	BE241717	Hs.9676	uncharacterized	DUF157,TM,	2.4
	422158	L10343	Hs.112341	protease inhibi	wap,,SS	2.4
	423217	NM_000094	Hs.1640	collagen, type	fn3,Collagen,Kunitz_BPTI,vwa,,SS	2.4
	408321	AW405882	Hs.44205	coristatin	TM	2.4
	419086	NM_000216	Hs.89591	Kallmann syndro	fn3,wap,,SS	2.4
	427722	AK000123	Hs.180479	hypothetical pr	PH,,SS	2.4
60	405454				TM	2.4
	422168	AA586894	Hs.112408	S100 calcium-bi	efhand,TM,	2.4
	421462	AF016495	Hs.104624	aquaporin 9	MIP,TM,	2.3
	403416	AI744626	Hs.301506	ESTs, Highly si	SS	2.3
65	448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.3
	423198	M81933	Hs.1634	cell division c	Rhodanese,,SS	2.3
	419926	AW900992	Hs.93796	DKFZP586D2223 p	SS	2.3
	429992	AL050053	Hs.227397	Homo sapiens mR	fn3,TM,SS	2.3
	446232	AI281848	Hs.165547	ESTs	7tm_3,TM,	2.3
	422493	AW474183	Hs.233816	ESTs	TM	2.3
70	407047	X65965		gb:H.sapiens SO	sodfe,TM,	2.3
	411096	U80034	Hs.68583	mitochondrial i	Peptidase_M3,,	2.3
	426457	AW894667	Hs.169965	chimerin (chima	DAG_PE-bind,RhoGAP,TM,	2.3
	446545	AI431798	Hs.164192	ESTs, Weakly si	TM	2.3
	422094	AF129535	Hs.272027	F-box only prot	TM	2.3
75	421933	R98881	Hs.109655	sex comb on mid	SAM,TM,	2.3
	430001	AI580056	Hs.98992	ESTs	TM	2.3
	420802	U22376	Hs.1334	v-myb avian mye	TM	2.3
	402053				gpdh,,SS	2.3
80	432743	AI146966	Hs.101656	ESTs	SS	2.3
	433409	AI278802	Hs.25661	ESTs	PWWP,PHD,bromodomain,TM,	2.3
	408330	AW182602	Hs.249954	ESTs	TM,SS	2.3
	407807	AL031427	Hs.40094	Human DNA seque	T4_deiodinase,TM,	2.3
	436972	AA284679	Hs.25640	claudin 3	PMP22_Claudin,TM,SS	2.3
	433730	AK002135	Hs.3542	hypothetical pr	TM,SS	2.3

5	414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	2.3
	438192	AJ859065	Hs.16808	ESTs, Weakly si	TM,SS	2.3
	415339	NM_015156	Hs.78398	KJAA0071 protei	ELM2,TM,	2.3
	449539	W80363	Hs.58446	ESTs	pkinae,Furin-like,Recep_L_domain,TM,SS	2.2
	450956	AW193531	Hs.205647	ESTs, Moderatel	pkinae,TM,SS	2.2
	430335	D80007	Hs.239499	KJAA0185 protei	S1,TM,	2.2
	417849	AW291587	Hs.82733	nidogen 2	EGF,ldl_recept_b,thyroglobulin_1,TM,SS	2.2
	412326	R07566	Hs.73817	small inducible	IL8,,SS	2.2
10	408349	BE546947	Hs.44276	homeo box C10	homeobox,TM,	2.2
	424704	AI263293	Hs.152096	cytochrome P450	p450,,SS	2.2
	409632	W74001	Hs.55279	serine (or cyst	serpin,TM,	2.2
	415323	BE269352	Hs.949	neutrophil cyto	SH3,TPR,TM,	2.2
	417531	NM_003157	Hs.1087	serine/threonin	pkinae,TM,	2.2
	403137				rm,TM,SS	2.2
15	428479	Y00272	Hs.184572	cell division c	pkinae,TM,SS	2.2
	430200	BE613337	Hs.234896	geminin	TM,SS	2.2
	425390	AI092634	Hs.156114	protein tyrosin	ig,Opioids_neuropep,TM,SS	2.2
	408380	AF123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,	2.2
	422424	AI186431	Hs.116577	prostate differ	TGF-beta,,SS	2.2
20	400298	AA032279	Hs.61635	six transmembra	TM	2.2
	411571	AA122393	Hs.70811	hypothetical pr	SS	2.2
	412802	U41518	Hs.74602	aquaporin 1 (ch	MIP,TM,	2.2
	414761	AU077228	Hs.77256	enhancer of zes	SET,TM,	2.2
	408432	AW195262		gb:xn67b05.x1 N	TM,SS	2.2
25	429558	AI088691	Hs.208414	Homo sapiens mR	mito_carr,TM,	2.2
	425300	AW601773	Hs.270259	ESTs	TM	2.2
	439653	AW021103	Hs.6631	hypothetical pr	TM,SS	2.2
	426827	AW067805	Hs.172655	methylene tetrah	THF_DHG_CYH_FTHFS,TM,	2.2
30	444514	AI682905	Hs.270431	ESTs, Weakly si	cnMP_binding,TM,SS	2.2
	425322	U63630	Hs.155637	protein kinase,	MCM,TM,	2.2
	421662	NM_014141	Hs.106552	cell recognitio	laminin_G,TM,SS	2.2
	438788	AA825716		gb:od29e10.s1 N	ank,death,RHD,TM,	2.2
	429058	AF138863	Hs.194827	hypothetical pr	TM	2.2
35	423104	AJ005273	Hs.123647	antigenic deter	TM	2.2
	410406	AI969703	Hs.301842	ESTs	FGGY,TM,	2.2
	421379	Y15221	Hs.103982	small inducible	IL8,TM,SS	2.2
	422809	AK001379	Hs.121028	hypothetical pr	IQ,TM,	2.2
	418049	AA211467	Hs.190488	hypothetical pr	TM	2.2
40	436209	AW850417	Hs.254020	ESTs, Moderatel	TM,SS	2.2
	408042	AL049233	Hs.42244	Homo sapiens mR	TM	2.2
	425692	D90041	Hs.155956	N-acetyltransfe	Acetyltransf2,TM,	2.2
	409665	NM_006731	Hs.55777	Fukuyama type c	SS	2.2
	428157	AI738719	Hs.298668	ESTs	hexokinase,TM,	2.2
45	410480	R97457	Hs.63984	cadherin 13, H-	cadherin,TM,SS	2.2
	429732	U20158	Hs.2488	lymphocyte cyto	SH2,TM,	2.2
	414747	U30872	Hs.77204	centromere prot	SS	2.2
	425843	BE313280	Hs.159627	death associate	TM	2.2
	445299	AI910382	Hs.118727	Homo sapiens cD	HLH,TM,	2.1
50	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.1
	430066	AI929659	Hs.237825	signal recognit	TPR,,SS	2.1
	427528	AU077143	Hs.179565	minichromosome	MCM,TM,SS	2.1
	448089	AI467945	Hs.173696	ESTs	TM,SS	2.1
	428728	NM_016625	Hs.191381	hypothetical pr	TM	2.1
55	409929	R38772	Hs.172619	KJAA1106 protei	TM	2.1
	405264				SS	2.1
	445625	BE246743	Hs.288529	Homo sapiens cD	TM	2.1
	408949	AF189011	Hs.49163	putative ribonu	Ribonuclease_3,TM,SS	2.1
	424513	BE385864	Hs.149894	mitochondrial t	GTP_EFTU,IF2,TM,	2.1
60	433683	AI817723	Hs.22678	hypothetical pr	SS	2.1
	442952	AI743261	Hs.131860	ESTs	TM	2.1
	432378	AI493046	Hs.146133	ESTs	TM	2.1
	417979	AU077284	Hs.83081	GTP cyclohydrol	TM,SS	2.1
	433849	BE465884	Hs.280728	ESTs	SS	2.1
65	437928	NM_005476	Hs.5920	UDP-N-acetylglu	ROK,Epimerase_2,TM,	2.1
	403055				filament,TM,SS	2.1
	432840	AK001403	Hs.279521	hypothetical pr	TM	2.1
	418994	AA296520	Hs.89546	selectin E (end	EGF,lectin_c,sushi,TM,SS	2.1
	440908	AI915225	Hs.126735	ESTs	TM	2.1
70	417621	AV654694	Hs.82316	interferon-indu	TM	2.1
	436895	AF037335	Hs.5338	carbonic anhydr	carb_anhydrase,TM,SS	2.1
	408420	NM_006915	Hs.299481	Homo sapiens mR	TM	2.1
	434064	AL049045	Hs.180758	hypothetical pr	cadherin,TM,SS	2.1
	404076				RmaAD,TM,	2.1
75	422515	AW500470	Hs.117950	multifunctional	AIRC,SAICAR_synt,TM,	2.1
	445867	AF272663	Hs.13405	gephyrin	MoCF_biosynth,TM,	2.1
	441021	AW578716	Hs.7644	H1 histone fami	linker_histone,TM,	2.1
	446595	T57448	Hs.15467	hypothetical pr	TM,SS	2.1
	417515	L24203	Hs.82237	ataxia-telangie	zf-B_box,,SS	2.1
80	412429	AV650262	Hs.75765	GRO2 oncogene	IL8,TM,SS	2.1
	449207	AL044222	Hs.23255	nucleoporin 155	TM,SS	2.1
	412095	AI624707	Hs.5921	Homo sapiens cD	TM,SS	2.1
	400861				pkinae,TM,	2.1
	440591	AA431599	Hs.132799	Homo sapiens cD	TM	2.1

442104	L20971	Hs.188	phosphodiesterase	PDEase,TM,	2.1
446921	AB012113	Hs.16530	small inducible	IL8,SS	2.1
446051	BE048061	Hs.153315	ESTs	Reprolysin,Pep_M12B_propep,TM,SS	2.1
422675	BE018517	Hs.119140	eukaryotic tran	elfF-5a,TM,	2.1
425170	AU077315	Hs.154970	transcription f	TM	2.1
453751	R36762	Hs.101282	Homo sapiens mR	TM	2.1
426283	NM_003937	Hs.169139	lynnurininase (L	TM	2.1
417874	BE516160	Hs.82829	protein tyrosin	Y_phosphatase,TM,	2.1
449555	AW450288	Hs.195390	ESTs	TM	2.1
439699	AF086534	Hs.187561	ESTs, Moderatel	TM	2.1
427413	BE547647	Hs.177781	superoxide dism	sodie,TM,	2.1
407802	D84145	Hs.39913	novel RGD-conta	hexapep,TM,SS	2.0
446035	NM_006558	Hs.13565	Sam68-like phos	TM	2.0
406981	S71129	Hs.296844	Acetylcholinest	COesterase,TM,SS	2.0
432343	NM_002960	Hs.2961	S100 calcium-bi	S_100,efhand,TM,SS	2.0
414890	BE281095	Hs.77573	uridine phospho	PNP_UDP_1,TM,SS	2.0
423019	AI640185	Hs.225816	ESTs	SS	2.0
422278	AF072873	Hs.114218	frizzled (Droso	Fz,Frizzled,TM,SS	2.0
405545				ABC_tran,ABC_membrane,TM,SS	2.0
446237	AW270515	Hs.149596	ESTs	bZIP,TM,	2.0
428074	BE387770	Hs.182378	colony stimulat	SS	2.0
423430	AF112481	Hs.128501	RAD54, S. cerev	SNF2_N,helicase_C,TM,	2.0
435767	H73505	Hs.117874	ESTs	Peptidase_S8,P,TM,	2.0
432945	AL043683	Hs.271357	ESTs, Weakly si	PK_SS	2.0
404170				sodie,TM,	2.0
422610	AF153820	Hs.1547	potassium inwar	IRK,TM,	2.0
417933	X02308	Hs.82962	thymidylate syn	thymidylat_synt,SS	2.0
441384	AA447849	Hs.288660	protease, serin	TM	2.0
414020	NM_002984	Hs.75703	small inducible	IL8,SS	2.0
427674	NM_003528	Hs.2178	H2B histone fam	histone,TM,SS	2.0
435425	H16263	Hs.31416	ESTs	TM	2.0
429782	NM_005754	Hs.220689	Ras-GTPase-acti	rm,MTF2,SS	2.0
417366	BE185289	Hs.1076	small proline-r	Crnifin,TM,	2.0
426746	J03626	Hs.2057	uridine monopho	Pribosyltran,OMPdecase,TM,	2.0
432677	NM_004482	Hs.278611	UDP-N-acetyl-al	Glycos_transf_2,Ricin_B_lectin,TM,	2.0

TABLE 43B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
408432	1058667_1	AW195262 R27868 AW811262
411560	1249443_1	AW851186 AW996967 BE143456
422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839
422285	214669_1	AI803103 AI885143 AW470793 AW450703 AI090784 AW271587 AW236950 AW242783
422689	219896_1	AW856665 AA315006 AW954733
423871	232749_1	AA331906 AA332484
438788	465159_1	AA825716 AW978859 AA828841
454456	1207088_1	AW850984 AW752836 M86124
454678	1228915_1	AW813089 W28102

TABLE 43C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400861	9757506	Plus	163855-164016
401644	8576138	Plus	82655-83959
401747	9789672	Minus	118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130468-130593, 131097-131258, 131866-131932, 132451-132575, 133580-134011
402053	8083229	Plus	62703-63179
402819	6729581	Plus	29217-29422
403055	8748904	Minus	109532-110225
403137	9211494	Minus	92349-92572, 92958-93084, 93579-93712, 93949-94072, 94591-94748, 95214-95337
403776	7770611	Minus	1414-1513, 1624-1756
404076	9931752	Minus	3848-3967
404170	9930793	Plus	168836-169248
405264	7329374	Plus	28556-28684
405454	7656675	Plus	133807-134053
405545	1054740	Plus	118677-118807, 119091-119296, 121626-121823
406434	9256651	Minus	17803-17931

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER

Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and denominator were switched.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number

Unigene Title: R1:		Unigene gene title Ratio of tumor to normal tissue		
	Pkey	ExAccn	UnigeneID	Unigene Title
5	412859	NM_000705	Hs.813	ATPase, H ⁺ -K ⁺ exchanging, beta polypepti
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible
	427469	AA403084	Hs.269347	ESTs
	407486	S69741		gb:hSCG-3=stomach cancer gene-3 (oncogen
10	428602	AL137479	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (f
	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e
	443547	AW271273	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (
	435473	N53550	Hs.260881	ESTs
15	455826	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo
	402015			
	430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo
	444515	AW204908	Hs.169979	ESTs
	429201	X03178	Hs.198246	group-specific component (vitamin D bind
20	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L
	450940	AI744943	Hs.300744	ESTs, Moderately similar to ALU7_HUMAN A
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto
	424596	AB020639	Hs.151017	estrogen-related receptor gamma
	403670			
25	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2
	407462	AJ252011		gb:Homo sapiens partial mRNA for amilor
	405110			
	402760			
	408947	AL080093	Hs.49117	Homo sapiens mRNA: cDNA DKFZp564N1662 (f
30	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT
	431514	AW972363		gb:EST384454 MAGE resequences, MAGL Homo
	451103	R52804	Hs.25956	DKFZP564D206 protein
	452033	AW273741	Hs.246977	ESTs
	440058	AJ932662	Hs.164073	ESTs
	405645			
35	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein
	445627	AW818475	Hs.7363	ESTs
	425679	X05997	Hs.159177	lipase, gastric
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,
40	443537	D13305	Hs.203	cholecystokinin B receptor
	435654	AW139612	Hs.131041	ESTs
	406326			
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164
	455541	AW993005		gb:RC2-BN0032-160200-013-d04 BN0032 Homo
45	453989	M63962	Hs.36992	ATPase, H ⁺ -K ⁺ exchanging, alpha polypept
	407261	L03172		gb:Homo sapiens cell-type T-cell immunog
	451062	AL110125	Hs.25910	Homo sapiens mRNA: cDNA DKFZp564C1416 (f
	429350	AJ754634	Hs.131987	ESTs
	411021	F00055	Hs.172004	titin
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi
	450572	AI700863	Hs.202494	Homo sapiens cDNA FLJ13245 fis, clone OV
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL
	421562	AA530994	Hs.105803	ghrelin precursor
	457432	NM_005136	Hs.268538	potassium voltage-gated channel, Isk-rel
55	418421	R58620	Hs.85050	phospholamban
	424104	AA669515	Hs.144950	ESTs
	422582	AA312660		gb:EST183335 Jurkat T-cells VI Homo sapi
	417332	AW972717	Hs.288462	Homo sapiens cDNA: FLJ21511 fis, clone C
	432440	X63597	Hs.2996	sucrase-isomaltase
60	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1
	401989			
	452528	AA742457	Hs.291479	ESTs
	412569	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s
	406255			
65	419293	AA746282	Hs.255659	ESTs
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle
	414502	AL133721	Hs.224680	ESTs
70	432113	AA935065	Hs.152385	ESTs
	413808	J00287	Hs.182183	caldesmon 1
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti
	434745	AW974445	Hs.185155	ESTs, Weakly similar to HuEMAP [H.sapien
	420444	AI905985	Hs.111805	ESTs
	445200	AA084460	Hs.12409	somatostatin
75	415314	N88802	Hs.5422	glycoprotein M6B
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970
	431152	AW970998		gb:EST383083 MAGE resequences, MAGK Homo
	432306	Y18207	Hs.274315	protein phosphatase 1, regulatory (inhib
	401775			
80	440059	AW467335	Hs.257676	ESTs
	436089	AA804957	Hs.119840	ESTs
	447071	AW236867	Hs.244376	ESTs
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04

5	423968	AF098277	Hs.136529	solute carrier family 23 (nucleobase tra	0.32
	445487	AI806287	Hs.201217	ESTs	0.32
	421296	NM_002666	Hs.103253	perilipin	0.32
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	0.33
	449916	T60525	Hs.299221	ESTs	0.33
10	446393	AW014174	Hs.151707	ESTs	0.33
	446632	AI333565	Hs.159073	diacylglycerol kinase, eta	0.33
	428070	T63918	Hs.182313	retinol-binding protein 2, cellular	0.33
	421451	AA291377	Hs.50831	ESTs	0.33
	405817				0.33
15	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
	413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	0.34
	404121				0.34
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.34
	413079	BE064382		gb:RC4-BT0310-110300-015-c12 BT0310 Homo	0.34
20	403059				0.35
	458987	AW750067	Hs.205386	ESTs	0.35
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.35
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.35
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	0.35
25	451818	AI819018		gb:ts54f01.x1 NCI_CGAP_Kid8 Homo sapiens	0.35
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	0.35
	405742				0.35
	403429				0.35
	443622	AI911527	Hs.11805	ESTs	0.36
30	404973				0.36
	444567	AV654020	Hs.184261	ESTs, Weakly similar to putative type II	0.36
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	0.36
	407110	AA018042	Hs.95078	ESTs	0.36
	411671	BE049094	Hs.278567	ESTs	0.36
35	430800	NM_000805	Hs.2681	gastrin	0.36
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	0.36
	444536	AI161068	Hs.14780	ESTs	0.36
	454042	H22570	Hs.172572	hypothetical protein FLJ20093	0.37
	444102	AV647953	Hs.282379	ESTs	0.37
40	424122	AA335593	Hs.116147	ESTs	0.37
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	0.37
	436277	R88520	Hs.120917	ESTs	0.37
	456350	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.37
	451027	AW519204	Hs.40808	ESTs	0.37
45	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	0.38
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	0.38
	436802	N34486	Hs.170504	ESTs	0.38
	448142	AI521768	Hs.164586	ESTs	0.38
	442378	R54033	Hs.21245	ESTs	0.38
50	446406	AI553681	Hs.25248	ESTs	0.38
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	0.38
	424903	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.38
	406714	AI219304	Hs.283108	hemoglobin, gamma G	0.39
	434340	AI193043	Hs.128685	ESTs	0.39
55	406036				0.39
	431078	U82827	Hs.249195	homeo box A13	0.39
	457663	AW371946	Hs.116119	ESTs	0.39
	451880	AI821032	Hs.209387	ESTs	0.39
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.39
60	446414	W93246	Hs.59187	ESTs	0.39
	442317	AI915599	Hs.129225	ESTs	0.39
	447261	NM_006691	Hs.17917	lymphatic vessel endothelial hyaluronan	0.39
	439569	AW602166	Hs.222399	CEGP1 protein	0.39
	433485	AI493076	Hs.78183	aldo-keto reductase family 1, member C1	0.40
65	432753	NM_014075	Hs.278915	PRO0593 protein	0.40
	420200	AI271429	Hs.88142	ESTs	0.40
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	0.40
	453950	AA156998	Hs.211568	eukaryotic translation initiation factor	0.40
	407408	AF054830		gb:Homo sapiens interleukin-1 type I rec	0.40
70	410732	AW984328		gb:PM3-HN0010-050400-001-h12 HN0010 Homo	0.40
	458272	AI797360	Hs.264899	ESTs, Weakly similar to ALU3_HUMAN ALU S	0.40
	401514	AF147186		gb:AF147186 Homo sapiens library (Schere	0.40
	436363	AA843926	Hs.124434	ESTs	0.40
	434445	AI349306	Hs.11782	ESTs	0.40
75	413272	AA127923	Hs.293256	ESTs	0.40
	409681	N51508	Hs.143718	ESTs	0.40
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.40
	450891	AI743118	Hs.238914	ESTs, Weakly similar to neuregulin-4 sho	0.40
	452078	AA022620	Hs.52170	ESTs	0.41
80	419278	AU076799	Hs.1247	apolipoprotein A-IV	0.41
	433637	AW024214	Hs.135405	ESTs	0.41
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	0.41
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcos	0.41
	453139	AA330620	Hs.240659	ESTs	0.41
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	0.41
	437931	AI249468	Hs.145274	ESTs	0.41
	402759				0.41

	450888	AW021446	Hs.80714	ESTs	0.41
	417318	AW953937	Hs.12891	ESTs	0.41
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	0.41
5	424884	AW299437	Hs.225717	ESTs	0.41
	439024	R96696	Hs.35598	ESTs	0.42
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	0.42
	409300	AA126190		gb:zm7803.r1 Stratagene neuroepithelium	0.42
	444237	AA336878	Hs.9842	Human DNA sequence from clone RP4-788L20	0.42
10	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	0.42
	447021	AI356564	Hs.161406	ESTs	0.42
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	0.42
	407850	AW086230	Hs.244912	ESTs	0.42
	449884	AI673110	Hs.222195	ESTs	0.42
15	436327	AA813075	Hs.120181	ESTs	0.42
	415972	H11436	Hs.260201	ESTs	0.42
	400917				0.43
	435309	AW089050	Hs.187993	ESTs	0.43
	424410	W79027	Hs.271762	ESTs	0.43
20	445577	N40696	Hs.146077	ESTs	0.43
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434i0428	0.43
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	0.43
	451123	AI927224	Hs.213480	ESTs	0.43
	457151	AW206116	Hs.253538	ESTs	0.43
25	459185	AI908222		gb:RC-BT165-300399-020 BT165 Homo sapien	0.43
	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	0.43
	424815	AA347287	Hs.104573	ESTs	0.43
	429704	AA584440	Hs.185812	ESTs	0.43
	411067	AI681006	Hs.301543	ESTs	0.43
30	430172	AA468591	Hs.161889	ESTs	0.43
	435124	AA725362	Hs.120456	ESTs	0.43
	445966	L17330	Hs.280	pre-T/NK cell associated protein	0.43
	443741	AW451759	Hs.145420	ESTs	0.43
	416275	H42823	Hs.155742	glyoxylate reductase/hydroxypyruvate red	0.44
35	451138	W92287	Hs.40268	ESTs	0.44
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	0.44
	426730	AL040738		gb:DKFZp434B1615_r1 434 (synonym: htes3)	0.44
	410066	AL117664	Hs.58419	DKFZP586L2024 protein	0.44
	427965	D00306	Hs.183864	elastase 3B	0.44
40	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.44
	408479	BE047329	Hs.144483	ESTs	0.44
	457994	AW136239	Hs.132922	ESTs	0.44
	435564	AF210652	Hs.16614	5(3)-deoxynucleotidase (dNT-2); nucl	0.45
	435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.45
45	434399	AA878845	Hs.125769	ESTs	0.45
	415797	AI291896	Hs.72800	ESTs	0.45
	430264	AA470519		gb:nc711i10.s1 NCI_CGAP_Pr1 Homo sapiens	0.45
	409435	AI810721	Hs.95424	ESTs	0.45
	433542	AA598869	Hs.173770	ESTs	0.45
50	455400	AW936342		gb:QV4-DT0021-281299-070-h12 DT0021 Homo	0.45
	412047	AA934589	Hs.49696	ESTs	0.45
	443948	T56148	Hs.9997	Homo sapiens mRNA full length insert cDN	0.45
	450307	AW450336	Hs.201783	ESTs	0.45
	434500	AF143877	Hs.215047	Homo sapiens clone IMAGE:113431 mRNA seq	0.45
55	420460	AA262331	Hs.135503	ESTs	0.45
	450752	AA012986	Hs.60466	ESTs	0.45
	418138	AA213626	Hs.136204	EST	0.45
	441088	AA916546	Hs.126546	ESTs	0.46
60	410990	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo	0.46
	438211	T08401		gb:EST06292 Infant Brain, Bento Soares H	0.46
	434349	NM_015678	Hs.3821	neurobeachin	0.46
	409824	AW501063		gb:UI-HF-BPOp-aiz-c-01-0-UI.r1 NIH_MGC_5	0.46
	403279				0.46
	434882	AW974752	Hs.269497	ESTs	0.46
65	404629				0.46
	427393	AB029018	Hs.177635	KIAA1095 protein	0.46
	454651	AW812091		gb:RC4-ST0173-191099-032-b04 ST0173 Homo	0.46
	401992				0.46
	457275	AA463422	Hs.209431	ESTs	0.46
70	403710				0.46
	419728	L36861	Hs.92858	guanylate cyclase activator 1A (retina)	0.46
	401075				0.46
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	0.46
	453404	AA035446	Hs.261224	ESTs	0.46
75	407208	T10695	Hs.102948	enigma (LIM domain protein)	0.46
	440681	AW449696	Hs.166547	ESTs	0.46
	454206	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	0.47
	402466				0.47
	429996	N90822	Hs.48969	ESTs	0.47
80	403680				0.47
	428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapi	0.47
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	0.47
	402851				0.47
	438421	AA806907	Hs.194451	ESTs	0.47

5	454661	BE244138		gb:TCBAP1E1218 Pediatric pre-B cell acut	0.47
	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.47
	409106	AW337854	Hs.177386	ESTs	0.47
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	0.47
	442799	AI564739	Hs.68505	ESTs	0.47
	457955	AI208986	Hs.143945	ESTs	0.47
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214 Homo	0.47
	407938	AA905097	Hs.85050	phospholamban	0.47
10	414141	BE255083		gb:601111390F1 NIH_MGC_16 Homo sapiens c	0.47
	448869	AI792798	Hs.12496	ESTs	0.47
	400749				0.47
	458745	AW207347	Hs.211101	ESTs	0.48
	418437	AA771738	Hs.295351	ESTs	0.48
15	452286	AI358570	Hs.123933	ESTs	0.48
	430369	AA477631	Hs.119484	ESTs	0.48
	453572	AA382590	Hs.31848	ESTs, Weakly similar to hypothetical pro	0.48
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	0.48
	445765	AV655102	Hs.117266	ESTs	0.48
20	400322	AF045576	Hs.247758	olfactory receptor, family 5, subfamily	0.48
	412526	M90366	Hs.73982	zona pellucida glycoprotein 2 (sperm rec	0.48
	407986	U32659	Hs.41724	interleukin 17 (cytotoxic T-lymphocyte-a	0.48
	455479	AW948312		gb:RC0-MT0015-280300-021-h04 MT0015 Homo	0.48
	450308	AI692571	Hs.201681	ESTs	0.48
25	411149	N68715	Hs.269128	ESTs	0.48
	453982	AW014252	Hs.252637	ESTs	0.48
	410971	AW812258		gb:RC0-ST0174-191099-031-b02 ST0174 Homo	0.48
	410839	NM_006849	Hs.66581	protein disulfide isomerase	0.48
	421553	AA536080	Hs.97302	ESTs	0.48
30	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fs, clone MA	0.48
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	0.48
	447858	AW080339	Hs.211911	ESTs	0.49
	422639	AI929377	Hs.173724	creatine kinase, brain	0.49
	402449				0.49
35	420440	NM_002407	Hs.97644	mammaglobin 2	0.49
	435056	AW023337	Hs.5422	glycoprotein M6B	0.49
	419543	AA244170	Hs.188719	ESTs	0.49
	407033	U78628		gb:Human leukemia inhibitory factor rece	0.49
	437468	AA457619		gb:aa89d11.1 Stratagene fetal retina 93	0.49
40	412639	AW961284	Hs.296235	ESTs	0.49
	406109				0.49
	404519				0.49
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	0.49
	406014				0.49
45	400938				0.49
	414290	AI568801	Hs.71721	ESTs	0.49
	432433	AW014734	Hs.157969	ESTs	0.49
	405273				0.49
50	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.49
	414383	BE279406		gb:601157981F1 NIH_MGC_21 Homo sapiens c	0.49
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	451241	AI767545	Hs.209572	ESTs	0.49
	428336	AA503115	Hs.183752	microseminoprotein, beta-	0.49
	418310	AA814100	Hs.86693	ESTs	0.49
55	452152	AL046755	Hs.28219	protein phosphatase 2 (formerly 2A), reg	0.49
	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	0.49
	400332	S66407	Hs.248032	FLT4	0.49
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	0.49
	408221	AA912183	Hs.47447	ESTs	0.49
60	440179	AI990151	Hs.125904	ESTs	0.50
	425360	BE547704		gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.50
	406600				0.50
	418594	AI732083	Hs.187619	ESTs	0.50
	432128	AA127221	Hs.117037	ESTs	0.50
65	458611	AI268407	Hs.211458	ESTs	0.50
	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	0.50
	441068	AA913897	Hs.233559	ESTs	0.50
	428108	AA421452	Hs.164851	ESTs	0.50
	400803				0.50
70	439996	AA916565	Hs.221675	ESTs	0.50

75	TABLE 44B:		
	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	

80	Pkey	CAT number	Accession
	409300	111676_1	AA126190 AA074486 AA074707 AA070059 AA084886
	409824	1155499_1	AW501063 AW503034 AW501523
	410285	119128_1	AA083609 AA083790 AA112048
	410495	1205826_1	N95428 W24040 AW751366 H81987
	410732	1218556_1	AW984328 AW984322 AW984318 AW984330 R58427 AW984332 AW799807 AW984321
	410971	1228216_1	AW812258 AW812252 AW812261 AW812263 AW812285 AW812277 AW812264
	410990	1228649_1	AW812929 AW812779 AW813088

	411607	1251251_1	AW853498 AW853442 AW853590 AW853433 AW853592
	413079	1348528_1	BE064382 BE064387 BE064385 BE064381 BE153367 BE153366 BE153401 BE153385 BE064372
	413679	1382784_1	BE156765 BE156770 BE156767 BE156769 BE156803 BE156802 BE156847 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779
5	414141	1420715_1	BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
	414383	1440279_1	BE255083 BE257634
	422582	218132_1	BE279406 BE280100
	425360	250631_1	AA312660 AJ474863
10	426730	271055_1	BE547704 AA355909
	428151	287658_1	AL040738 AA383683
	430264	315008_1	AA422028 W79191
	430664	321423_1	AA470519 BE303010 BE302954 BE384120
	431152	328675_1	AW969834 AA528493 AA483165 AW969842
15	431514	334213_1	AW970998 AW971004 AA574217 AA493538
	437468	43743_1	AW972363 AA506335 AI077445
	438211	45225_1	AA457619 AL390167
	449923	81926_1	T08401 ZB3934 T16897
	451818	887271_1	BE258051 R45758 AA004732 BE256126
20	454206	1050848_1	AJ819018 RD5492 W27615
			AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515
			AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263
			AW810325 AW810443 AW810198 AW810321 AW810265 AW810567 AW810447 AW810328 AW810513 BE146674 AW810257 AW810185 AW810281
			AW810258 BE062400 AW810323 AW810293 BE146652 AW810516 BE146689 AW810289 AW810566 AW810636 AW178842 BE062434 BE146653
			AW810536 AW846649
25	454554	1223842_1	AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156
			AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431
			BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330
			AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998
			BE061745 BE061753
30	454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
	454561	1228069_1	AW812091 AW812228 AW812106 AW938581 AW812080
	454561	1228527_1	BE241138 BE244727 AW812636 AW812647
	454738	1232449_1	BE072139 BE157977 BE157974 AW857974 AW817778
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265
			AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454790	1234752_1	AW820852 AW820773 AW821088
	454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
			AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
	455175	1257335_1	AW993247 AW861464
40	455400	1288135_1	AW936342 AW936366
	455479	1293163_1	AW948312 AW948286 AW948289 AW948297 AW948279 AW948295
	455541	1323705_1	AW993005 AW993285 AW993290
	455753	1356070_1	BE075124 BE075229 BE075278
	455826	1373392_1	BE144228 BE144291
45	458147	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
	459185	922823_1	AJ908222 AJ908224 AJ908217

TABLE 44C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	NT_position
	400749	7331445	Minus	9162-9293
	400803	8567875	Minus	18267-19088
	400917	7283186	Minus	173258-173631
	400938	7652890	Minus	92074-92423
	401075	3687273	Plus	81218-81395
60	401514	7622355	Plus	93224-93292,94913-95065,95163-95334
	401775	9966311	Minus	110228-110340
	401989	4309964	Minus	118611-118821
	401992	4153858	Plus	31452-31649
	402015	7417802	Minus	48791-49043,50038-50205,51530-51672,54448-54565,55933-56073
65	402449	9796674	Plus	59867-60039,62588-62828,63465-63623,64923-65108
	402466	9796919	Plus	57659-57866,58839-58908
	402759	9213869	Plus	134117-134281
	402760	9213869	Plus	136829-136952,137336-137521
	402851	9650753	Minus	63022-63136,63683-63783
70	403059	8954192	Minus	69553-69702
	403279	8072597	Plus	162569-162768,163918-164168
	403429	9719566	Minus	52789-52917
	403670	7259739	Minus	88377-88537
	403680	7331517	Minus	157184-157415
75	403710	6437516	Plus	27413-28978
	404121	9796219	Plus	59256-59401
	404519	8152000	Plus	12817-13000
	404629	9796665	Plus	55584-55796
	404973	3213020	Plus	101602-102591
80	405110	8096888	Minus	118940-119100
	405273	4156137	Minus	98141-98754
	405645	4926864	Minus	92231-92380,92724-92869
	405742	7283744	Minus	54424-55488

405817	4071056	Plus	19914-20112,25655-25810
406014	6758904	Minus	23738-24076
406036	6758919	Plus	17942-18163
406109	9127147	Minus	58328-58485
406255	7417729	Plus	2959-3200
406326	9212385	Plus	84508-84655
406600	8248616	Minus	36296-36610

TABLE 45A: ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES
Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" stomach cancer level was set to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of stomach cancer compared to normal stomach

Pkey	ExAccn	UnigenID	Unigene Title	R1
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	66.80
411243	AB039886	Hs.69319	CA11	61.16
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	42.36
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	35.80
425679	X05997	Hs.159177	lipase, gastric	28.34
409041	AB033025	Hs.50081	KIAA1199 protein	26.91
452121	NM_004081	Hs.70936	deleted in azoospermia	26.22
403776			NA	25.00
444783	AK001468	Hs.62180	anilin (Drosophila Scraps homolog), act	23.90
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.90
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	23.35
424252	AK000520	Hs.143811	hypothetical protein FLJ20513	22.26
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	21.06
415989	AI267700	Hs.317584	ESTs	20.72
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	19.84
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	15.50
438639	AI278360	Hs.31409	ESTs	15.16
426427	M86699	Hs.169840	TTK protein kinase	14.54
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	14.26
443211	AI128388	Hs.143655	ESTs	14.22
421470	R27496	Hs.1378	annexin A3	13.96
400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	13.94
424086	AI351010	Hs.102267	lysyl oxidase	13.73
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.38
409757	NM_001898	Hs.123114	cystatin SN	13.33
447033	AI357412	Hs.157601	ESTs	13.20
447164	AF026941	Hs.17518	Homo sapiens cigs mRNA, partial sequence	12.80
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fs, clone C	12.66
432596	AJ224741	Hs.278461	matrilin 3	12.64
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	12.46
413582	AW295647	Hs.71331	hypothetical protein MGC5350	12.32
423020	AA383092	Hs.1608	replication protein A3 (14kD)	12.18
448693	AW004854	Hs.228320	hypothetical protein FLJ23537	11.74
442660	AW138174	Hs.130651	ESTs	11.73
441693	AA384673	Hs.7943	RPB5-mediated protein	11.16
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	11.08
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fs, clone HE	10.90
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.48
443715	AI583187	Hs.9700	cyclin E1	10.44
420900	AL045633	Hs.44269	ESTs	10.38
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.36
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.20
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	10.18
410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fs, clone PL	10.14
414422	AA147224	Hs.337232	ESTs	10.12
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.02
414972	BE263782	Hs.77695	KIAA0008 gene product	10.02
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	9.80
428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fs, clone CO	9.72
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.68
400195	NA		NA	9.66
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.64
420170	U43374	Hs.95631	Human normal keratinocyte mRNA	9.60
414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fs, clone L	9.58
417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	9.34
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f	9.26
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	9.16
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	8.95
431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	8.84
419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.80
425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.78

	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT	8.69
	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	8.68
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	8.68
	452461	N78223	Hs.108106	transcription factor	8.68
5	425916	NM_006786	Hs.162200	urotensin 2	8.64
	422805	AA436989	Hs.121017	H2A histone family, member A	8.54
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	8.52
	441377	BE218239	Hs.202656	ESTs	8.41
	445891	AW391342	Hs.199460	ESTs	8.31
10	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.30
	439521	AI808955	Hs.58248	ESTs	8.30
	425087	R62424	Hs.126059	ESTs	8.28
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.22
	441795	N58115	Hs.21137	AD024 protein	8.02
15	427878	C05766	Hs.181022	CGI-07 protein	8.00
	413583	AL120806	Hs.5888	ESTs	7.98
	407853	AA336797	Hs.40499	dicckopf (Xenopus laevis).homolog 1	7.98
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFp566A1046 (f	7.97
	404996			NA	7.96
20	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.96
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	7.94
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.91
	418895	AA894638	Hs.14600	ESTs	7.90
25	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fs, clone Y7	7.86
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	7.82
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.80
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFp564F093 (fr	7.72
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.70
30	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	7.70
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	7.69
	427718	AI798680	Hs.25933	ESTs	7.66
	434032	AW009951	Hs.206892	ESTs	7.60
35	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	7.58
	450480	X82125	Hs.25040	zinc finger protein 239	7.51
	418678	NM_001327	Hs.167379	cancer/testis antigen	7.49
	431494	AA991355	Hs.298312	hypothetical protein DKFp434A1315	7.44
	452705	H49805	Hs.246005	ESTs	7.36
40	443646	AI085198	Hs.164226	ESTs	7.32
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	7.30
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	7.28
	421155	H87879	Hs.102267	lysyl oxidase	7.24
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.24
45	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.22
	435473	N53550	Hs.260881	ESTs	7.20
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	7.14
	449347	AV649748	Hs.295901	KIAA0493 protein	7.11
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	7.11
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.11
50	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	7.10
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	7.02
	426890	AA393167	Hs.41294	ESTs	6.98
	404440			NA	6.97
55	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.96
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFp564B2062 (f	6.95
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.94
	426249	F05422	Hs.168352	nucleoporin-like protein 1	6.94
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	6.92
60	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.85
	423903	M57765	Hs.1721	interleukin 11	6.84
	431041	AA490967	Hs.197955	KIAA0704 protein	6.74
	417256	U94332	Hs.81791	tumor necrosis factor receptor superfam	6.74
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.70
	407771	AL138272	Hs.62713	ESTs	6.69
65	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.66
	407162	N63855	Hs.142634	zinc finger protein	6.64
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	6.64
	427920	Z11502	Hs.181107	annexin A13	6.59
70	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	6.58
	427401	U20582	Hs.2149	actin like protein	6.55
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	6.54
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	6.54
	435159	AA668879	Hs.116649	ESTs	6.54
75	440209	H05049	Hs.22269	neurexin 3	6.54
	418134	AA397769	Hs.86617	ESTs	6.50
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.47
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	6.40
	422505	AL120862	Hs.124165	ESTs	6.34
80	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	6.32
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	6.31
	408380	AF123050	Hs.44532	diubiquitin	6.31
	420218	AW958037	Hs.286	ribosomal protein L4	6.29
	405817	NA		NA	6.28

	406747	AJ925153	Hs.217493	annexin A2	6.24
	448743	AB032962	Hs.21896	KIAA1136 protein	6.24
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	6.20
5	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	6.17
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	6.17
	401644			NA	6.16
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.13
	427335	AA448542	Hs.251677	G antigen 7B	6.12
10	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	6.07
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	6.06
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.06
	413573	AJ733859	Hs.149089	ESTs	6.06
	408758	NM_003686	Hs.47504	exonuclease 1	6.02
15	444188	AJ393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	6.02
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.00
	446364	AB006624	Hs.14912	KIAA0286 protein	5.98
	418939	AW630803	Hs.89497	lamin B1	5.90
	424639	AJ917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HE	5.88
20	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	5.86
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	5.84
	430849	AJ940727	Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.82
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	5.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.74
25	442957	AJ949952	Hs.49397	ESTs	5.72
	444577	AJ207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.72
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.71
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	5.68
	428618	AA885360	Hs.160199	NADPH oxidase, EF hand calcium-binding d	5.68
30	432867	AW016936	Hs.233364	ESTs	5.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.63
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.62
	418379	AA218940	Hs.137516	fidgetin-like 1	5.57
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.57
35	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.56
	427386	AW836261	Hs.337717	ESTs	5.54
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.52
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	5.51
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.50
40	431118	BE264901	Hs.250502	carbonic anhydrase VIII	5.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.50
	453931	AL121278	Hs.25144	ESTs	5.49
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	5.48
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.45
45	448336	RS3848	Hs.44976	ESTs	5.44
	454018	AW016892	Hs.100855	ESTs	5.42
	457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	5.42
	412246	AI160873	Hs.69233	zinc finger protein	5.40
50	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.40
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	5.40
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.40
	452862	AW378065	Hs.8687	ESTs	5.38
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.36
	412811	H06382	Hs.21400	ESTs	5.34
55	448390	AL035414	Hs.21068	hypothetical protein	5.32
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	5.30
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	5.29
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	5.28
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	5.27
60	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	5.26
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	5.25
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	5.24
	452150	W42490	Hs.260844	ESTs	5.24
	432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	5.22
65	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	5.22
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	5.22
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.22
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.20
	429625	AA455568	Hs.193814	ESTs	5.20
70	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	5.20
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	5.19
	444059	R69743	Hs.116774	integrin, alpha 1	5.18
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	5.17
	412719	AW016610	Hs.129911	ESTs	5.15
75	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.14
	425739	T19016	Hs.159410	molybdopter synthase sulfurylase	5.12
	452198	AJ097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	5.12
	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	5.10
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	5.09
80	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	5.08
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.06
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.06
	448811	AI590371	Hs.174759	ESTs	5.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.04

	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	5.04
	421373	AA808229	Hs.167771	ESTs	5.04
	448991	AW771565	Hs.189594	ESTs	5.02
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	5.00
5	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.98
	405770			NA	4.96
	421110	AJ250717	Hs.1355	cathepsin E	4.96
	452588	AA889120	Hs.110637	homeo box A10	4.92
10	433159	AB035898	Hs.150587	kinesin-like protein 2	4.91
	420952	AA282067	Hs.88972	ESTs, Moderately similar to A46010 X-in	4.88
	408321	AW405882	Hs.44205	coristatin	4.87
	441801	AW242799	Hs.86366	ESTs	4.84
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fs, clone NT	4.83
15	452909	NM_015368	Hs.30985	pannexin 1	4.82
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.82
	451105	AJ761324		gb:wf60b11.x1 NCL CGAP_Co16 Homo sapiens	4.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	4.80
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.80
20	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	4.78
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	4.78
	432874	W94322	Hs.279651	melanoma inhibitory activity	4.78
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.78
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fs, clone PL	4.77
25	442980	AA857025	Hs.8878	kinesin-like 1	4.76
	432437	W07088	Hs.293685	ESTs	4.76
	414869	AA157291	Hs.21479	ubiquitin 1	4.74
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fs, clone NT	4.74
	418380	AA425473	Hs.84429	KIAA0971 protein	4.74
30	419343	AA456245	Hs.85603	down-regulated by Ctnnb1, a	4.74
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.72
	425813	AA364136	Hs.210553	hypothetical protein DKFZp7611172	4.71
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.71
	412733	AA984472	Hs.74554	KIAA0080 protein	4.68
35	444325	AW152618	Hs.16757	ESTs	4.66
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.66
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.66
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.64
	449448	D60730	Hs.57471	ESTs	4.62
40	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.62
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	4.62
	421987	AJ133161	Hs.286131	CGI-101 protein	4.60
	430217	N47863	Hs.336901	ribosomal protein S24	4.58
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	4.57
45	425932	M81650	Hs.1968	semenogelin I	4.57
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.56
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	4.55
	451254	AI571016	Hs.172967	ESTs	4.54
	422426	W79117	Hs.58559	ESTs	4.54
50	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fs, clone HE	4.53
	435420	AI928513	Hs.59203	ESTs	4.53
	447519	U46258	Hs.339665	ESTs	4.52
	424176	AL137273	Hs.142307	hypothetical protein	4.52
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.51
55	438069	N80701	Hs.33790	ESTs	4.50
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	4.50
	438159	Z83947		gb:H.sapiens mRNA; clone CD 117	4.50
	433925	AI183551	Hs.26481	SBB126 protein	4.48
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.48
60	433384	AI021992	Hs.124244	ESTs	4.47
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.47
	453941	U39817	Hs.36820	Bloom syndrome	4.45
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	4.44
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.43
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	4.42
65	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	4.42
	417956	AA210704	Hs.190465	ESTs	4.42
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	4.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	4.42
70	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.41
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.41
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.40
	425142	AW954397	Hs.154762	HIV-1 rev binding protein 2	4.40
	441720	AI346487	Hs.28739	ESTs	4.40
75	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	4.39
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.38
	430044	AA464510	Hs.152812	ESTs	4.37
	436246	AW450963	Hs.119991	ESTs	4.37
	409582	R27430	Hs.271565	ESTs	4.37
80	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	4.35
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.34
	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.34
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	4.34
	442470	AW273860	Hs.5759	ESTs	4.33

5	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	4.32
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	4.31
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	4.31
	433397	AW079766	Hs.134880	ESTs, Weakly similar to unnamed protein	4.30
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.29
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.29
	451592	AI805416	Hs.213897	ESTs	4.28
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.28
10	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.26
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	4.26
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	4.24
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.23
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	4.22
15	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.21
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.20
	422232	D43945	Hs.113274	transcription factor EC	4.18
	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	4.18
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	4.16
20	434217	AW014795	Hs.23349	ESTs	4.16
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	4.14
	407768	AW002841	Hs.29475	ESTs	4.14
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.13
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	4.12
25	443691	AI081724	Hs.17267	ESTs	4.12
	409640	U78722	Hs.55481	zinc finger protein 165	4.12
	438176	AW138970	Hs.122113	ESTs	4.10
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	4.10
	419606	AW294795	Hs.198529	ESTs	4.08
30	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	4.08
	414152	NM_003248	Hs.75774	thrombospondin 4	4.08
	418688	T85017	Hs.1192	KIAA0074 protein	4.07
	404253			NA	4.06
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	4.06
35	428218	AA424266	Hs.123642	EphA3	4.06
	428858	AA436760		gb:zv67d11.r1 Soares_fetal_fetus_Nb2HF8_	4.06
	428336	AA503115	Hs.183752	microseminoprotein, beta-	4.05
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.04
	421841	AA908197	Hs.108850	MAK-related kinase	4.04
40	451177	AI969716	Hs.13034	ESTs	4.04
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	4.04
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	4.03
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	4.02
45	438777	AA825487	Hs.142179	ESTs	4.02
	423343	AA324643	Hs.246106	ESTs	4.02
	425788	BE466417	Hs.231899	ESTs, Weakly similar to rab3 effector-li	4.02
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.01
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	4.01
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	4.00
50	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	4.00
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	4.00
	452022	AW072330	Hs.293875	ESTs	4.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.99
	423541	AA295922	Hs.129778	gastrointestinal peptide	3.99
55	414132	AI801235	Hs.48480	ESTs	3.99
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	3.98
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.98
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	3.98
	453160	AI263307	Hs.239884	H2B histone family, member L	3.97
60	417235	AA810278	Hs.24250	ESTs	3.96
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	3.95
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.94
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	3.94
	431753	X76029	Hs.2841	neuromedin U	3.94
65	453161	AA628608	Hs.61656	ESTs	3.94
	454821	AW833504		gb:QV4-TT0008-091199-025-03 TT0008 Homo	3.94
	427961	AW293165	Hs.143134	ESTs	3.94
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.93
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.93
70	418396	AI765805	Hs.26691	ESTs	3.92
	451411	AA017492	Hs.135655	EST	3.92
	445885	AI734009	Hs.127699	KIAA1603 protein	3.92
	407698	AA058900	Hs.32646	hypothetical protein FLJ21901	3.91
	442896	R37725	Hs.261108	ESTs	3.90
75	433361	AW469373	Hs.300141	ribosomal protein L39	3.90
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.89
	413775	AW409934	Hs.75528	nucleolar GTPase	3.88
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.86
	428549	AA430064	Hs.220929	Homo sapiens cDNA FLJ14369 fis, clone HE	3.86
80	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	3.86
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.85
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	3.85
	417720	AA205625	Hs.208067	ESTs	3.85
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	3.84

	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	3.84
	421246	AW582962	Hs.102897	CGI-47 protein	3.83
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	3.83
5	428698	AA852773	Hs.334838	KIAA1866 protein	3.82
	435202	AI971313	Hs.170204	KIAA0551 protein	3.82
	454074	R63503	Hs.28419	ESTs	3.82
	448917	AI683598	Hs.201615	ESTs	3.82
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.82
10	452571	W31518	Hs.34665	ESTs	3.82
	445663	AI247343	Hs.149232	ESTs	3.82
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.80
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	3.80
	425656	AB018284	Hs.158688	KIAA0741 gene product	3.80
15	407168	RA5175	Hs.117183	ESTs	3.79
	403422	NA		NA	3.79
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.79
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.79
	457325	AA744550	Hs.136345	ESTs	3.78
20	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.77
	428865	BE544095	Hs.164960	BarH-like homeobox 1	3.76
	424188	AW954552	Hs.142634	zinc finger protein	3.75
	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	3.75
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.75
25	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	3.74
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	3.74
	459000	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.74
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	3.73
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.73
30	414883	AA926960	Hs.334883	CDC28 protein kinase 1	3.73
	415064	AA159840	Hs.149305	hypothetical protein MGC2603	3.72
	432198	AI475306	Hs.50458	ESTs	3.72
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	3.72
	415263	AA948033	Hs.130853	ESTs	3.71
35	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.71
	408460	AA054726	Hs.285574	ESTs	3.71
	437496	AA452378	Hs.170144	Homo sapiens mRNA: cDNA DKFZp547J125 (fr	3.70
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.68
	432021	AA524470	Hs.58753	ESTs	3.68
40	420092	AA814043	Hs.88045	ESTs	3.68
	414923	AW445008	Hs.77637	homeo box A4	3.68
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	3.68
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.67
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.67
45	432542	AW083920	Hs.16098	claudin 2	3.67
	410782	AW504860	Hs.288836	hypothetical protein FLJ12673	3.66
	421106	AA877124	Hs.172844	ESTs	3.64
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.64
	418735	N48769	Hs.44609	ESTs	3.64
50	411598	BE336654	Hs.70937	H3 histone family, member A	3.63
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.63
	436411	AW674352	Hs.50883	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.63
	429774	AI522215	Hs.50883	KIAA1804 protein	3.62
	448844	AI581519	Hs.177164	ESTs	3.61
55	402473	AB033035	Hs.51965	KIAA1209 protein	3.61
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.61
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.60
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.60
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.59
60	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.59
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	3.58
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.58
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	3.58
	440717	AA904527	Hs.42207	ESTs	3.58
65	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypotheti	3.58
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.58
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.57
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	3.55
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	3.55
70	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.54
	439225	AA192669	Hs.45032	ESTs	3.54
	429183	AB014604	Hs.197955	KIAA0704 protein	3.54
	419948	AB041035	Hs.93847	NADPH oxidase 4	3.53
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.52
75	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	3.52
	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	3.52
	432101	AI918950	Hs.123642	EphA3	3.52
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.51
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	3.51
80	422093	AF151852	Hs.111449	CGI-94 protein	3.50
	404766	NA		NA	3.50
	441513	AW014557	Hs.112420	ESTs	3.50
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.50
	417315	AI080042	Hs.336901	ribosomal protein S24	3.50

	407182	AA312551	Hs.230157	ESTs	3.49
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.49
	432289	AI860145	Hs.55118	ESTs	3.49
	453644	AI813444	Hs.42197	ESTs	3.48
5	427986	NA5214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.48
	405466		NA		3.48
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.48
	430357	AW976789	Hs.165607	ESTs	3.46
10	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.46
	422260	AA315993	Hs.105484	regenerating gene type IV	3.46
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.46
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.46
	406117		NA		3.46
15	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	3.46
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	3.45
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	3.45
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	3.45
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.45
20	444478	W07318	Hs.240	M-phase phosphoprotein 1	3.45
	425904	AI805990	Hs.82238	POP4 (processing of precursor, S. cerev	3.44
	416702	AA186428	Hs.85591	ESTs	3.44
	448668	AI560305	Hs.199852	ESTs	3.42
	410004	AI298027	Hs.5057	carboxypeptidase D	3.42
25	428771	AB028992	Hs.193143	KIAA1069 protein	3.42
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.42
	429628	H09604	Hs.13268	ESTs	3.40
	448816	AB033052	Hs.22151	KIAA1226 protein	3.40
	456032	AW957446	Hs.301711	ESTs	3.39
30	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.39
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	3.38
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	3.38
	416057	AI927382	Hs.29857	ESTs	3.38
	430704	AW813091	Hs.335799	ESTs	3.38
35	423600	AI633559	Hs.310359	ESTs	3.38
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	3.38
	430178	AW449612	Hs.152475	ESTs	3.37
	417791	AW965339	Hs.111471	ESTs	3.37
	408867	AA437199	Hs.656	cell division cycle 25C	3.37
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	3.37
	457003	S78234	Hs.172405	cell division cycle 27	3.36
	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.36
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.36
	418782	AI792648	Hs.14665	ESTs	3.34
45	449722	BE280074	Hs.23960	cyclin B1	3.34
	447984	AI457263	Hs.37244	ESTs	3.34
	451103	R52804	Hs.25956	DKFZP564D206 protein	3.34
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	3.34
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	3.34
50	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.33
	450531	AW301032	Hs.203800	ESTs	3.32
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.32
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.31
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	3.30
55	421037	AI684808	Hs.197653	ESTs	3.30
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.30
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.30
	447078	AW885727	Hs.301570	ESTs	3.30
	402408	NA		NA	3.29
60	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	3.29
	423126	AA322245	Hs.290165	ESTs	3.28
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.27
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.27
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.26
65	411078	AI222020	Hs.182364	CocoaCrisp	3.26
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	3.26
	427119	AW880562	Hs.114574	ESTs	3.26
	400250	NA		NA	3.26
	429044	AI261490	Hs.145527	ESTs	3.25
70	451050	AW937420	Hs.69662	ESTs	3.24
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.24
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.23
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.22
	442028	AI239437	Hs.48945	ESTs	3.22
75	409110	AA191493	Hs.48778	niban protein	3.22
	418926	AA232658	Hs.105794	UDP-glucose:glycoprotein glucosyltransfe	3.22
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.21
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.20
	442979	AW440782	Hs.174743	ESTs	3.20
80	439292	AA090421	Hs.5355	hypothetical protein MGCS347	3.20
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.20
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	3.20
	451181	AI796330	Hs.207461	ESTs	3.19
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.19

	411573	AB029000	Hs.70823	KIAA1077 protein	3.19
	424539	L02911	Hs.150402	activin A receptor, type I	3.18
	443179	A928402	Hs.6933	hypothetical protein FLJ12684	3.18
5	452545	N31940	Hs.14434	ESTs, Weakly similar to I38022 hypotheti	3.18
	433024	AA573847	Hs.26549	KIAA1708 protein	3.18
	414737	A1160386	Hs.125087	ESTs	3.18
	444230	H95537	Hs.146067	ESTs	3.18
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.17
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	3.17
10	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.17
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.17
	443598	AW499970	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.16
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.16
	434389	AA971223	Hs.128098	ESTs	3.16
15	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.15
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.15
	453331	A1240665	Hs.8895	ESTs	3.15
	410286	A1739159	Hs.61898	DKFZP586N2124 protein	3.14
20	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (tr	3.14
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.14
	419078	M93119	Hs.89584	insulinoma-associated 1	3.14
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.14
	451525	AW001757	Hs.14005	ESTs	3.13
25	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.13
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.12
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associate	3.12
	413170	BE068819		gb:MR0-BT0374-220300-001-b03 BT0374 Homo	3.12
	437181	A1306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	3.12
30	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.11
	453867	A1929383	Hs.33032	hypothetical protein DKFZp434N185	3.11
	437641	AA811452	Hs.291911	ESTs	3.10
	428651	AF196478	Hs.188401	annexin A10	3.09
	427927	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP).	3.09
35	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.09
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.09
	408633	AW963372	Hs.46677	PRO2000 protein	3.09
	403381			NA	3.08
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	3.08
40	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.08
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.07
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.07
	436556	A1364997	Hs.7572	ESTs	3.07
	427043	AA397679	Hs.3991	ESTs	3.06
45	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.06
	419229	A827237	Hs.282884	ESTs	3.05
	414718	H95348	Hs.107987	ESTs	3.05
	439737	A1751438	Hs.41271	Homo sapiens mRNA full length insert cDN	3.05
	448587	A1539652	Hs.28338	KIAA1546 protein	3.04
50	448595	AB014544	Hs.21572	KIAA0644 gene product	3.04
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.04
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	3.04
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	3.04
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.04
55	429410	X98494	Hs.201676	M-phase phosphoprotein 10 (U3 small nucl	3.04
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.03
	441031	A110584	Hs.7645	fibrinogen, B beta polypeptide	3.03
	446142	A1754693	Hs.145968	ESTs	3.02
	402167			NA	3.02
60	402299			NA	3.02
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.02
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.02
	424001	W67883	Hs.137476	paternally expressed 10	3.01
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.01
65	439924	A1985897	Hs.125293	ESTs	3.01
	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.01
	432201	A1538613	Hs.298241	Transmembrane protease, serine 3	3.00
	445845	A1261870	Hs.145555	ESTs	3.00
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.00
70	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.00
	403637	NA		NA	3.00
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	3.00
	413430	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.99
75	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.99
	442204	A1635450	Hs.21914	ESTs	2.98
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.98
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.97
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	2.97
	441826	AW503603	Hs.129915	phosphotriesterase related	2.97
80	433404	T32982	Hs.102720	ESTs	2.96
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.96
	423880	BE278111	Hs.134200	DKFZP564C186 protein	2.96
	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.96

	408155	AB014528	Hs. 43133	KIAA0628 gene product	2.96
	424131	AA335714	Hs. 199665	ESTs	2.96
	451250	AA491275	Hs. 236940	hypothetical protein FLJ12542	2.96
5	425154	NM_001851	Hs. 154850	collagen, type IX, alpha 1	2.96
	447829	AI433029	Hs. 164104	ESTs	2.95
	410561	BE540255	Hs. 6994	Homo sapiens cDNA: FLJ22044 fts, clone H	2.95
	417873	BE266659	Hs. 293659	Homo sapiens, Similar to RIKEN cDNA A430	2.95
	452693	T79153	Hs. 48589	zinc finger protein 228	2.95
10	407742	AF186252	Hs. 38084	sulfotransferase family, cytosolic, 1C,	2.94
	421430	AW207555	Hs. 97093	Homo sapiens cDNA: FLJ23004 fts, clone L	2.94
	407995	AI094748	Hs. 100134	hypothetical protein FLJ12787	2.94
	413281	AA861271	Hs. 222024	transcription factor BMAL2	2.94
	452381	H23329	Hs. 290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.94
15	441020	W79283	Hs. 35962	ESTs	2.94
	425397	J04088	Hs. 156346	topoisomerase (DNA) II alpha (170kD)	2.94
	420005	AW271106	Hs. 133294	ESTs	2.93
	412530	AA766268	Hs. 266273	hypothetical protein FLJ13346	2.93
	435602	AF217515	Hs. 283532	uncharacterized bone marrow protein BM03	2.93
20	447247	AW369351	Hs. 287955	Homo sapiens cDNA FLJ13090 fts, clone NT	2.93
	443341	AW631480	Hs. 8688	ESTs	2.92
	436481	AA379597	Hs. 5199	HSPC150 protein similar to ubiquitin-con	2.92
	410144	W07189	Hs. 68185	ESTs, Weakly similar to ARL3_HUMAN ADP-R	2.92
	434450	S78664	Hs. 87	retinoblastoma-like 1 (p107)	2.92
25	450402	BE218027	Hs. 89968	ESTs	2.92
	422026	U80736	Hs. 110826	trinucleotide repeat containing 9	2.92
	421562	AA530994	Hs. 334471	ghrelin precursor	2.92
	410434	AF051152	Hs. 63668	toll-like receptor 2	2.92
	422665	AJ011812	Hs. 119018	transcription factor NRF	2.91
30	428966	AF059214	Hs. 194687	cholesterol 25-hydroxylase	2.90
	412416	AI628253	Hs. 22580	alkylglycerone phosphate synthase	2.90
	446232	AI281848	Hs. 194691	retinoic acid induced 3	2.90
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	2.90
35	438018	AK001160	Hs. 5999	hypothetical protein FLJ10298	2.90
	433252	AB040957	Hs. 151343	KIAA1524 protein	2.90
	444355	BE383686	Hs. 191621	ESTs, Moderately similar to ALU6_HUMAN A	2.90
	443054	AI745185	Hs. 8939	yes-associated protein 65 kDa	2.89
	421308	AA687322	Hs. 192843	leucine zipper protein FKSG14	2.89
	411643	AI924519	Hs. 192570	hypothetical protein FLJ22028	2.89
40	419559	Y07828	Hs. 91096	ring finger protein	2.89
	433527	AW235613	Hs. 133020	ESTs	2.88
	426274	D38122	Hs. 2007	tumor necrosis factor (ligand) superfamily	2.88
	406182	NA		NA	2.88
	432731	R31178	Hs. 287820	fibronectin 1	2.88
45	429274	AI379772	Hs. 99206	ESTs	2.87
	418216	AA662240	Hs. 283099	AF15q14 protein	2.87
	410166	AK001376	Hs. 59346	hypothetical protein FLJ10514	2.86
	452665	AW839326	Hs. 330414	ESTs, Moderately similar to S65657 alpha	2.86
	424696	BE439547	Hs. 151903	GrpE-like protein cochaperone	2.86
50	410174	AA306007	Hs. 59461	DKFZP434C245 protein	2.85
	443640	AI872643	Hs. 134218	ESTs	2.85
	432912	BE007371	Hs. 200313	ESTs	2.85
	431611	U58766	Hs. 264428	tissue specific transplantation antigen	2.85
	446565	D13757	Hs. 311	phosphoribosyl pyrophosphate amidotransf	2.85
55	424770	AA425562	Hs. 11065	Homo sapiens HDCME13P mRNA, partial cds	2.84
	418845	AA852985	Hs. 89232	chromobox homolog 5 (Drosophila HP1 alph	2.84
	403639	NA		NA	2.84
	451110	AI955040	Hs. 265398	ESTs, Weakly similar to transformation-r	2.84
	416185	AW975861	Hs. 47367	KIAA1785 protein	2.84
60	444665	BE613126	Hs. 47783	B aggressive lymphoma gene	2.83
	423441	R68649	Hs. 278359	absent in melanoma 1 like	2.83
	450584	AA040403	Hs. 60371	ESTs	2.83
	420191	AW003565	Hs. 192323	Homo sapiens mRNA for FLJ00057 protein,	2.83
	425599	AW366745	Hs. 214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83
65	424408	AI754813	Hs. 146428	collagen, type V, alpha 1	2.83
	448769	N66037	Hs. 38173	ESTs	2.82
	444946	AW139205	Hs. 156457	hypothetical protein FLJ22408	2.82
	435347	AW014873	Hs. 116963	ESTs	2.82
	438435	AA807142	Hs. 42194	hypothetical protein FLJ22649 similar to	2.82
70	427687	AW003867	Hs. 1570	histamine receptor H1	2.82
	426951	AA393636	Hs. 97454	ESTs	2.82
	427970	AA418187	Hs. 330515	ESTs	2.82
	442577	AA292998	Hs. 163900	ESTs	2.82
	441016	AW138653	Hs. 25845	ESTs	2.81
75	414774	X02419	Hs. 77274	plasminogen activator, urokinase	2.81
	417160	N76497	Hs. 1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.81
	409346	AL162066	Hs. 54320	hypothetical protein DKFZp762D096	2.81
	410407	X66839	Hs. 63287	carbonic anhydrase IX	2.81
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.81
80	435849	BE305242	Hs. 16098	claudin 2	2.80
	426695	AW118191	Hs. 112729	ESTs	2.80
	428301	AW628666	Hs. 98440	ESTs, Weakly similar to I38022 hypotheti	2.80
	420759	T11832	Hs. 127797	Homo sapiens cDNA FLJ11381 fts, clone HE	2.80
	421341	AJ243212	Hs. 279611	deleted in malignant brain tumors 1	2.80

	419423	D26488	Hs.90315	KIAA0007 protein	2.79
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.79
	425826	U97698	Hs.159593	mucin 6, gastric	2.79
5	457465	AW301344	Hs.122908	DNA replication factor	2.79
	426472	BE246138	Hs.30853	ESTs	2.79
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.78
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	2.78
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.78
10	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	2.78
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	2.78
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	2.78
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	2.77
	414043	AI521210	Hs.97977	ESTs	2.77
15	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.77
	439223	AW238299	Hs.250618	UL16 binding protein 2	2.76
	425956	M50828	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.76
	437612	AA827715	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	2.76
	426119	W94997	Hs.189917	ESTs	2.76
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.76
	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	2.76
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.76
	418217	AI910647	Hs.13442	ESTs	2.76
	420022	AA256253	Hs.120817	ESTs	2.76
25	408243	Y00787	Hs.624	interleukin 8	2.75
	421346	Z34277	Hs.103707	apomucin	2.75
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.75
	425773	N21279	Hs.237749	ESTs	2.75
	449611	AI970394	Hs.197075	ESTs	2.74
30	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.74
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
	428523	AW974540	Hs.98626	ESTs	2.73
	410839	NM_005849	Hs.66581	protein disulfide isomerase	2.73
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	2.73
35	424641	AB001106	Hs.151413	glia maturation factor, beta	2.73
	431708	AI698136	Hs.108873	ESTs	2.73
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	2.73
	441790	AW294909	Hs.132208	ESTs	2.73
40	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.73
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	2.73
	423482	BE280172	Hs.129228	galactokinase 2	2.73
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.72
	448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae) 11	2.72
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	2.72
45	447803	BE620578	Hs.30858	ESTs, Weakly similar to S65657 alpha-1C-	2.72
	429703	T93154	Hs.28705	ESTs	2.72
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	2.72
	410902	AW809665		gb:MR4-ST0124-261099-015-g07 ST0124 Homo	2.72
50	424745	AA214618	Hs.152759	activator of S phase kinase	2.72
	454469	AW792775		gb:CM0-UM0001-010300-258-g10 UM0001 Homo	2.72
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	2.72
	452012	AA307703	Hs.279766	kinesin family member 4A	2.72
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.72
	438008	AA775026	Hs.203802	ESTs	2.72
55	420552	AK000492	Hs.98806	hypothetical protein	2.71
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.71
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.71
	425371	D49441	Hs.155981	mesothelin	2.71
	439857	AA847194	Hs.232002	ESTs	2.71
60	455309	AW894017		gb:RC4-NN0027-150400-012-g04 NN0027 Homo	2.71
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	2.70
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.70
	435039	AW043921	Hs.130526	ESTs	2.70
	438796	W67821	Hs.109590	genethonin 1	2.70
65	407013	U35637		gb:Human nebulin mRNA, partial cds	2.70
	445413	AA151342	Hs.12677	CGI-147 protein	2.70
	418416	U11700	Hs.84999	ATPase, Cu++ transporting, beta polypept	2.70
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.69
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.69
70	441868	AI400276	Hs.183485	ESTs	2.69
	449076	AI627826	Hs.209109	ESTs	2.69
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	2.69
	427617	D42063	Hs.199179	RAN binding protein 2	2.69
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.69
75	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.68
	419310	AA236233	Hs.188716	ESTs	2.68
	445279	R41900	Hs.22245	ESTs	2.68
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	2.68
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	2.68
	449300	AI656959	Hs.222165	ESTs	2.68
80	444585	AW170015	Hs.6594	ESTs	2.68
	444384	BE174527	Hs.11065	Homo sapiens HDOME13P mRNA, partial cds	2.68
	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	2.67
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.67

	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.67
	418971	AA360392	Hs.87113	ESTs	2.66
	446152	AI292036	Hs.150028	ESTs	2.66
5	441553	AA281219	Hs.121296	ESTs	2.66
	403548			NA	2.66
	452699	AW295390	Hs.213062	ESTs	2.66
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.66
	453985	N44545	Hs.251865	ESTs	2.65
10	409956	AW103354	Hs.727	inhibin, beta A (activin A, activin AB a	2.65
	409446	AI561173	Hs.67688	ESTs	2.65
	422094	AF129535	Hs.272027	F-box only protein 5	2.65
	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.64
	432670	AA806536	Hs.291841	ESTs	2.64
15	418634	AK000064	Hs.86905	ATPase, H+ transporting, lysosomal (vacu	2.64
	453628	AW243307	Hs.83937	hypothetical protein	2.64
	442117	AW664964	Hs.128899	ESTs	2.64
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.64
	414631	AW970130	Hs.65406	ESTs	2.64
20	423268	BE386898	Hs.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.64
	413597	AW302885	Hs.117183	ESTs	2.63
	446031	AI271704	Hs.18987	Homo sapiens BAC clone RP11-505D17 from	2.63
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	2.63
	436304	AA339622	Hs.108887	ESTs	2.63
25	439832	T81829	Hs.14870	Homo sapiens, Similar to hect domain and	2.63
	449207	AL044222	Hs.23255	nucleoporin 159kD	2.62
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	2.62
	423811	AW299598	Hs.50895	homeo box C4	2.62
30	439474	AI824060	Hs.211501	ESTs	2.62
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.62
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	2.62
	442821	BE391929	Hs.8752	transmembrane protein 4	2.62
	418245	AA088767	Hs.83883	transmembrane, prostatic androgen induced	2.62
35	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	2.61
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.61
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.61
	403056	RS8624	Hs.2186	eukaryotic translation elongation factor	2.61
	433037	NM_014158	Hs.279938	HSPC067 protein	2.61
40	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.60
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.60
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.60
	457233	AI355009	Hs.221698	ESTs	2.60
	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	2.60
45	418946	AI798841	Hs.164526	ESTs	2.60
	441891	AW129145	Hs.128076	ESTs	2.60
	443742	AW627805	Hs.145421	ESTs	2.60
	433868	AA612960	Hs.337300	ESTs	2.60
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.59
50	444542	AI161293	Hs.280380	aminopeptidase	2.59
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	2.59
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	2.59
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.59
	401458			NA	2.58
55	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	2.58
	430980	AW971904	Hs.122164	diaphanous (Drosophila, homolog) 3	2.58
	441581	BE551408	Hs.127196	ESTs	2.58
	435693	AI033134	Hs.119887	ESTs	2.58
	431814	BE256242	Hs.270847	delta-tubulin	2.58
60	448269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.58
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.58
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	2.58
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.58
	434423	NM_006769	Hs.3844	LIM domain only 4	2.57
65	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	2.57
	433929	AI375499	Hs.27379	ESTs	2.57
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	2.57
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	2.57
	435627	W88774	Hs.118370	ESTs	2.57
70	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	2.57
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	2.57
	424057	AI339874	Hs.126593	ESTs	2.57
	424315	AW614850	Hs.193384	putative 28 kDa protein	2.57
	435663	AI023707	Hs.134273	ESTs	2.56
75	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	2.56
	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.56
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.56
	421102	AI470093	Hs.283085	protocadherin beta 6	2.56
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.56
80	448243	AW369771	Hs.52620	integrin, beta 8	2.56
	442881	AI023175	Hs.167022	ESTs	2.56
	422165	AL041199	Hs.1481	histidine decarboxylase	2.56
	425843	BE313280	Hs.159627	death associated protein 3	2.56
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.55

5	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	2.55
	438113	AI467908	Hs.8882	ESTs	2.55
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.55
	448275	BE514434	Hs.20830	kinesin-like 2	2.55
	419987	NM_005014	Hs.94070	osteomodulin	2.55
	439929	S73205		gb:insulin activator factor (human, panc	2.55
	452240	AI591147	Hs.61232	ESTs	2.55
	417806	AI867277	Hs.183733	ESTs	2.55
10	421482	AL135462	Hs.104715	inversin	2.55
	456884	AA054679	Hs.155150	ribonuclease P (14kD)	2.55
	442961	BE614474	Hs.289074	F-box only protein 22	2.55
	411274	NM_002776	Hs.69423	kallikrein 10	2.55
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.54
15	448666	NM_014953	Hs.323346	KIAA1008 protein	2.54
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	2.54
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fs, clone C	2.54
	430733	AW975920	Hs.283361	ESTs	2.54
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	2.54
20	435361	AI168596	Hs.117117	ESTs	2.54
	452833	BE559681	Hs.30736	KIAA0124 protein	2.54
	422330	D30783	Hs.115263	epiregulin	2.54
	424962	NM_012288	Hs.153954	TRAM-like protein	2.54
25	430264	AA470519		gb:nc71f10.s1 NCL CGAP_Pr1 Homo sapiens	2.53
	447178	AW594641	Hs.192417	ESTs	2.53
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.53
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.53
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fs, clone PL	2.53
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.53
30	409435	AI810721	Hs.95424	ESTs	2.52
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.52
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.52
	422314	K01900	Hs.73890	interferon, alpha 8	2.52
	441343	AI970348	Hs.132230	ESTs	2.52
35	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	2.52
	401747			NA	2.52
	448526	AB028946	Hs.21361	KIAA1023 protein	2.52
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.52
40	413627	BE182082	Hs.246973	ESTs	2.51
	441285	NM_002374	Hs.167	microtubule-associated protein 2	2.51
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.51
	429357	AA779725	Hs.164589	ESTs	2.51
	443171	BE281128	Hs.9030	TONDU	2.50
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	2.50
45	420795	AA323037	Hs.128645	sorting nexin 16	2.50
	448582	AI538880	Hs.94812	ESTs	2.50
	445459	AI478629	Hs.158465	likely ortholog of mouse putative IKK re	2.50
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	2.50
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal m	2.50
50	407568	AA740964	Hs.62699	ESTs	2.50
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	2.50
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (2.50
	433843	AW021423	Hs.112819	ESTs	2.50
	456254	T19844		gb:B711F Heart Homo sapiens cDNA clone B	2.50
55	403137			NA	2.50
	425895	AI269484	Hs.161427	zinc finger protein 215	2.50
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	2.50

TABLE 45B:

60	Pkey:	Unique Eos probaset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

65	Pkey	CAT Number	Accessions
	410784	1221005_1	AW803201 BE079700 BE062940
	410902	1226078_1	AW809665 AW810108 AW809781 AW809844
	411765	125700_1	H43346 AA248302 AA095182
	413170	1351880_1	BE068819 BE068821 BE068825
	413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
	414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
70	428858	296453_1	AA436760 AW237453 BE327496 N47347 N56967
	430264	315008_1	AA470519 BE303010 BE302954 BE384120
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	436411	419334_1	AW674352 AA715374 Z25205
75	438159	45106_2	Z83947
	439929	48059_1	S73205
	451105	859083_1	AI761324 AW880941 AW880937
	452453	918300_1	AI902519 AI902518 AI902516
	454469	1213727_1	AW792775 BE072509 AW792958
80	454600	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006
	454821	1236365_1	AW809672 AW809694 AW810552 AW810345 AW810432 AW809950
	455309	1278153_1	AW833504 AW833751 AW833493 AW833341
			AW894017 AW893956 AW894032

456254 1699246_1 T19844 T11755 T11830 T20136 T11957 R45834 R45828 R15595

TABLE 45C:

5 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
 Strand: sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 NL_position: Indicates DNA strand from which exons were predicted.
 Indicates nucleotide positions of predicted exons.

10	Pkey	Ref	Strand	NL_position
	401458	9187886	Plus	76485-77597
	401644	8576138	Plus	82655-83959
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
15	402167	8571795	Plus	109122-110357
	402299	6693370	Plus	23367-25175
	402408	9796239	Minus	110326-110491
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
20	403381	9438267	Minus	26009-26178
	403422	9665041	Minus	151169-151561
	403548	8081591	Minus	38760-39352
	403637	8671936	Minus	142647-142771,145531-145762
	403639	8671948	Plus	113234-113326,115186-115287,119649-119786
25	403776	7770611	Minus	1414-1513,1624-1756
	404253	9367202	Minus	55675-56055
	404440	7528051	Plus	80430-81581
	404766	7882612	Minus	158681-158882,160838-160973
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
30	405466	7767904	Minus	64498-64675
	405770	2735037	Plus	61057-62075
	405817	4071056	Plus	19914-20112,25655-25810
	406117	9142932	Plus	54304-54584
	406182	5923650	Minus	28256-28935

TABLE 46A: ABOUT 1303 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH

Table 46A lists about 1303 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 45A except using non-malignant stomach specimens in determining the denominator value and the ratio was equal to or greater than 5.0.

40 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

45	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	80.50
	414152	NM_003248	Hs.75774	thrombospondin 4	70.52
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	65.30
50	428698	AA852773	Hs.334838	KIAA1866 protein	61.90
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	50.60
	409041	AB033025	Hs.50081	KIAA1199 protein	44.50
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	41.10
	452862	AW378065	Hs.8687	ESTs	33.50
55	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	32.10
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	26.90
	428398	AI249368	Hs.98558	ESTs	26.40
	409757	NM_001898	Hs.123114	cystatin SN	25.48
	403776			NA	24.90
60	427674	NM_003528	Hs.2178	H2B histone family, member Q	23.80
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	23.10
	427108	AB028976	Hs.173571	KIAA1053 protein	21.76
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	20.70
	400419	AF084545		NA	20.40
65	415989	AI267700	Hs.317584	ESTs	19.80
	432101	AI918950	Hs.123642	EphA3	19.70
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	19.00
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	18.40
	412652	AI801777	Hs.6774	ESTs	18.20
70	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	17.71
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	17.38
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	17.36
	437446	AA788946	Hs.16859	ESTs, Moderately similar to CA1C RAT COL	17.00
	440594	AW445167	Hs.126036	ESTs	17.00
75	430044	AA464510	Hs.152812	ESTs	17.00
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	16.90
	414737	AI160386	Hs.125087	ESTs	16.50
	427335	AA448542	Hs.251677	G antigen 7B	16.30
	423453	AW450737	Hs.128791	CGI-09 protein	15.50
80	414569	AF109298	Hs.118258	prostate cancer associated protein 1	15.40
	401951	NA		NA	15.40
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	15.40
	432069	AW975888	Hs.294100	ESTs	15.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	15.30

	409062	AL157488	Hs.50150	Homo sapiens mRNA: cDNA DKFZp564B182 (tr	15.30
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	15.20
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	15.20
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	15.19
5	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	15.10
	438639	AI276360	Hs.31409	ESTs	15.10
	458997	AW937420	Hs.69662	ESTs	15.00
	432731	R31178	Hs.287820	fibronectin 1	14.90
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	14.70
10	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	14.70
	452242	R50956	Hs.159993	glycosyltransferase	14.70
	426427	M86699	Hs.169840	TTK protein kinase	14.50
	439924	AI985897	Hs.125293	ESTs	14.45
	414869	AA157291	Hs.21479	ubiquitin 1	14.40
15	411573	AB029000	Hs.70823	KIAA1077 protein	14.40
	418693	AI750878	Hs.87409	thrombospondin 1	14.37
	421823	N40850	Hs.28625	ESTs	14.30
	423903	M57765	Hs.1721	interleukin 11	14.20
	419227	BES37383	Hs.89739	cholinergic receptor, nicotinic, beta po	14.10
20	447417	AW732858	Hs.143067	KIAA1602 protein	13.96
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	13.90
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	13.90
	412863	AA121673	Hs.59757	zinc finger protein 281	13.90
	449509	AA001615	Hs.84561	ESTs	13.80
25	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fs, clone NT	13.80
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	13.60
	428769	AW207175	Hs.106771	ESTs	13.60
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.41
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	13.40
30	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fs, clone PL	13.30
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	13.26
	406972	M32053		gb:Human H19 RNA gene, complete cds.	13.19
	432368	AW970244	Hs.162188	ESTs	13.16
	424806	AA382523	Hs.105689	MSTP031 protein	13.08
35	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	12.98
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	12.90
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	12.80
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	12.80
	402363	NA		NA	12.78
40	444301	AK000136	Hs.10760	asporin (LRR class 1)	12.76
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	12.60
	435706	W31254	Hs.7045	GL004 protein	12.50
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	12.50
45	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	12.49
	405770			NA	12.46
	418678	NM_001327	Hs.167379	cancer/testis antigen	12.45
	414132	AI801235	Hs.48480	ESTs	12.40
	410434	AF051152	Hs.63668	tol-like receptor 2	12.30
50	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	12.26
	407891	AA486620	Hs.41135	endomucin-2	12.20
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	12.01
	411213	AA676939	Hs.69285	neuropilin 1	12.00
	436476	AA326108	Hs.33829	bHLH protein DEC2	12.00
55	413582	AW295647	Hs.71331	hypothetical protein MGC5350	11.90
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	11.90
	401747			NA	11.88
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	11.84
	432596	AJ224741	Hs.278461	matrilin 3	11.80
60	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	11.73
	425688	U48361	Hs.159223	NGF-A binding protein 2 (ERG1 binding p	11.72
	407938	AA905097	Hs.85050	phospholamban	11.70
	419948	AB041035	Hs.93847	NADPH oxidase 4	11.70
	459645	AA074346	Hs.250715	ESTs	11.51
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	11.50
65	434851	AA806164	Hs.116502	ESTs	11.50
	418699	BES39639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	11.47
	413453	AA129640	Hs.128065	ESTs	11.40
	442028	AI239437	Hs.48945	ESTs	11.40
70	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	11.39
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	11.20
	421633	AF121860	Hs.106260	sorting nexin 10	11.20
	410339	AI916499	Hs.298258	ESTs	11.20
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	11.15
75	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.15
	430217	N47863	Hs.336901	ribosomal protein S24	11.10
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	11.10
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	11.06
	416854	H40164	Hs.80296	Purkinje cell protein 4	10.90
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	10.90
80	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	10.80
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.80
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	10.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	10.80

	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	
	441693	AA384673	Hs.7943	RPB5-mediated protein	10.80
	414922	000723	Hs.77631	glycine cleavage system protein H (amino	10.80
5	441801	AW242799	Hs.86366	ESTs	10.80
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	10.80
	415727	BE501389	Hs.20848	ESTs, Weakly similar to APAF_HUMAN APOPT	10.80
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fs, clone HE	10.80
	421650	AA781795	Hs.122587	ESTs	10.80
10	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.80
	421814	L12350	Hs.108623	thrombospondin 2	10.70
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	10.69
	421462	AF016495	Hs.104624	aquaporin 9	10.67
	410444	W73484		gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	10.66
15	409743	N48721	Hs.183506	hypothetical protein FLJ14213	10.61
	446142	AJ754693	Hs.145968	ESTs	10.60
	444114	T58003	Hs.10323	Homo sapiens mRNA from chromosome 5q31-3	10.60
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.60
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	10.55
20	417352	AA195919		gb:zp95h09.r1 Stratagene muscle 937209 H	10.50
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	10.46
	427718	AJ798680	Hs.25933	ESTs	10.42
	412589	R28660	Hs.24305	ESTs	10.40
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	10.40
25	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.40
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.30
	409044	AJ129586	Hs.33033	hypothetical protein FLJ14623	10.30
	423600	AJ633559	Hs.310359	ESTs	10.30
	433819	AW511097	Hs.112765	ESTs	10.30
30	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.18
	410503	AW575746	Hs.188662	KIAA1702 protein	10.10
	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	10.10
	429357	AA779725	Hs.164589	ESTs	10.10
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	10.00
35	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	10.00
	416198	H27332	Hs.99598	hypothetical protein MGCS338	10.00
	413918	AW015898	Hs.71245	ESTs	10.00
	400570	NA		NA	10.00
	439333	AW384710	Hs.125258	Homo sapiens cDNA FLJ13795 fs, clone TH	10.00
40	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	9.97
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	9.93
	434352	AF129505	Hs.86492	small muscle protein, X-linked	9.90
	453160	AJ263307	Hs.239884	H2B histone family, member L	9.90
	433929	AJ375499	Hs.27379	ESTs	9.90
45	413273	U75679	Hs.75257	stem-loop (histone) binding protein	9.89
	437536	X91221	Hs.144465	ESTs	9.81
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	9.80
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	9.80
50	438913	AJ380429	Hs.172445	ESTs	9.80
	417849	AW291587	Hs.82733	nidogen 2	9.80
	424086	AJ351010	Hs.102267	lysyl oxidase	9.78
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	9.72
	414422	AA147224	Hs.337232	ESTs	9.70
	419197	N48921	Hs.27441	KIAA1615 protein	9.70
55	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	9.70
	449347	AV649748	Hs.295901	KIAA0493 protein	9.70
	409643	AW450866	Hs.257359	ESTs	9.70
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	9.70
	439608	AW864696	Hs.301732	hypothetical protein MGCS306	9.70
60	430290	AJ734110	Hs.136355	ESTs	9.60
	447124	AW976438	Hs.17428	RBP1-like protein	9.60
	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fs, clone H	9.60
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	9.60
	418067	AJ127958	Hs.83393	cystatin E/M	9.58
65	424001	W67883	Hs.137476	paternally expressed 10	9.54
	443037	AW500305	Hs.299166	syntaxin 7	9.50
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	9.50
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	9.50
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	9.50
70	443162	T49951	Hs.9029	DKFZP434G032 protein	9.50
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	9.45
	424026	AJ798295	Hs.137576	ribosomal protein L34 pseudogene 1	9.43
	440052	AJ633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	9.40
	403137			NA	9.40
75	418051	AW192535	Hs.19479	ESTs	9.37
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	9.35
	430291	AV660345	Hs.238126	CGI-49 protein	9.30
	426137	AL040683	Hs.167031	DKFZP566D133 protein	9.30
	400195	NA		NA	9.30
80	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fs, clone NT	9.30
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	9.20
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fs, clone L	9.20
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.20
	405543	NA		NA	9.20

	420900	AL045633	Hs.44269	ESTs	9.11
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	9.10
	410929	H47233	Hs.30643	ESTs	9.10
5	427319	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	9.10
	443745	AB039670	Hs.9728	ALEX1 protein	9.10
	436574	AW293527	Hs.126465	ESTs	9.10
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	9.08
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	9.07
10	408778	AI500519	Hs.63382	hypothetical protein PRO2714	9.03
	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	9.00
	404440			NA	9.00
	407168	R45175	Hs.117183	ESTs	9.00
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	9.00
	431946	AJ018336	Hs.131730	ESTs	8.92
15	408875	NM_015434	Hs.48604	DKFZP434B168 protein	8.90
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	8.90
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	8.89
	445029	AF196481	Hs.12256	mdline 2	8.86
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	8.80
20	409089	NM_014781	Hs.50421	KIAA0203 gene product	8.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.80
	416190	N54000		gb:yy99d02.r1 Soares_multiple_sclerosis_	8.80
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.77
	416440	AI823912	Hs.79335	Homo sapiens, Similar to SWI/SNF related	8.76
25	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	8.70
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	8.70
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.70
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	8.70
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	8.65
30	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	8.65
	412054	W87482	Hs.302209	ESTs	8.64
	450236	AW162998	Hs.24684	KIAA1376 protein	8.63
	418782	AJ792648	Hs.14665	ESTs	8.60
	452631	AI188658	Hs.87496	ESTs	8.60
35	425268	AJ807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	8.60
	432014	H66741	Hs.38540	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.60
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	8.60
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	8.60
40	426809	BE313114	Hs.29706	ESTs	8.60
	419704	AA429104	Hs.45057	ESTs	8.60
	452909	NM_015368	Hs.30985	pannexin 1	8.60
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	8.60
	430418	R98852	Hs.35029	heart and neural crest derivatives expre	8.58
45	450480	X82125	Hs.25040	zinc finger protein 239	8.58
	444984	H15474	Hs.132898	fatty acid desaturase 1	8.58
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	8.57
	430518	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (8.50
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	8.50
50	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	8.50
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	8.50
	441079	AW150697	Hs.107418	ESTs	8.50
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	8.50
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	8.50
55	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	8.50
	441540	C01367	Hs.127128	ESTs	8.50
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	8.50
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	8.50
	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (tr	8.48
60	436515	AJ278111	Hs.195292	putative tumor antigen	8.43
	416315	AA179483	Hs.73605	ESTs	8.42
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	8.40
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	8.40
	419198	AA234938	Hs.87384	ESTs	8.36
65	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	8.36
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	8.31
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (tr	8.30
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	8.30
	459060	H89244	Hs.303627	heterogeneous nuclear ribonucleoprotein	8.30
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	8.30
70	443977	AL120986	Hs.150627	ESTs, Weakly similar to I38022 hypotheti	8.30
	457997	AA806616	Hs.209523	ESTs	8.30
	451934	AI540842	Hs.61082	ESTs	8.30
	404335			NA	8.30
75	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	8.30
	431566	AF176012	Hs.260720	J domain containing protein 1	8.29
	446307	TS0083	Hs.9094	ESTs	8.28
	423928	AA332680		gb:EST36768 Embryo, 8 week 1 Homo sapien	8.26
	436420	AA443966	Hs.31595	ESTs	8.25
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	8.25
80	442988	AI026130	Hs.131683	ESTs	8.25
	402408	NA		NA	8.24
	438707	L08239	Hs.5326	amino acid system N transporter 2; porcu	8.23
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	8.22

	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	8.21
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.20
	411984	NM_005419	Hs.72988	signal transducer and activator of trans	8.20
5	420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	8.20
	437048	AA743240	Hs.91582	ESTs	8.20
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.20
	447066	BE167667	Hs.32163	ESTs	8.20
	425932	M81650	Hs.19668	semenogelin I	8.20
10	431819	AA515995	Hs.152334	ESTs	8.20
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	8.20
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	8.20
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	8.18
	413109	AW389845	Hs.110855	ESTs	8.17
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	8.16
	424335	AW021508	Hs.28170	ESTs	8.10
	453096	AW294631	Hs.11325	ESTs	8.10
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	8.10
	457796	AA913389	Hs.126691	ESTs	8.10
20	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	8.10
	445165	AV652831		gb:AV652831 GLC Homo sapiens cDNA clone	8.08
	418046	W49670	Hs.56044	ESTs	8.06
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.04
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.02
25	419559	Y07828	Hs.91096	ring finger protein	8.02
	409268	AA625304	Hs.188554	ESTs	8.00
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	8.00
	446977	AW863613	Hs.156798	ESTs	8.00
30	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	8.00
	407013	U35637		gb:Human nebulin mRNA, partial cds	7.99
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	7.98
	440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	7.96
	417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	7.95
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	7.94
35	415585	R59946	Hs.184852	KIAA1553 protein	7.92
	453331	AI240665	Hs.8895	ESTs	7.92
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	7.90
	417318	AW953937	Hs.12891	ESTs	7.90
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	7.90
40	444769	AI191650	Hs.221436	ESTs	7.90
	444272	AI138596	Hs.154619	ESTs	7.90
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	7.90
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	7.90
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	7.90
45	421558	AB011125	Hs.105749	KIAA0553 protein	7.90
	446444	AI743737	Hs.24370	ESTs	7.90
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	7.86
	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	7.86
	409582	R27430	Hs.271565	ESTs	7.84
50	419235	AW470411	Hs.288433	neurotrimin	7.83
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	7.82
	441690	R81733	Hs.33106	ESTs	7.80
	417735	AA188175	Hs.82506	KIAA1254 protein	7.80
	441795	N58115	Hs.21137	AD024 protein	7.80
55	442992	AI914699	Hs.13297	ESTs	7.80
	422554	AA312219	Hs.296338	ESTs	7.80
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	7.80
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	7.80
	429228	AI553633	Hs.337139	ESTs	7.80
60	429399	AA452244	Hs.16727	ESTs	7.80
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	7.77
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	7.76
	429396	AW954598	Hs.201626	Homo sapiens clone 25015 mRNA sequence	7.75
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	7.75
65	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	7.71
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	7.71
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	7.70
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	7.70
	404996			NA	7.70
70	418947	W52990	Hs.22860	ESTs	7.70
	427401	U20582	Hs.2149	actin like protein	7.70
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	7.70
	426262	AI792141	Hs.196270	folate transporter/carrier	7.70
	446955	AW613138	Hs.156747	ESTs	7.70
75	449199	AI990122	Hs.196988	ESTs	7.70
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	7.70
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	7.70
	427164	AB037721	Hs.173871	KIAA1300 protein	7.70
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	7.70
80	452588	AA889120	Hs.110637	homeo box A10	7.70
	451838	AW005866	Hs.193969	ESTs	7.67
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	7.66
	451227	R84429	Hs.151944	ESTs, Weakly similar to high-risk human	7.66
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	7.65

	432695	D63480	Hs.278634	KIAA0146 protein	7.63
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.60
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	7.60
5	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	7.60
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	7.60
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	7.60
	450628	AW382884	Hs.204715	ESTs	7.60
	418995	H39599	Hs.294008	ESTs	7.60
10	416402	NM_000715	Hs.1012	complement component 4-binding protein, NA	7.60
	405545			hypothetical protein MGC16275	7.60
	440866	AJ703103	Hs.271360	ESTs	7.60
	421281	AI299139	Hs.17517	cartilage intermediate layer protein, nu	7.60
15	424634	NM_003613	Hs.151407	ESTs, Moderately similar to I38022 hypot	7.60
	421041	N36914	Hs.14691	hypothetical protein FLJ11457	7.54
	453311	AW104911	Hs.126707	hypothetical protein MGC15754	7.50
	453060	AW294092	Hs.21594	hypothetical protein FLJ14813	7.50
	417655	AA780791	Hs.14014	serine/threonine kinase 2	7.50
20	417531	NM_003157	Hs.1087	solute carrier family 7 (cationic amino	7.50
	444099	D87432	Hs.10315	dickkopf (Xenopus laevis) homolog 1	7.50
	407853	AA336797	Hs.40499	fibronectin leucine rich transmembrane p	7.50
	408920	AL120071	Hs.48998	ESTs, Weakly similar to I38022 hypotheti	7.48
	447806	W03616	Hs.10432	ESTs	7.48
25	424748	AA346257	Hs.134933	KIAA1350 protein	7.46
	421089	AB037771	Hs.101799	ESTs	7.42
	444856	AI888057	Hs.12097	acylphosphatase 1, erythrocyte (common)	7.41
	447425	AI963747	Hs.18573	ESTs, Weakly similar to alternatively sp	7.40
	418450	R84397	Hs.193651	ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.40
30	434539	AW748078	Hs.214410	ESTs	7.40
	437036	AI571514	Hs.133022	hemoglobin, alpha 2	7.40
	414680	AA743331	Hs.272572	Homo sapiens cDNA: FLJ21880 fis, clone H	7.40
	451815	AW974911	Hs.184793	ESTs	7.40
	433577	AW007080	Hs.8817	ESTs, Moderately similar to S65657 alpha	7.40
35	453652	AW009640	Hs.28368	transcription factor NRF	7.40
	422655	AJ011812	Hs.119018	zinc finger protein	7.40
	424188	AW954552	Hs.142634	gb:zn43e07.s1 Stratagene HeLa cell s3 93	7.40
	407300	AA102616		hypothetical protein DKFZp434A1315	7.40
	431494	AA991355	Hs.298312	ESTs	7.40
	452958	AA883929	Hs.40527	hypothetical protein FLJ20212	7.40
40	418763	AK000219	Hs.88367	ESTs, Weakly similar to A47582 B-cell gr	7.40
	428279	AA425310	Hs.155766	Homo sapiens mRNA: cDNA DKFZp434K2172 (f	7.40
	449570	F07693	Hs.23869	ESTs, Weakly similar to putative p150 [H	7.40
	449601	AA461509	Hs.293565	ESTs	7.40
	438490	AW593272	Hs.301299	highly expressed in cancer, rich in leuc	7.40
45	410044	BE566742	Hs.58169	ras homolog gene family, member B	7.38
	429509	AW614420	Hs.204354	itchy (mouse homolog) E3 ubiquitin prote	7.38
	433393	AF038564	Hs.98074	pleiomorphic adenoma gene-like 1	7.37
	434096	AW662958	Hs.75825	ESTs	7.36
	425773	N21279	Hs.237749	RAN binding protein 8	7.36
50	422755	T25365	Hs.119587	Homo sapiens cDNA FLJ13585 fis, clone PL	7.35
	410566	AA373210	Hs.43047	ESTs	7.35
	412851	AI826502	Hs.106149	E2F transcription factor 3	7.35
	418661	NM_001949	Hs.1189	ESTs	7.34
	436246	AW450963	Hs.119991	kinesin-like protein 2	7.33
55	433159	AB035898	Hs.150587	GPI-anchored metastasis-associated prote	7.32
	444781	NM_014400	Hs.11950	DC32	7.31
	453878	AW964440	Hs.19025	Niemann-Pick disease, type C1	7.31
	414696	AF002020	Hs.76918	novel Ras family protein	7.31
	402250	AV655272	Hs.20252	ESTs	7.30
60	439039	AI656707	Hs.48713	interleukin 18 (interferon-gamma-inducin	7.30
	417976	BE565892	Hs.83077	hypothetical protein DKFZp434K1421	7.30
	419436	AA991639	Hs.242413	aspartyl-tRNA synthetase	7.30
	417006	AW673606	Hs.80758	hypothetical protein NUF2R	7.30
	425420	BE536911	Hs.234545	tachykinin receptor 2	7.29
65	425889	M57414	Hs.161305	ESTs	7.26
	442969	AI025499	Hs.132238	homolog of mouse transient receptor pote	7.25
	446360	N42553	Hs.267914	NOD2 protein	7.25
	438022	AW517524	Hs.135201	gb:EST66864 Fetal lung III Homo sapiens	7.24
70	407183	AA358015		hypothetical protein similar to small G	7.24
	429882	AA278898	Hs.225979	transcription elongation factor A (SII)-	7.22
	420120	AL049610	Hs.95243	NA	7.20
	400212			ESTs	7.20
	431812	AA515902	Hs.130650	15 kDa selenoprotein	7.20
	419481	AI879195	Hs.90606	ESTs	7.20
75	447078	AW885727	Hs.301570	ESTs	7.20
	413200	AA127395	Hs.222414	KIAA0112 protein; homolog of yeast ribos	7.20
	411750	BE562298	Hs.71827	ESTs	7.20
	439901	N73885	Hs.124169	leucine-rich repeat-containing 2	7.20
	411815	AA156679	Hs.125790	gb:MR1-ST0206-170400-024-h09 ST0206 Homo	7.20
80	459279	AW814996		KIAA1560 protein	7.20
	445263	H57646	Hs.42586	ESTs, Highly similar to unnamed protein	7.20
	413801	M62246	Hs.35406	nuclear transcription factor Y, beta	7.20
	418407	AL044818	Hs.84928	hypothetical protein FLJ22242	7.20
	452221	C21322	Hs.288057		

	425202	AW962282	Hs.152049	ESTs, Weakly similar to t38022 hypothe	7.20
	403764			NA	7.20
	416896	A1752862	Hs.5638	KIAA1572 protein	7.20
5	416636	N32536	Hs.42645	ESTs	7.20
	428071	AF212848	Hs.182339	ets homologous factor	7.20
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	7.18
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	7.17
	409759	N40285	Hs.81182	histamine N-methyltransferase	7.16
10	452448	AW182440	Hs.61389	ESTs, Weakly similar to unnamed protein	7.16
	427951	A1826125	Hs.43546	ESTs	7.16
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	7.15
	419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	7.12
	411769	A1694575	Hs.27207	KIAA0982 protein	7.11
15	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, be	7.10
	419511	AA429750	Hs.75113	general transcription factor IIIA	7.10
	409032	AW301807	Hs.297260	ESTs	7.10
	424539	L02911	Hs.150402	actinin A receptor, type I	7.10
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	7.10
20	430719	AA488988	Hs.293796	ESTs	7.10
	408020	AA127940	Hs.62781	ESTs	7.10
	420218	AW958037	Hs.286	ribosomal protein L4	7.10
	443487	A1073491	Hs.269887	ESTs, Highly similar to KPBB_HUMAN PHOSP	7.10
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.10
25	428724	AL390128	Hs.191268	KIAA1530 protein	7.10
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	7.10
	419126	A1810144	Hs.135276	ESTs	7.09
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	7.09
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	7.07
30	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	7.07
	457019	AA421844	Hs.12830	hypothetical protein	7.07
	409697	AB018348	Hs.55947	KIAA0805 protein	7.06
	400977	NA		NA	7.06
	436668	AA831857	Hs.209071	ESTs	7.03
35	451684	AF216751	Hs.26813	COA14	7.03
	404029			NA	7.02
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	7.02
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	7.00
	419647	AA348947	Hs.91816	hypothetical protein	7.00
40	442075	AW136928		gb:U1-H-B11-adp-d-08-0-U1.s1 NCI_CGAP_Su	7.00
	429598	AA811257	Hs.269710	ESTs	7.00
	450832	AW970602	Hs.105421	ESTs	7.00
	421389	AA531291	Hs.101064	Homo sapiens cDNA FLJ12777 fis, clone NT	7.00
	453931	AL121278	Hs.25144	ESTs	7.00
45	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	7.00
	452979	AW167599	Hs.232282	ESTs	7.00
	431696	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	7.00
	413583	AL120806	Hs.5888	ESTs	7.00
	436758	AW977167	Hs.155272	ESTs	7.00
50	455944	BE160643		gb:PM1-HT0422-291299-002-f03 HT0422 Homo	6.98
	430302	AL137502	Hs.238679	Rag D protein	6.96
	437613	R19892	Hs.10267	MIL1 protein	6.96
	440524	R71264	Hs.16798	ESTs	6.95
	451047	AB022317	Hs.25887	sema domain, immunoglobulin domain (Ig).	6.93
55	450377	AB033091	Hs.74313	KIAA1265 protein	6.93
	457396	Z20964	Hs.323817	DKFZP547E1010 protein	6.93
	417393	R10484	Hs.82071	Cbp/p300-interacting transactivator, wit	6.92
	414417	BE299433	Hs.68533	KIAA1679 protein	6.92
	412246	A1160873	Hs.69233	zinc finger protein	6.90
60	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	6.90
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.90
	405696	NA		NA	6.90
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.90
	414429	R51494	Hs.71818	ESTs	6.90
65	424641	AB001106	Hs.151413	glia maturation factor, beta	6.90
	418895	AA894638	Hs.14600	ESTs	6.90
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	6.90
	432038	AA524746	Hs.162110	ESTs	6.87
70	446610	AV659433	Hs.282984	ESTs, Weakly similar to t38022 hypothe	6.86
	451286	AW139789	Hs.16370	Homo sapiens cDNA FLJ11652 fis, clone HE	6.86
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	6.85
	418934	T83845	Hs.191116	ESTs	6.82
	435143	R12375	Hs.194600	ESTs	6.82
75	442660	AW138174	Hs.130651	ESTs	6.82
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	6.81
	435990	A1015862	Hs.131793	ESTs	6.80
	449062	AJ272268	Hs.22958	calcium channel, voltage-dependent, alph	6.80
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	6.80
80	421476	AW953805	Hs.21887	ESTs	6.80
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.80
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	6.80
	410298	A1693821	Hs.182185	ESTs	6.80
	420560	AW207748	Hs.59115	ESTs	6.80

	427752	AA470687	Hs.104772	ESTs	6.80
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	6.80
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	6.80
5	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	6.80
	426890	AA393167	Hs.41294	ESTs	6.80
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	6.80
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.79
	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	6.79
10	434267	AI206589	Hs.116243	ESTs	6.79
	419358	T78763	Hs.90063	neurocalcin delta	6.79
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prole	6.78
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	6.77
	443184	AI638728	Hs.131973	ESTs	6.77
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	6.77
15	429483	AA974832	Hs.128708	ESTs	6.76
	425605	BE544300	Hs.7076	KIAA1705 protein	6.76
	425045	AW953186	Hs.92400	ESTs	6.76
	438776	AW245243	Hs.334368	hypothetical protein MGC11257	6.75
20	458174	AA781530	Hs.127236	hypothetical protein FLJ12879	6.74
	445129	R39878	Hs.21394	ESTs	6.74
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.73
	444442	AI149234	Hs.298423	ESTs, Moderately similar to I54374 gene	6.73
	431240	AA496790	Hs.179481	ESTs	6.72
25	422109	S73265	Hs.1473	gastrin-releasing peptide	6.70
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.70
	423811	AW299598	Hs.50895	homeo box C4	6.70
	443695	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	6.70
	420686	AI950339	Hs.40782	ESTs	6.70
30	419574	AK001989	Hs.91165	hypothetical protein	6.70
	418269	AA806113	Hs.189025	ESTs	6.70
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.70
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	6.70
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	6.70
35	409506	NM_006153	Hs.54589	NCK adaptor protein 1	6.70
	454029	W05150	Hs.37034	homeo box A5	6.70
	413365	AW205188	Hs.124304	Homo sapiens cDNA FLJ14635 fis, clone NT	6.70
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	6.70
	426566	AF131836	Hs.170453	tropomodulin	6.70
40	446261	AA313893	Hs.306219	hypothetical protein FLJ12615 similar to	6.70
	408547	AA574291	Hs.57837	ESTs	6.70
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	6.70
	413627	BE182082	Hs.246973	ESTs	6.70
	410498	AA355749		gb:EST64459 Jurkat T-cells VI Homo sapie	6.70
45	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	6.70
	453691	H12235	Hs.226505	ESTs	6.68
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.68
	415885	D79983	Hs.78894	KIAA0161 gene product	6.68
	405529	AW410458	Hs.5258	chromosome 11 open reading frame2	6.68
50	438242	AW241910	Hs.122254	ESTs, Weakly similar to JX0369 collagen	6.68
	442643	U82756	Hs.8551	PRP4/STK/WD splicing factor	6.67
	424802	X79201	Hs.153221	synovial sarcoma, translocated to X chro	6.67
	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	6.67
	458714	R20916	Hs.202501	ESTs	6.66
55	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.65
	433260	AB040966	Hs.83575	KIAA1533 protein	6.65
	400268	NA		NA	6.63
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	6.62
	403973	NA		NA	6.60
60	436862	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	6.60
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.60
	453387	AI990741	Hs.252809	ESTs	6.60
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	6.60
	418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	6.60
65	448172	N75276	Hs.135904	ESTs	6.60
	409571	AA504249	Hs.187585	ESTs	6.60
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	6.60
	430701	AI760833	Hs.293971	ESTs	6.60
	450373	AI915790	Hs.337282	ESTs	6.60
70	419384	AA490866	Hs.39429	ESTs	6.60
	429828	AB019494	Hs.225767	IDN3 protein	6.60
	441761	AI222880		gb:qp40c06.x1 NCI_CGAP_Co8 Homo sapiens	6.60
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	6.60
	421111	BE299047	Hs.43532	ESTs, Weakly similar to T20177 hypotheti	6.60
75	407424	AF120493		gb:Homo sapiens elastase 1 precursor (EL	6.59
	412396	AW947895		gb:PM1-MT0010-200300-001-110 MT0010 Homo	6.57
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.57
	406674	AA332152	Hs.288036	tRNA isopentenylpyrophosphate transferas	6.57
	400860			NA	6.56
80	457893	AA744292		gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens	6.55
	426108	AA622037	Hs.166468	programmed cell death 5	6.54
	422133	AW612779	Hs.333159	Homo sapiens laryngeal carcinoma related	6.54
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	6.54
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	6.53

5	400351	AF060169	Hs.272369	Homo sapiens AS11 protein mRNA, partial	6.52
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	6.52
	410416	BE410072	Hs.63304	protein phosphatase methyltransferase-1	6.50
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	6.50
	419677	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	6.50
10	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	6.50
	429774	AI522215	Hs.50883	KIAA1804 protein	6.50
	428228	AA424352	Hs.210586	ESTs	6.50
	418134	AA397769	Hs.86617	ESTs	6.50
	403859	NA		NA	6.50
15	422704	AA972147	Hs.132275	ESTs	6.50
	416737	AF154335	Hs.79691	LIM domain protein	6.50
	429854	R55508	Hs.99472	ESTs	6.50
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	6.50
	453600	BE246211	Hs.119120	E3 ubiquitin ligase SMURF1	6.49
20	454835	AW833763		gb:QV4-TT0008-130100-077-d10 TT0008 Homo	6.48
	434603	AF147384		gb:Homo sapiens full length insert cDNA	6.48
	408243	Y00787	Hs.624	interleukin 8	6.48
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	6.47
	451316	AI770011	Hs.208310	ESTs	6.46
25	448339	AL035920	Hs.20938	RNA binding motif, single stranded inter	6.46
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	6.44
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	6.44
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.42
	440526	AI832243	Hs.211471	ESTs	6.42
30	432727	AA305233	Hs.278712	eukaryotic translation initiation factor	6.41
	433009	AA761668		gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	6.40
	435782	N49433	Hs.285737	Homo sapiens cDNA: FLJ20895 fis, clone A	6.40
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	6.40
	407162	N63855	Hs.142634	zinc finger protein	6.40
35	446152	AI292036	Hs.150028	ESTs	6.40
	422828	AL133396	Hs.121281	prion protein 2 (dublet)	6.40
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	6.40
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.40
	429039	AI524793	Hs.301897	ESTs	6.40
40	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.40
	435159	AA668879	Hs.116649	ESTs	6.40
	429625	AA455568	Hs.193814	ESTs	6.40
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	6.40
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	6.40
45	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	6.40
	449911	AI262106	Hs.12653	ESTs	6.40
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	6.40
	440395	AA884412	Hs.216342	ESTs	6.37
	429500	X78565	Hs.289114	hexabrachion (lenscrin C, cytotoxin)	6.37
50	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	6.36
	417092	H97508	Hs.181165	eukaryotic translation elongation factor	6.36
	412227	AW902282		gb:QV3-NN1023-260400-169-g10 NN1023 Homo	6.36
	400845			NA	6.36
	403546	NA		NA	6.36
55	412345	AW938386		gb:PM4-DT0057-201299-002-G10 DT0057 Homo	6.35
	422186	AW962364	Hs.129051	ESTs	6.34
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6.34
	417687	AI828596	Hs.250691	ESTs	6.33
	426223	AW977812	Hs.130391	ESTs	6.32
60	417588	Z44510		gb:HSC22D091 normalized infant brain cDN	6.32
	432629	AW860548	Hs.280658	ESTs	6.31
	440495	AA887212	Hs.14161	hypothetical protein DKFZp434i1930	6.31
	407771	AL138272	Hs.62713	ESTs	6.31
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	6.30
65	431041	AA490967	Hs.197955	KIAA0704 protein	6.30
	445571	AI378000	Hs.158489	ESTs, Weakly similar to Z184_HUMAN ZINC	6.30
	433309	AA807060	Hs.126558	ESTs	6.30
	415659	W27214	Hs.78547	zinc finger protein (clone 647)	6.30
	420271	AI954365	Hs.42892	ESTs	6.30
70	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.30
	400950	NA		NA	6.30
	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypothe	6.30
	439813	AA846321	Hs.124501	ESTs	6.30
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.30
75	453596	AA441838	Hs.62905	hypothetical protein FLJ14834	6.30
	446847	TS1454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.30
	435820	AA700580	Hs.189000	ESTs	6.30
	452576	AB023177	Hs.29900	KIAA0960 protein	6.30
	448924	AW450569	Hs.188399	ESTs	6.30
80	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.30
	412591	BE217736	Hs.292653	ESTs, Weakly similar to T26845 hypothe	6.30
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.30
	419088	AI538323	Hs.52620	integrin, beta 8	6.30
	401424			NA	6.30
	412189	R60982	Hs.22581	ESTs	6.30
	435501	AW051819	Hs.129908	KIAA0591 protein	6.30
	408221	AA912183	Hs.47447	ESTs	6.28

	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	6.28
	416845	H95279		gb:yu20h02.s1 Soares fetal liver spleen	6.27
	402732	NA		NA	6.26
5	413224	AI732470	Hs.191157	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.24
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	6.24
	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	6.24
	419548	AW978142	Hs.326248	Homo sapiens cDNA: FLJ22071 fis, clone H	6.23
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	6.22
10	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	6.22
	413384	NM_000401	Hs.75334	exostosins (multiple) 2	6.21
	445584	AF217518	Hs.8360	PTD012 protein	6.21
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	6.21
	420807	AA280627	Hs.57846	ESTs	6.20
15	421155	H87879	Hs.102267	lysyl oxidase	6.20
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	6.20
	440209	H05049	Hs.22269	neurexin 3	6.20
	408170	AW204516	Hs.31835	ESTs	6.20
	433590	N98410	Hs.48364	Homo sapiens regulator of G-protein sign	6.20
20	442008	AI457814	Hs.270272	ESTs	6.20
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	6.20
	402343			NA	6.20
	432682	AI376400	Hs.159588	ESTs	6.20
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	6.20
25	429954	AI918130	Hs.21374	ESTs	6.20
	417256	U94332	Hs.81791	tumor necrosis factor receptor superfam	6.20
	435525	AI831297	Hs.123310	ESTs	6.20
	413604	R51767		gb:yg73g11.r1 Soares infant brain 1N1B H	6.20
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	6.20
30	443285	AI301918	Hs.334264	ESTs	6.20
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	6.20
	451027	AW519204	Hs.40808	ESTs	6.20
	452243	AL355715	Hs.28555	programmed cell death 9	6.19
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	6.17
35	424060	X92108	Hs.138629	H.sapiens mRNA for subtelomeric repeat s	6.17
	432494	AA551060		gb:bnk74f02.s1 NCI_CGAP_Sch1 Homo sapiens	6.16
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	6.14
	419638	N46504	Hs.91747	profilin 2	6.13
	445595	W25950	Hs.14512	DIPB protein	6.13
40	433036	AA574091	Hs.105964	ESTs	6.13
	457155	AL110243	Hs.187991	DKFZP564A122 protein	6.13
	443715	AI583187	Hs.9700	cyclin E1	6.13
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.12
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	6.11
45	424897	D63216	Hs.153684	frizzled-related protein	6.11
	429188	AB011171	Hs.198037	KIAA0599 protein	6.11
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	6.10
	413339	AI818080	Hs.194290	ESTs	6.10
	453685	AL110309		gb:DKFZp564L0278_r1 564 (synonym: hfr2)	6.10
50	421195	BE464560	Hs.133017	ESTs	6.10
	453296	AA034413	Hs.62560	ESTs	6.10
	444985	AI677737	Hs.28329	hypothetical protein FLJ14005	6.10
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	6.10
	419841	BE005848	Hs.7326	ESTs	6.10
55	429190	H18650	Hs.92602	ESTs	6.10
	426116	AA868729	Hs.144694	ESTs	6.10
	451441	AA017601	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	6.10
	401740			NA	6.10
	441953	H11695	Hs.322901	disrupter of silencing 10	6.10
60	401464	AF039241	Hs.9028	histone deacetylase 5	6.10
	405033			NA	6.10
	410743	AA089474	Hs.272153	ESTs	6.10
	454758	AW845266		gb:IL2-CT0031-160999-003-808 CT0031 Homo	6.10
	417728	AW138437	Hs.24790	KIAA1573 protein	6.10
65	418553	T88964		gb:yd97a07.r1 Soares fetal liver spleen	6.09
	431617	AK000738	Hs.264636	hypothetical protein FLJ20731	6.08
	455608	BE011437		gb:CM4-BN0220-080500-170-03 BN0220 Homo	6.08
	450755	AA010984	Hs.159464	ESTs	6.07
	455217	AW867534		gb:MR0-SN0037-160400-004-e05 SN0037 Homo	6.07
70	437179	AA393508	Hs.300642	serologically defined colon cancer anti	6.06
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	6.06
	415308	F05251		gb:HSC04H101 normalized infant brain cDN	6.06
	428417	AK001699	Hs.184227	F-box only protein 21	6.05
	426501	AW043782	Hs.293616	ESTs	6.03
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	6.03
75	403040			NA	6.02
	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	6.02
	415637	R25517		gb:yg44f01.r1 Soares infant brain 1N1B H	6.02
	427925	N51323	Hs.255935	Homo sapiens, clone IMAGE:3448993, mRNA	6.02
	404702	NA		NA	6.02
80	433183	AF231338	Hs.222024	transcription factor BMAL2	6.01
	437762	T78028	Hs.154679	synaptotagmin I	6.01
	443833	AI654108	Hs.135125	ESTs	6.01
	422263	AA307639	Hs.129908	KIAA0591 protein	6.00

	420909	AI640551	Hs.88878	Homo sapiens cDNA: FLJ23536 fis. clone L	6.00
	407612	U26403	Hs.37142	ephrin-A5	6.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	6.00
5	453853	AL040600	Hs.188083	ESTs	6.00
	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	422505	AL120862	Hs.124165	ESTs	6.00
	420734	AW972872	Hs.293736	ESTs	6.00
10	455082	BE148180		gb:RC0-HT0232-211099-011-e04 HT0232 Homo	6.00
	444200	AA327113	Hs.149057	ESTs	6.00
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	6.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.00
	428412	AA428240	Hs.126083	ESTs	6.00
15	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis. clone PL	6.00
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	6.00
	431878	AA521207	Hs.270202	ESTs, Weakly similar to ALU4_HUMAN ALU S	6.00
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	6.00
	401093			NA	6.00
20	411861	AW867875		gb:MR0-SN0040-050500-003-f11 SN0040 Homo	6.00
	411800	N39342	Hs.103042	microtubule-associated protein 1B	5.99
	446925	AW974605	Hs.176669	ESTs	5.98
	401708	NA		NA	5.98
	449894	AK001578	Hs.24129	CLLL7 protein	5.97
25	403278	NA		NA	5.96
	455212	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	5.96
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	5.96
	441271	AA927290	Hs.130462	ESTs	5.95
	404072			NA	5.95
30	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.94
	421622	AB037748	Hs.106204	KIAA1327 protein	5.93
	441300	R35063	Hs.181536	ESTs	5.92
	445517	AF208855	Hs.12830	hypothetical protein	5.91
	429559	AI985345	Hs.26425	ESTs	5.91
35	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	5.91
	440510	H08427	Hs.309165	ESTs, Weakly similar to ISHUS protein d	5.90
	414727	BE466904		gb:h22803.x1 NCI_CGAP_GC6 Homo sapiens	5.90
	451686	AA059246	Hs.110293	ESTs	5.90
	438032	BE045624	Hs.152992	ESTs	5.90
40	450470	Z75330	Hs.286148	stromal antigen 1	5.90
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	5.90
	432662	AL049314	Hs.280700	ESTs	5.90
	451742	T77609	Hs.117970	ankyrin 2, neuronal	5.90
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	5.90
45	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	5.90
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	5.90
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	5.90
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.90
	433865	N29862	Hs.44104	ESTs	5.90
50	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis. clone PL	5.90
	448743	AB032962	Hs.21896	KIAA1136 protein	5.90
	447153	AA805202	Hs.315562	ESTs	5.90
	425793	AA363946	Hs.20969	ESTs	5.90
	404632			NA	5.90
55	445364	AB006624	Hs.14912	KIAA0286 protein	5.90
	452240	AI591147	Hs.61232	ESTs	5.90
	410424	AA084984		gb:zn11a08.r1 Stratagene hNT neuron (937	5.90
	404170			NA	5.89
60	458390	AI792585	Hs.133272	ESTs, Weakly similar to ALLUC_HUMAN !!!!	5.89
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	5.88
	444406	AI147237	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.87
	413894	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	5.87
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.86
	446700	AW208257	Hs.156326	Human DNA sequence from clone RP11-145L2	5.86
65	443377	AI792547	Hs.133292	ESTs	5.86
	419162	AA234591	Hs.304123	ESTs	5.85
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	5.84
	428650	AI560456	Hs.107319	ESTs	5.84
	437410	AW023340	Hs.14880	ESTs	5.84
70	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	5.84
	401004			NA	5.83
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	5.83
	410979	BE151480		gb:RC0-HT0295-071199-011-a01 HT0295 Homo	5.82
	424576	BE154142	Hs.96833	ESTs	5.82
75	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	5.81
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	5.80
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.80
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.80
	451367	AA923729	Hs.26322	cell cycle related kinase	5.80
80	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	5.80
	421589	AW954177	Hs.82919	cullin 2	5.80
	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	5.80
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.80
	436096	H55931	Hs.269582	ESTs	5.80

	443353	AI052659	Hs.133255	ESTs	5.80
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I38022 hypothe	5.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.80
5	440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	5.80
	445745	AB007924	Hs.13245	KIAA0455 gene product	5.80
	405637	NA		NA	5.80
	415293	R49462	Hs.106541	ESTs	5.80
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	5.80
10	442227	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	5.80
	423395	AA326613		gb:EST29922 Cerebellum II Homo sapiens c	5.80
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.80
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	5.80
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	5.80
15	430818	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	5.80
	444749	AI190672	Hs.65926	ESTs	5.80
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	5.79
	456192	D84109	Hs.80248	RNA-binding protein gene with multiple s	5.78
	411253	AW833897		gb:QV0-TT0009-111199-055-b07 TT0009 Homo	5.78
20	417219	AW973473	Hs.220936	ESTs	5.78
	409450	AW628650	Hs.61260	hypothetical protein FLJ13164	5.76
	412013	AA400753	Hs.43761	ESTs, Weakly similar to A46010 X-linked	5.76
	425566	AW162943	Hs.250618	UL16 binding protein 2	5.75
	417877	AI025829	Hs.86320	ESTs	5.75
25	437114	AA836641	Hs.163085	ESTs	5.75
	421238	AB033101	Hs.102796	Homo sapiens cDNA FLJ110708 fis, clone NT	5.74
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	5.73
	415209	F00183	Hs.172004	titin	5.73
	429922	Z97630	Hs.226117	H1 histone family, member 0	5.72
30	420022	AA256253	Hs.120817	ESTs	5.71
	431485	BE621320	Hs.257486	hypothetical protein FLJ20062	5.71
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	5.71
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	5.71
	438085	R52518	Hs.7967	ESTs	5.70
35	444379	N99035	Hs.222657	ESTs	5.70
	401348	NA		NA	5.70
	428878	AA436884	Hs.48926	ESTs	5.70
	422564	AI148006	Hs.222120	ESTs	5.70
	452560	BE077084	Hs.336432	ESTs	5.70
40	408384	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	5.70
	409948	AA078643		gb:7P08801 Chromosome 7 Placental cDNA L	5.70
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	5.70
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	5.70
	439203	AA448930	Hs.8453	KIAA1587 protein	5.70
45	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	5.70
	451922	BE463995	Hs.211033	ESTs	5.70
	407808	AA663559	Hs.279789	histone deacetylase 3	5.70
	428161	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi	5.70
	413430	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.70
50	428223	AA424313	Hs.98402	ESTs	5.70
	427972	AA864870	Hs.181304	putative gene product	5.70
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	5.70
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	5.70
	458044	AW979114	Hs.326135	ESTs	5.70
55	432911	AW807634	Hs.279799	putative zinc finger protein NY-REN-34 a	5.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	5.70
	408867	AA437199	Hs.656	cell division cycle 25C	5.70
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.70
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	5.70
60	409570	AW418720	Hs.167583	ESTs	5.70
	457441	BE467737	Hs.146125	ESTs	5.70
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	5.70
	420192	AA256281	Hs.105040	ESTs	5.69
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	5.69
65	454511	AW948146		gb:RC0-MT0013-280300-031-e02 MT0013 Homo	5.68
	419586	AI088485	Hs.144759	ESTs, Weakly similar to I38022 hypothe	5.67
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	5.67
	435849	BE305242	Hs.16098	claudin 2	5.67
	457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens	5.66
70	450191	AW137243	Hs.222446	ESTs	5.66
	438653	AW188099	Hs.131813	ESTs	5.66
	422910	AI269508	Hs.121591	Human DNA sequence from PAC 257A7 on chr	5.66
	453694	AW504918	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	5.66
	445302	AK001537	Hs.12488	hypothetical protein FLJ10675	5.66
75	446080	AI221741	Hs.117777	ESTs	5.65
	425474	Z48054	Hs.158084	peroxisome receptor 1	5.65
	432542	AW083920	Hs.16098	claudin 2	5.65
	446983	AA157484	Hs.97199	complement component C1q receptor	5.65
	420898	AB002379	Hs.100113	KIAA0381 protein	5.65
80	401372			NA	5.64
	428541	AI862570	Hs.299214	Homo sapiens, clone IMAGE:2822295, mRNA,	5.63
	426249	F05422	Hs.168352	nucleoporin-like protein 1	5.63
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	5.63
	451863	AL120634	Hs.305923	ATPase, Ca ⁺⁺ transporting, plasma membra	5.62

	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced translocation)	5.62
	401183			NA	5.62
	426029	AW294138	Hs.255277	ESTs	5.61
5	443462	AI064690	Hs.171176	ESTs	5.61
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypothetical protein	5.60
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous)	5.60
	444577	AI207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.60
	423605	AF047826	Hs.129887	cadherin 19, type 2	5.60
10	413447	AW969388	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	5.60
	442957	AI949952	Hs.49397	ESTs	5.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	5.60
	430679	R44428	Hs.22801	ESTs	5.60
	449358	AA001229	Hs.131436	ESTs	5.60
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	5.60
15	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	5.60
	444059	R69743	Hs.116774	integrin, alpha 1	5.60
	438157	AW137011	Hs.49576	ESTs	5.60
	428233	AI358831	Hs.20578	ESTs	5.60
20	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	5.60
	451652	AA018968	Hs.133536	ESTs	5.59
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.59
	447591	AI675417	Hs.282855	ESTs	5.58
	417958	AA767382	Hs.193417	ESTs	5.57
25	438146	Z36842	Hs.57548	ESTs	5.57
	413595	AW235215	Hs.16145	ESTs	5.57
	422406	AF025441	Hs.116206	Opa-interacting protein 5	5.56
	420529	D25259	Hs.319844	ESTs, Moderately similar to I54374 gene	5.56
	439582	W79161	Hs.118327	Homo sapiens cDNA FLJ11522 fis, clone HE	5.56
30	408744	AW806177		gb:MR1-UM0108-130400-003-d04 UM0108 Homo	5.56
	447230	AW972147	Hs.101395	hypothetical protein MGC11352	5.54
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	5.54
	446813	AA971436	Hs.16218	KIAA0903 protein	5.53
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.53
35	410516	BE537917	Hs.90034	hypothetical protein FLJ21916	5.53
	453994	BE180964	Hs.165590	ribosomal protein S13	5.53
	435583	AA767714	Hs.291627	ESTs	5.52
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.51
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	5.51
	427966	R97130	Hs.189699	ESTs	5.51
	433611	AW327692	Hs.3446	mitogen-activated protein kinase kinase	5.51
	401244			NA	5.50
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	5.50
45	434006	AF113688		gb:Homo sapiens clone FLB4630	5.50
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	5.50
	427507	AF240467	Hs.179152	tol1-like receptor 7	5.50
	423268	BE386898	Hs.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.50
	405065	NA		NA	5.50
50	444302	AI140115	Hs.225130	ESTs	5.50
	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	5.50
	435586	AI279137	Hs.151498	ESTs	5.50
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	5.50
	427189	H82453	Hs.5635	ESTs	5.50
	415263	AA948033	Hs.130853	ESTs	5.50
55	441818	AI630451	Hs.7976	KIAA0332 protein	5.50
	407834	AW084991	Hs.26100	ESTs	5.50
	404012	NA		NA	5.50
	449932	AI675444	Hs.263024	ESTs	5.50
60	423760	AA775891	Hs.191980	ESTs	5.50
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	5.50
	423172	R15652		gb:HH503-F Adult heart, Clontech Homo sa	5.50
	422295	AF051151	Hs.114408	tol1-like receptor 5	5.50
	429044	AI261490	Hs.145527	ESTs	5.50
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	5.50
65	414323	NM_014759	Hs.334688	KIAA0273 gene product	5.50
	405511	NA		NA	5.49
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	5.49
	434434	AA633516	Hs.157201	ESTs	5.48
	421997	R66740	Hs.110613	KIAA0220 protein	5.47
70	410276	AI554545	Hs.68301	ESTs	5.47
	435867	AA954229	Hs.114052	ESTs	5.47
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	5.47
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	5.47
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.47
75	401629	NA		NA	5.46
	433071	BE150229	Hs.281564	retinal outer segment membrane protein 1	5.46
	458247	R14439	Hs.209194	ESTs	5.46
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	5.45
	418247	R55174		gb:yg87h04.r1 Soares infant brain 1N1B H	5.45
80	453716	AA037675	Hs.152675	ESTs	5.44
	431157	AI823969	Hs.132678	ESTs	5.44
	426873	AI190540	Hs.131092	ESTs	5.43
	437092	AA744292		gb:ny51d05.s1 NCL_CGAP_Pr18 Homo sapiens	5.42
	445782	AW407672	Hs.315367	Homo sapiens, Similar to hypothetical pr	5.42

	447393	AI377458	Hs.158831	EST	5.42
	425283	AA354338	Hs.131100	ESTs	5.42
	401208	NA		NA	5.42
5	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	5.42
	405523			NA	5.42
	409012	AL117435	Hs.49725	DKFZP434I216 protein	5.41
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	5.41
	436982	AB018305	Hs.5378	spodion 1, (f-spondin) extracellular mat	5.40
10	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	5.40
	456027	BE327387	Hs.13913	KIAA1577 protein	5.40
	411897	AW875066	Hs.326876	Homo sapiens SOX6 mRNA, complete cds	5.40
	449689	AF228421	Hs.23889	DKFZP564A032 protein	5.40
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	5.40
	408248	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	5.40
15	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.40
	423289	N77774		gb:yz83e01.r1 Soares_multiple_sclerosis_	5.40
	453365	AA035211	Hs.17404	ESTs	5.40
	406465			NA	5.40
20	441858	AW173339	Hs.135665	ESTs	5.40
	432507	BE391093	Hs.324667	ESTs	5.40
	440570	AI205712	Hs.125998	ESTs	5.40
	445062	AI339915	Hs.44324	ESTs	5.40
	421639	NM_012082	Hs.106309	Friend of GATA2	5.40
25	410406	AI969703	Hs.1466	glycerol kinase	5.40
	418939	AW630803	Hs.89497	lamin B1	5.40
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.40
	400250	NA		NA	5.40
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	5.40
30	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.39
	433384	AI021992	Hs.124244	ESTs	5.38
	428781	AF164799	Hs.193384	putative 28 kDa protein	5.38
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	5.38
	400639			NA	5.38
35	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-	5.37
	424205	AA336825		gb:EST41732 Endometrial tumor Homo sapie	5.36
	459596	H29554	Hs.113871	ESTs	5.36
	408234	AW993356	Hs.285814	sprouty (Drosophila) homolog 4	5.36
	414547	T47770	Hs.191463	ESTs	5.35
40	419851	AA287987	Hs.13477	ESTs, Weakly similar to 1207289A reverse	5.35
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	5.34
	425764	AW996009	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.34
	405352			NA	5.33
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	5.32
45	424284	BE541008	Hs.6193	hypothetical protein FLJ14590	5.32
	427741	AW753185	Hs.180628	dynamitin 1-like	5.31
	426021	AW770897	Hs.34392	ESTs, Weakly similar to I38022 hypotheti	5.31
	442186	AA984083	Hs.269746	ESTs, Weakly similar to T03306 PSD-95/SA	5.30
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	5.30
	405287	NA		NA	5.30
50	427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p	5.30
	415371	R15239		gb:yf89b02.r1 Soares infant brain 1N1B H	5.30
	420024	AA252905	Hs.194477	E3 ubiquitin ligase SMURF2	5.30
	434408	AI031771	Hs.132586	ESTs	5.30
55	434739	AA804487	Hs.144130	ESTs	5.30
	421327	AA837295	Hs.188802	ESTs	5.30
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	5.30
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.30
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	5.30
60	430264	AA470519		gb:nc71110.s1 NCI_CGAP_P1 Homo sapiens	5.30
	411402	BE297855	Hs.69855	NRAS-related gene	5.30
	419220	AA811938	Hs.291759	ESTs	5.30
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	5.30
	459256	AW967468	Hs.99821	hypothetical protein FLJ14547	5.30
65	452449	AW068658	Hs.20943	ESTs	5.30
	430366	AI057368	Hs.105575	ESTs	5.30
	434360	AW015415	Hs.127780	ESTs	5.30
	422560	F11469	Hs.118281	zinc finger protein 266	5.29
	441704	AI458766	Hs.201988	ESTs	5.29
70	443635	AI080230	Hs.134214	ESTs	5.29
	434342	AI791138	Hs.116768	ESTs	5.29
	423409	NM_006466	Hs.128207	polymerase (RNA) III (DNA directed)-{39k	5.29
	449000	U69560	Hs.3826	kelch-like protein C3IP1	5.29
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.29
75	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	5.29
	434860	AA932386	Hs.292667	ESTs	5.28
	408096	BE250162	Hs.83765	dihydrofolate reductase	5.28
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	5.28
	435443	AI248674	Hs.14295	ESTs	5.26
80	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	5.26
	408371	AF161545	Hs.279883	hypothetical protein	5.26
	401205	NA		NA	5.26
	450904	R07118	Hs.189924	ESTs	5.26
	416351	H49704	Hs.173522	ESTs	5.26

	426524	AA380611	Hs.163841	ESTs	
	412901	A1127359	Hs.289088	heat shock 90kD protein 1, alpha	5.25
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	5.25
5	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase	5.24
	412953	Z45794	Hs.238809	ESTs	5.24
	404117	NA		NA	5.24
	427956	AL046175	Hs.108169	Homo sapiens mRNA; cDNA DKFZp586C1619 ff	5.22
	421787	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m	5.22
10	437255	R58970	Hs.9887	ESTs	5.22
	424897	AL136169	Hs.250708	CAAX box 1	5.22
	449771	A1668702	Hs.54976	ESTs	5.20
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.20
	438885	A1886558	Hs.184987	ESTs	5.20
15	407182	AA312551	Hs.230157	ESTs	5.20
	452150	W42490	Hs.260844	ESTs	5.20
	419680	AA249720	Hs.59335	ESTs	5.20
	438940	AF075045	Hs.271609	ESTs	5.20
	405362	NA		NA	5.20
20	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.20
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.20
	409331	M36634	Hs.53973	vasoactive intestinal peptide	5.20
	415397	H10818		gb:ym04f10.r1 Soares infant brain 1N1B H	5.20
	406735	AA603092		gb:np37a01.s1 NCI_CGAP_Lu1 Homo sapiens	5.20
25	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	5.20
	431480	AA837274	Hs.257005	hypothetical protein FLJ20837	5.20
	425523	A8007948	Hs.158244	KIAA0479 protein	5.20
	425673	R70318	Hs.339730	ESTs	5.20
	439267	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	5.20
30	457030	A1301740	Hs.173381	dihydropyrimidinase-like 2	5.20
	424638	A1472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	5.20
	454434	AA083558	Hs.261286	ESTs	5.20
	448336	R53848	Hs.44976	ESTs	5.20
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	5.20
35	434803	AW974640	Hs.303413	ESTs	5.20
	403199	NA		NA	5.20
	435225	A1021912	Hs.187983	ESTs	5.20
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	5.20
	440385	AA884283	Hs.192136	ESTs	5.20
40	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	5.20
	400484			NA	5.20
	425757	AA363171		gb:EST72986 Ovary II Homo sapiens cDNA 5	5.19
	449841	A1671602	Hs.199602	ESTs	5.19
	420303	AA258282	Hs.278436	KIAA1474 protein	5.19
45	429687	A1675749	Hs.211608	nucleoporin 153kD	5.19
	453345	AA302862	Hs.90063	neurocalcin delta	5.18
	447499	AW262580	Hs.147674	protocadherin beta 16	5.18
	404913			NA	5.18
	405114	NA		NA	5.18
50	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	5.18
	411995	W49701	Hs.29667	ESTs	5.17
	401736	NA		NA	5.17
	425250	AA353495	Hs.269762	ESTs, Weakly similar to A47582 B-cell gr	5.16
55	454388	AA630905	Hs.333300	hypothetical protein FLJ14026	5.16
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	5.16
	443646	A1085198	Hs.164226	ESTs	5.15
	436032	AA150797	Hs.109276	latexin protein	5.15
	456896	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	5.15
60	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	5.15
	432826	X75363	Hs.250770	ACO for serine protease homologue	5.14
	439441	W67993	Hs.323135	ESTs	5.14
	400205	NA		NA	5.14
	430854	AW440369	Hs.47026	ESTs	5.14
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	5.14
65	456804	A1421645	Hs.139851	caveolin 2	5.14
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	5.13
	449210	A1635363	Hs.197636	ESTs	5.12
	419013	T90378	Hs.14463	ESTs	5.12
	425843	BE313280	Hs.159627	death associated protein 3	5.12
	422545	X02761	Hs.287820	fibronectin 1	5.12
70	424785	R23519	Hs.6126	hypothetical protein dJ1141E15.2	5.11
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	5.10
	422411	AW749443	Hs.22511	ESTs	5.10
	457565	BE294029	Hs.279903	Ras homolog enriched in brain 2	5.10
75	437722	AW292947	Hs.122872	ESTs, Weakly similar to J00033 hypothe	5.10
	446893	A1610818	Hs.7110	ESTs	5.10
	401581			NA	5.10
	417511	AL049176	Hs.82223	chordin-like	5.10
80	422336	A1761322	Hs.115285	dihydrodipamide S-acetyltransferase (E2	5.10
	437662	AA765387	Hs.145095	ESTs	5.10
	429526	AA454182	Hs.98360	ESTs	5.10
	447332	AW445012	Hs.160918	ESTs	5.10
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	5.10
	428155	H17012	Hs.14633	ESTs	5.10

5	420185	AL044056	Hs.158047	ESTs	5.10
	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	5.10
	440913	AI267491	Hs.160593	ESTs	5.10
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	5.10
	428603	BE241619	Hs.24541	cytoskeleton associated protein 2	5.10
10	436577	W84774	Hs.17643	ESTs	5.10
	400241	NA		NA	5.10
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	5.10
	423654	AI674253	Hs.35828	ESTs	5.10
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	5.10
15	430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.10
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	5.10
	440381	AA917808	Hs.190495	ESTs	5.10
	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens c	5.10
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	5.10
20	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.10
	442150	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	5.10
	415651	AI207162	Hs.3815	slathmin-like-protein RB3	5.10
	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	5.09
	434442	AA737415	Hs.152826	ESTs	5.09
25	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PL	5.09
	435419	AI281068	Hs.152835	ESTs	5.09
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	5.09
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	5.08
	424071	R71340	Hs.12876	ESTs	5.08
30	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.08
	426400	M78361	Hs.169743	Homo sapiens clone Z5121 neuronal octact	5.08
	429026	AA443385	Hs.221993	ESTs	5.08
	455847	BE146775		gb:QV4-HT0222-181099-013-e04 HT0222 Homo	5.08
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	5.08
35	436854	AA749167	Hs.173911	ESTs	5.08
	421799	AW972292	Hs.292998	ESTs	5.08
	452154	AW953265	Hs.302746	MSTP028 protein	5.06
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	5.06
	445950	AI267957	Hs.145706	ESTs	5.06
40	443124	AI033500	Hs.132895	ESTs	5.06
	440698	AI348455	Hs.147492	Homo sapiens cDNA FLJ11777 fis, clone HE	5.06
	444713	AW812074	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	5.06
	447970	AW086109	Hs.20136	chromosome X open reading frame 6	5.06
	419307	AW953190	Hs.23180	ESTs	5.06
45	421954	AA410245	Hs.40323	BU83 (budding uninhibited by benzimidazo	5.06
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	5.05
	421782	AB029290	Hs.108258	actin binding protein; macrophin (microf	5.05
	407976	AI633875	Hs.77823	hypothetical protein FLJ21343	5.05
	400869			NA	5.04
50	416153	R13894		gb:yf62a06.r1 Soares infant brain 1NIB H	5.04
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	5.04
	406038	Y14443	Hs.88219	zinc finger protein 200	5.03
	440659	AF134160	Hs.7327	claudin 1	5.03
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.02
55	446051	BE048061	Hs.37054	ephrin-A3	5.02
	443387	BE139135	Hs.254629	ESTs	5.02
	414407	AA147026	Hs.76704	ESTs	5.02
	408349	BE546947	Hs.44276	homeo box C10	5.01
	452510	Z33566	Hs.301491	ESTs	5.01
60	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	5.00
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	5.00
	447857	AA081218	Hs.58508	Homo sapiens cDNA FLJ14206 fis, clone NT	5.00
	423648	AK000456	Hs.130546	hypothetical protein FLJ20449	5.00
	412997	BE046600		gb:hn41d08.x1 NCL_CGAP_RDF2 Homo sapiens	5.00
65	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	5.00
	411636	AW855001		gb:PM3-CT0263-091299-007-R05 CT0263 Homo	5.00
	418111	R42003	Hs.106513	ESTs	5.00
	402709	NA		NA	5.00
	408677	AI279892	Hs.46801	sorting nexin 14	5.00
70	411350	AW877011		gb:QV2-PT0010-250300-096-b05 PT0010 Homo	5.00
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	5.00
	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.00
	408512	AW902013	Hs.255937	ESTs	5.00
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566G133	5.00
75	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	5.00
	423896	AA332216	Hs.130584	ESTs	5.00
	429091	AA935658	Hs.187939	ESTs	5.00
	410968	AA199907	Hs.67397	homeo box A1	5.00
	436859	AA732681	Hs.270053	ESTs	5.00
80	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	5.00
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	414631	AW970130	Hs.65406	ESTs	5.00
	405481			NA	5.00
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	5.00
	421373	AA808229	Hs.167771	ESTs	5.00
	424916	AW867440	Hs.23096	ESTs	5.00
	433106	AB002443	Hs.184418	ESTs	5.00

5	427386	AW836261	Hs.337717	ESTs	5.00
	441998	A173236	Hs.128312	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	420161	A1683069	Hs.175319	ESTs	5.00
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.00
	415188	BE007531	Hs.258791	ESTs	5.00
	420429	AW293291	Hs.255180	ESTs	5.00
	439038	AV655045	Hs.8366	ESTs	5.00
	457031	AM97955	Hs.304802	ESTs, Weakly similar to KIAA0944 protein	5.00
10	430865	A1073424	Hs.5232	HSPC125 protein	5.00
	420583	H77859	Hs.65450	reticulum 4	5.00
	432229	AW290976	Hs.143587	ESTs	5.00
	455208	BE180276		gb:RC3-HT0622-130400-022-a02 HT0622 Homo	5.00
	419263	AW583874	Hs.89832	insulin	5.00
15	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.00
	419100	AA464362	Hs.6748	hypothetical protein PP1665	5.00
	438585	AA811371	Hs.123362	ESTs	5.00
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fs, clone NT	5.00
	428775	AA34579	Hs.143691	ESTs	5.00
20	422471	AA311027	Hs.271894	ESTs, Weakly similar to I38022 hypothe	5.00
	402524		NA	NA	5.00
TABLE 46B:					
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	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
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	408248	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817		
	408432	1058667_1	AW195262 R27868 AW811262		
	408744	1078309_1	AW806177 AW806178 AW265775		
	409948	116139_1	AA078643 BE535933 AA132607		
	410424	120166_1	AA084984 Z18302 AW502279 AW499519		
	410444	1203699_1	W73484 AW748569 AW748532 AW748585		
35	410498	120611_1	AA355749 AA085520 AW966333 AA340319 BE170936		
	410784	1221005_1	AW803201 BE079700 BE062940		
	410979	1228509_1	BE151480 D63282 AW812615		
	411253	1236671_1	AW833897 AW833907 AW833908 AW833920 AW833953 AW833881 AW833878 AW833879 AW833952 AW833919 AW833921 AW833915		
40	411350	1239976_1	AW877011 AW877066 AW877136 AW876980 AW991827 AW877073 AW877070 AW882665 AW876972 AW877068 AW877064 AW838297 AW877065		
	411636	1252525_1	AW855001 AW855031 BE062221		
	411861	1261785_1	AW867875 BE067343 BE067350 BE067305 BE067347 BE067306 BE067304 BE067303 BE067302 AW938147		
	412227	1284297_1	AW902282 AW902508 AW902509 AW902605 AW902606 AW902643 AW902490		
	412345	1289783_1	AW938386 AW938411 AW938426 AW938397		
45	412396	1292796_1	AW947895 AW947891 AW947933 AW947892 AW947930 AW947889 AW947894 AW947931 AW947893 AW947932 AW947929		
	412997	1343205_1	BE046600 BE046677 BE046236		
	413604	1379715_1	R51767 BE152515 Z44834 H23397		
	413894	1397740_1	BE177983 BE178322		
	414727	1481204_1	BE466904 W28721		
50	415308	1533673_1	F05251 R13748 Z44028 H14747		
	415371	1535066_1	R15239 Z45189 F06836		
	415397	1535937_1	H10818 F07831 Z43072		
	415637	1540904_1	R25517 F13222 T75465		
	416153	1573947_1	R13894 H23037 R56371		
55	416190	1576789_1	N54000 H26494 T83818		
	416845	1624038_1	H95279 H95331 H95933		
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499		
	417352	166908_1	AA195919 D79180 BE543135 BE008355 BE008353 BE008315 BE008317		
	417588	1688092_1	Z44510 R24958 R00714 T82024		
60	418247	1733290_1	R55174 Z19829 X97508		
	418553	1767393_1	T88964 R99447 T84773		
	418647	177521_1	AA226198 AA226513 AA383773		
	418866	179788_1	T65754 AA229857 AA229658		
	423172	225618_1	R15652 AA322742 AW961639 AW961637		
65	423289	226804_1	N77774 AA324125 AW955199 AA452230		
	423395	227885_1	AA326613 AA325417 AW962164		
	423928	233416_1	AA332680 AA332831 AW962684		
	424205	236651_1	AA336825 AA337256 AA337682 AA337525		
	425757	255956_1	AA363171 AW963347 AA371863		
70	428679	294049_1	AA431765 AA432015		
	430264	315008_1	AA470519 BE303010 BE302954 BE384120		
	430818	324239_1	A1311928 AA936030 T51931 AA609816 AA487195 AA664207		
	432494	348522_1	AA551060 AW979274 AA847429 AA878487		
	432639	351744_1	AW973785 H60163 AA557608		
75	433009	357371_1	AA761668 AA573621 R92814 R09670		
	434006	37855_1	AF113688 A1114617		
	434603	38944_1	AF147384 T60126 T60244		
	436411	419334_1	AW674352 AA715374 Z25205		
	437092	432938_1	AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923		
80	437237	43506_-2	BE513073		
	441033	50807_-1	BE562555		
	441761	525307_1	A1222880 A1242392 AA961560 A1242524 A1719648 A1718138 AW275807		
	442075	532052_1	AW136928 A1685655 BE218584 BE455078 N68963 AA975338 BE147199 N76377		

445165 63181_1 AV652831 AA191140 AA329706 AJ267893 AJ796986 AW675672 AW195369 BE002835 BE003284 AA190592 AA769594 AW275548 R56781 AA807313
 AW169695 N31806
 447197 711623_1 R36075 AJ366546 R36167
 453685 977734_1 AL110309 AW088119 H22881
 454511 1220533_1 AW948146 AW948135 AW802578
 454758 1233743_1 AW845266 AW845254 AW819440 AW819430 AW819425 AW819423
 454835 1236507_1 AW833763 AW833704 AW833618
 455082 1252687_1 BE148180 AW855210 AW855243
 455208 1260551_1 BE180276 AW866156 BE180165
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 455217 1261522_1 AW867534 AW867539
 455608 1337389_1 BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
 455847 1375358_1 BE146775 BE146789 BE146792 BE147010 BE146941 BE146801 BE146998 BE147011 BE146903 BE146901
 455944 1385569_1 BE160643 BE160585
 457892 432926_1 AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
 457893 432938_1 AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923
 459279 975649_1 AW814996 AL047199 AW850979

TABLE 46C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400484	8569067	Minus	52725-52912
400570	9884797	Minus	156787-156862,178082-178208,186819-186957
400639	9887597	Plus	23150-23580
400845	9188605	Plus	34428-34612
400860	9757499	Minus	151830-152104,152649-152744
400869	9838306	Plus	29152-30102
400950	7658481	Minus	157920-158564
400977	8072510	Plus	73950-74364
401004	7229982	Plus	62580-62772
401093	8516137	Minus	22335-23166
401183	7670214	Minus	39921-40601
401205	9743388	Plus	167373-167433,167936-168031
401208	7712287	Plus	163145-163281
401244	4827300	Minus	55359-56376
401348	9930791	Minus	9365-9490
401372	9944181	Plus	127056-127196
401424	8176894	Plus	24223-24428
401581	9502454	Plus	9440-10165
401629	8575965	Minus	169336-169788
401708	2951946	Plus	154511-155298
401736	3219338	Plus	1771-1894
401740	2982169	Plus	148357-148484,148591-148690
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401961	4581193	Minus	124054-124209
402343	8099256	Plus	4677-6084
402363	9454515	Plus	25693-25991
402408	9796239	Minus	110326-110491
402524	9798518	Minus	20529-21096
402709	8901246	Minus	56847-57055
402732	9211639	Minus	147904-148107
403040	3133144	Minus	91632-91788,97918-98115
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403199	9958183	Minus	58895-59036,66618-66789
403278	8072597	Plus	146823-146986
403546	8078400	Plus	94703-94849
403764	7717105	Minus	118692-118853
403776	7770611	Minus	1414-1513,1624-1756
403859	7708954	Plus	113738-113858
403973	8575876	Plus	93873-94384
404012	8655948	Plus	551356-552233
404029	7671252	Plus	108716-111112
404072	9931705	Plus	49546-50498
404117	9796029	Plus	149723-149920
404170	9930793	Plus	168836-169248
404335	9838027	Minus	21030-21145,26504-26692
404440	7528051	Plus	80430-81581
404632	9796668	Plus	45096-45229
404702	7630798	Plus	78043-78890
404913	7341740	Plus	97717-97976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405065	7684500	Minus	13855-14027
405114	8096938	Minus	97013-97560
405287	3928029	Plus	89802-89999
405352	2822162	Minus	97253-97742
405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641

5	405481	3688109	Plus	5718-5837,8719-8818
	405511	9454623	Plus	57731-57852
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405543	9857582	Minus	104338-104449
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405637	6289229	Plus	189852-189978
	405696	4309923	Minus	1865-2013,2124-2231
	405770	2735037	Plus	61057-62075
10	406465	9795550	Plus	94502-94706,96776-96914,98795-98928,102423-102576,105087-105191,107023-107127,108852-108992

TABLE 47A: ABOUT 370 GENES SIGNIFICANTLY DOWN-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH

Table 47A lists about 370 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 46A, except that the numerator and denominator were switched and the ratio was equal to or less than 0.33.

Pkey: Unique Eos probe/identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	412859	NM_000705	Hs.813	ATPase, H ⁺ /K ⁺ exchanging, beta polypept	0.02
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.02
25	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	0.04
	429050	X81333	Hs.194777	meprin A, beta	0.04
	421996	AW583807	Hs.1460	glucagon	0.05
	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.05
	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	0.06
30	403697	NA		NA	0.07
	402760	NA		NA	0.08
	428285	AW340797	Hs.98434	ESTs	0.08
	419279	AA235900	Hs.87500	ESTs	0.08
	422459	K02100	Hs.117050	ornithine carbamoyltransferase	0.09
35	422992	AF016833	Hs.122785	maltase-glucoamylase (alpha-glucosidase)	0.09
	430867	M16404	Hs.248099	cholinergic receptor, muscarinic 2	0.09
	453989	M63962	Hs.36992	ATPase, H ⁺ /K ⁺ exchanging, alpha polypept	0.10
	443022	AL046485	Hs.207604	ESTs	0.10
	413382	BE090689		gb:RC1-BT0720-280300-011-008 BT0720 Homo	0.10
40	450769	AA057418	Hs.33654	ESTs	0.10
	428070	T63918	Hs.182313	retinol-binding protein 2, cellular	0.10
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	0.11
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.11
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	0.12
45	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.12
	405650	NA		NA	0.12
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.12
	401623	NA		NA	0.12
	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	0.13
50	455826	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	0.13
	414949	C15314	Hs.323349	ESTs	0.13
	407486	S69741		gb:hSCG-3=stomach cancer gene-3 (oncogen	0.13
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	0.13
	401015	NA		NA	0.13
55	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.14
	450926	A1744361	Hs.205591	ESTs, Weakly similar to T46608 zinc fing	0.14
	443564	A1921685	Hs.199713	ESTs	0.14
	457955	A1208986	Hs.143945	ESTs	0.14
	457345	A1699933	Hs.192175	ESTs	0.14
60	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.14
	408518	BE162203	Hs.314758	ESTs	0.14
	444938	AW470690	Hs.148814	ESTs	0.15
	403670	NA		NA	0.15
	432440	X63597	Hs.2996	sucrase-isomaltase	0.15
65	428492	AW662740	Hs.259391	ESTs	0.15
	443607	A1452512	Hs.134069	ESTs	0.15
	446914	BE044496	Hs.166994	FAT tumor suppressor (Drosophila) homolo	0.15
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	0.15
	430350	BE169639		gb:PM1-HT0527-280200-005-a05 HT0527 Homo	0.16
70	431094	AW972276	Hs.116195	ESTs	0.16
	401683	NA		NA	0.16
	419278	AU076799	Hs.1247	apolipoprotein A-IV	0.16
	455071	BE145826		gb:MR0-HT0208-101299-202-e12 HT0208 Homo	0.16
	454282	AW296422		gb:UL-H-BW0-aio-h-05-0-UL.s1 NCI_CGAP_Su	0.16
75	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	0.16
	451729	AW160725	Hs.312469	ESTs	0.16
	451103	RS2804	Hs.25956	DKFZP564D206 protein	0.16
	428602	AL137479	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (f	0.16
	437157	BE048860	Hs.120655	ESTs	0.17
80	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	0.17
	402015	NA		NA	0.17
	414758	H82022	Hs.282847	pregnancy specific beta-1-glycoprotein 3	0.17
	412793	AW997986		gb:RC1-BN0056-230200-021-e11 BN0056 Homo	0.17
	438152	AW292520	Hs.122082	ESTs	0.17

	401685	NA	NA	0.17
	441519	AA972740	ESTs	0.17
	438327	H87407	chorionic gonadotropin, beta polypeptide	0.17
5	402761	BE387621	chaperonin containing TCP1, subunit 7 (e	0.17
	424268	AA397653	Human DNA sequence from clone 495010 on	0.18
	414507	AW102637	Homo sapiens cDNA FLJ14647 fis, clone NT	0.18
	413808	J00287	Homo sapiens mRNA for caldesmon, 3' UTR	0.18
	401132	NA	NA	0.18
10	412374	X01388	apolipoprotein C-III	0.18
	423417	AP000365	potassium large conductance calcium-acti	0.18
	447677	AI419235	gb:lf21d02.x1 NCL_CGAP_Bm23 Homo sapien	0.18
	448828	AI580296	ESTs, Weakly similar to KIAA1437 protein	0.18
	424122	AA335593	ESTs	0.18
15	417332	AW972717	hypothetical protein FLJ21511	0.18
	434597	AW974668	gb:EST386757 MAGE resequences, MAGM Homo	0.19
	428804	AK000713	hypothetical protein FLJ20706	0.19
	410280	AA083558	ESTs	0.19
	408382	AA071244	gb:zm73g03.r1 Stratagene neuroepithelium	0.19
20	428062	AA420683	hypothetical protein FLJ14103	0.19
	426069	H10807	Homo sapiens cDNA FLJ14028 fis, clone HE	0.19
	430135	NM_000035	aldolase B, fructose-bisphosphate	0.19
	414802	AI793107	Ris	0.19
	457432	NM_005136	potassium voltage-gated channel, Isk-rel	0.19
25	446909	AA004895	ESTs	0.19
	435447	AI872932	gb:wm72e03.x1 NCL_CGAP_U12 Homo sapiens	0.20
	408611	NM_004367	chemokine (C-C motif) receptor 6	0.20
	423577	AW810107	Homo sapiens cDNA: FLJ22145 fis, clone H	0.20
	439328	W07411	ESTs, Moderately similar to ALU3_HUMAN A	0.20
30	436741	AA860163	ESTs	0.20
	426635	BE395109	hypothetical protein MGC13057	0.20
	418277	AW135221	ESTs	0.20
	448871	BE616709	kruppel-related zinc finger protein hckr	0.20
	459370	AA889982	ESTs, Weakly similar to I38022 hypothe	0.21
35	427469	AA403084	ESTs, Weakly similar to 2109260A B cell	0.21
	432887	AI926047	ESTs	0.21
	421296	NM_002666	pentipin	0.21
	449216	AW295417	ESTs	0.21
	414835	AA156720	ESTs	0.21
40	459233	AI939966	gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.21
	439756	AL359651	Homo sapiens mRNA full length insert cDN	0.21
	427167	AI239607	hypothetical protein MGC11324	0.21
	400410	AF154915	homeo box D12	0.21
	409828	AW501137	gb:U1-HF-BP0p-ait-e-12-0-U1.r1 NIH_MGC_5	0.22
45	428470	AC002301	Homo sapiens Chromosome 16 BAC clone CIT	0.22
	455968	BE168828	gb:QV1-HT0517-020400-145-f04 HT0517 Homo	0.22
	404145	NA	NA	0.22
	454011	M31008	alkaline phosphatase, intestinal	0.22
	430588	AI741461	ESTs	0.22
50	403652	NA	NA	0.22
	440410	AW204436	ESTs	0.22
	453871	BE300380	Homo sapiens cDNA FLJ12758 fis, clone NT	0.22
	458567	AI222075	ESTs	0.22
	436004	AA703332	folate transporter/carrier	0.22
55	417408	F17211	Homo sapiens skeletal myosin light chain	0.22
	448643	AI557531	gb:pt2.1-06.D06.r tumor2 Homo sapiens cD	0.22
	404401	NA	NA	0.22
	428088	AA421130	EST	0.22
	427074	AA527435	hepatocellular carcinoma antigen gene 52	0.22
60	421972	M18185	gastric inhibitory polypeptide	0.22
	429001	AF098951	ATP-binding cassette, sub-family G (WHIT	0.22
	441155	AW161008	GABA(A) receptor-associated protein	0.22
	402750	NA	NA	0.22
	438587	AA811450	ESTs	0.22
65	404848	NA	NA	0.22
	427833	AA416615	ESTs	0.23
	439907	AA853978	ESTs	0.23
	414373	AW162907	proline-rich protein with nuclear target	0.23
	446817	AI700684	ESTs	0.23
70	437333	AA748898	gb:ny76h10.s1 NCL_CGAP_GCB1 Homo sapiens	0.23
	404097	NA	NA	0.23
	446393	AW014174	zinc finger protein	0.23
	456328	T41368	gb:ph1d1_19/1TV Outward Alu-primed hncDN	0.23
	401042	NA	NA	0.23
75	458441	AW842283	cyclin I	0.23
	435547	AW117431	ESTs	0.23
	429060	AW139155	hypothetical protein DKFZp434O0320	0.23
	425158	AW954631	t-complex-associated-testis-expressed 1-	0.23
	448758	AB018311	KIAA0768 protein	0.23
80	441240	AA923749	ESTs	0.23
	436562	H71937	ESTs, Weakly similar to I38022 hypothe	0.23
	424104	AA669515	ESTs	0.23
	447452	BE618258	Homo sapiens, clone IMAGE:3869590, mRNA,	0.23
	444515	AW204908	ESTs	0.24

	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.24
	406560	NA		NA	0.24
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	0.24
5	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	0.24
	453979	M68895	Hs.76800	alcohol dehydrogenase 6 (class V)	0.24
	439657	W93589		gb:zd95g05.s1 Soares_fetal_heart_NbHH19W	0.24
	407512	X15674		gb:Human pTR5 mRNA for repetitive sequen	0.24
	440875	AW138036	Hs.201788	ESTs	0.24
10	404753	NA		NA	0.24
	411119	MG0627	Hs.753	formyl peptide receptor 1	0.24
	418692	AK000268	Hs.87383	hypothetical protein	0.24
	415327	H22769		gb:ym54c02.r1 Soares infant brain 1N1B H	0.24
	429446	A1547111		gb:PN2.1_A01_G12 r mynorm Homo sapiens c	0.24
15	455391	BE156230		gb:QV0-HT0367-310100-102-c11 HT0367 Homo	0.25
	422818	AA404290	Hs.97848	ESTs	0.25
	435338	AA678071	Hs.194300	ESTs, Weakly similar to I38022 hypotheti	0.25
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.25
	403941	NA		NA	0.25
20	414383	BE279406		gb:601157981F1 NIH_MGC_21 Homo sapiens c	0.25
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	0.25
	424985	A1907236	Hs.279935	Homo sapiens cDNA FLJ11780 fs, clone HE	0.25
	450736	AW970060		gb:EST382140 MAGE resequences, MAGK Homo	0.25
	431185	H02767	Hs.28944	ESTs	0.25
25	455308	AW893949		gb:RC4-NN0027-060400-011-a09 NN0027 Homo	0.25
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	0.25
	418525	AW450369	Hs.86937	ESTs	0.25
	402790			NA	0.25
	411869	W20027	Hs.23439	ESTs	0.25
30	400332	S66407	Hs.248032	FLT4	0.25
	424884	AW299437	Hs.225717	ESTs	0.25
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [0.25
	439780	AL109688		gb:Homo sapiens mRNA full length insert	0.25
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.25
35	404900	NA		NA	0.25
	441918	A1733373	Hs.128119	ESTs	0.25
	441639	A1133287	Hs.303953	ESTs	0.25
	459396	A1907536	Hs.103869	ESTs	0.25
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	0.25
40	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	0.25
	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fs, clone NT	0.26
	429450	AA824451	Hs.94292	hypothetical protein FLJ23311	0.26
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	0.26
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	0.26
45	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	0.26
	455802	BE141491		gb:MR0-HT0080-011099-002-h06 HT0080 Homo	0.26
	414003	AA134472		gb:zo13c01.s1 Stratagene colon (937204)	0.26
	436363	AA843926	Hs.124434	ESTs	0.26
	456074	BE409525	Hs.902	neurofibromin 2 (bilateral abouctic neur	0.26
50	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	0.26
	445635	A1769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.26
	405953	NA		NA	0.26
	411021	F00055	Hs.172004	titin	0.26
55	428443	BE618106	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	0.26
	434345	AF127772		gb:Homo sapiens cell-line E8CASS clone E	0.26
	455743	BE073754		gb:RC0-BT0561-210100-032-d07 BT0561 Homo	0.26
	451138	W92287	Hs.40268	ESTs	0.26
	449528	H63337	Hs.38178	hypothetical protein FLJ23468	0.26
	441040	AW449782	Hs.178803	ESTs	0.26
60	458830	AW501248	Hs.250824	Homo sapiens cDNA: FLJ23435 fs, clone H	0.26
	428861	AW352234	Hs.269365	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.26
	435469	AW388237	Hs.191204	ESTs	0.27
	427562	R56424	Hs.26534	ESTs	0.27
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	0.27
65	423528	AB011137	Hs.300938	KIAA0565 gene product	0.27
	406589			NA	0.27
	450059	BE220223	Hs.279626	ESTs	0.27
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	0.27
70	454007	AW015870	Hs.232081	ESTs	0.27
	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	0.27
	441665	AJ301355	Hs.151285	ESTs	0.27
	405037	NA		NA	0.27
	446820	AW295037	Hs.254986	ESTs	0.27
	448487	AJ523720	Hs.172567	ESTs	0.27
75	447567	AW474513	Hs.224397	ESTs, Weakly similar to I38931 Wiskott-A	0.27
	408540	L13220	Hs.639	calbindin 3, (vitamin D-dependent calciu	0.27
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.27
	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	0.27
	401350	NA		NA	0.27
80	417569	R00271	Hs.144651	ESTs	0.27
	443542	AJ927065	Hs.146040	ESTs	0.27
	437105	AA744554	Hs.222127	ESTs	0.27
	432119	T80289	Hs.302041	Homo sapiens clone 24762 mRNA sequence	0.27
	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	0.28

	427812	AA770424	Hs.98162	ESTs	0.28
	423557	AB011176	Hs.129801	KIAA0604 gene product	0.28
	445311	AW027556	Hs.156286	ESTs	0.28
	402758	NA		NA	0.28
5	448240	AJ478345	Hs.191034	ESTs	0.28
	401333	NA		NA	0.28
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.28
	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.28
10	442896	R37725	Hs.261108	ESTs	0.28
	447949	AJ446820	Hs.165839	EST	0.28
	435625	H50654	Hs.113999	ESTs	0.28
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	0.28
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	0.28
15	442967	AI025460	Hs.220977	ESTs	0.28
	448062	AW295923	Hs.255472	KIAA1843 protein	0.28
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	0.28
	451839	AI820516	Hs.16857	ESTs	0.28
	446000	AV656052	Hs.1504	hemopexin	0.28
20	443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.28
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	0.28
	445481	AW661846	Hs.148836	ESTs	0.28
	409337	H71289	Hs.220535	ESTs	0.28
	411414	AW897236		gb:CMO-NN0057-150400-335-c06 NN0057 Homo	0.28
25	427642	R40761	Hs.9834	ESTs	0.28
	456392	W28766		gb:51d3 Human retina cDNA randomly prime	0.28
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	0.28
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	0.28
	442496	R55073	Hs.124130	ESTs	0.28
30	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	0.28
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	0.29
	458716	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29
	423235	AW410698	Hs.169917	neurabin II	0.29
	431087	H12723	Hs.290791	ESTs	0.29
35	459106	AW589793	Hs.224713	ESTs	0.29
	414870	N72264	Hs.300670	KIAA1204 protein	0.29
	402243			NA	0.29
	432628	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	0.29
	404364	NA		NA	0.29
40	400480			NA	0.29
	456083	U46922	Hs.77252	fragile histidine triad gene	0.29
	446598	AW250546		gb:2821774.5prime NIH_MGC_7 Homo sapiens	0.29
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	0.29
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	0.29
45	453948	AI970797	Hs.64859	ESTs	0.29
	403792	NA		NA	0.29
	418957	AI792615	Hs.188712	ESTs	0.29
	457960	AA771881	Hs.298149	ESTs	0.29
	404269			NA	0.29
50	439309	AF090097	Hs.6524	Homo sapiens clone IMAGE 25997	0.29
	458239	BE439877	Hs.283389	ESTs	0.30
	414941	C14865	Hs.332341	ESTs	0.30
	404954			NA	0.30
	441609	AA946764	Hs.133460	ESTs	0.30
55	426895	AA416880	Hs.225738	ESTs	0.30
	403182	NA		NA	0.30
	402319			NA	0.30
	429699	AI383469	Hs.159300	ESTs	0.30
	405669	NA		homeo box HB9	0.30
60	459312	AF107457	Hs.37035	homeo box HB9	0.30
	431853	AA521034	Hs.70834	ESTs	0.30
	449768	AI972746	Hs.102945	ESTs, Weakly similar to I78885 serine/th	0.30
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	0.30
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	0.30
65	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.30
	400128	NA		NA	0.30
	423208	AA323191	Hs.137064	cytoplasmic polyadenylation element bind	0.30
	434227	AF119893	Hs.63382	hypothetical protein PRO2714	0.30
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.30
70	401165	NA		NA	0.30
	415394	R19249	Hs.22654	sodium channel, voltage-gated, type I, a	0.30
	443110	AW352243	Hs.132665	ESTs	0.30
	426724	AA383623	Hs.293616	ESTs	0.30
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.30
75	409753	AA234847		gb:zs37b10.r1 Soares_NhHMPu_S1 Homo sapi	0.31
	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	0.31
	408895	AA058730	Hs.191464	ESTs	0.31
	405110	NA		NA	0.31
	432430	AW079984	Hs.262480	ESTs, Weakly similar to PIHUB6 salivary	0.31
80	426442	AA378656	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	0.31
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	0.31
	431854	AA383550	Hs.271699	polymerase (DNA directed) iota	0.31
	457553	AI861895	Hs.304505	ESTs	0.31
	412301	AW936328		gb:QV4-DT0021-281299-070-07 DT0021 Homo	0.31

5	418626	AW299508	Hs.135230	ESTs	0.31
	416156	Z41922		gb:HSC03B101 normalized infant brain cDN	0.31
	416275	H42823	Hs.155742	glyoxylate reductase/hydroxypyruvate red	0.31
	419091	T85332	Hs.178294	ESTs	0.31
	420118	AW295297	Hs.182585	KIAA1276 protein	0.31
	451094	A1949825	Hs.260395	ESTs	0.31
	403214	NA		NA	0.31
	412717	W00973	Hs.334728	ESTs	0.31
10	428782	X12830	Hs.193400	interleukin 6 receptor	0.31
	449202	AW295154	Hs.255396	ESTs	0.31
	433138	AB029496	Hs.59729	semaphorin sem2	0.31
	436602	A1793222	Hs.166817	ESTs	0.31
	424844	D61524		gb:HUM413E07B Clontech human fetal brain	0.32
15	435253	W91884		gb:zh47D8.s1 Soares_fetal_liver_spleen_	0.32
	455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	0.32
	416320	H47867	Hs.34024	ESTs	0.32
	406333			NA	0.32
	443652	A1080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	0.32
20	457103	A1421187	Hs.189192	ESTs, Weakly similar to T COMPLEX TESTIS	0.32
	423593	AA328144		gb:EST31752 Embryo, 12 week 1 Homo sapie	0.32
	453242	T98327	Hs.18343	ESTs	0.32
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.32
	403847	NA		NA	0.32
25	458711	AL036877	Hs.282878	ESTs	0.32
	406242	NA		NA	0.32
	433493	AA594915	Hs.155087	ESTs	0.32
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214 Homo	0.32
30	437403	A1208149	Hs.121196	ESTs	0.32
	407823	D44744	Hs.247447	ESTs	0.32
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fts, clone C	0.32
	436089	AA804957	Hs.119840	ESTs	0.32
	457463	AW877031	Hs.272321	hypothetical protein FLJ12571	0.32
	433370	A084343	Hs.122310	ESTs	0.32
35	436298	AW293496	Hs.180138	ESTs	0.32
	419768	T72104	Hs.93194	apolipoprotein A-I	0.32
	449428	A1651280	Hs.195685	ESTs	0.33
	406291	NA		NA	0.33
40	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	0.33
	418162	T11958		gb:A802R Heart Homo sapiens cDNA clone A	0.33
	408316	AW807771		gb:MR4-ST0098-090300-003-c05 ST0098 Homo	0.33
	404187	NA		NA	0.33
	452992	A1792376	Hs.31290	Homo sapiens clone 23832 mRNA sequence	0.33
45	448355	A1493734	Hs.329374	ESTs	0.33
	442423	BE326264	Hs.246842	ESTs	0.33
	439474	A1824060	Hs.211501	ESTs	0.33
	457149	AA429575	Hs.297493	ESTs	0.33
	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	0.33
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
50	419372	W28781		gb:51h3 Human retina cDNA randomly prime	0.33
	406293	NA		NA	0.33
	422933	AF073931	Hs.122359	calcium channel, voltage-dependent, alph	0.33
	451818	A1819018	Hs.339668	ESTs	0.33
	441912	AA971484	Hs.159938	ESTs	0.33
55	429013	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	0.33
	422304	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.33
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	0.33
	406597			NA	0.33
	451636	AW173270	Hs.140444	ESTs	0.33
60	424226	N94153	Hs.19155	ESTs	0.33

TABLE 47B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

65	Pkey	CAT Number	Accession
	408316	1051210_1	AW807771 AW179260 AW807851 AW179240 AW845961 AW807693 BE141176 AW807594 AW807772 AW846003 AW845963 AW179239
	409382	112508_1	AA071244 AA071477
70	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
	409753	115305_1	AA234847 AA077472
	409828	1155571_1	AW501137 AW501295 AW501212
	410285	119128_1	AA083609 AA083790 AA112048
	411414	1245024_1	AW897236 AW845406
75	411765	125700_1	H43346 AA248302 AA095182
	412301	1288123_1	AW936328 AW936539
	412793	1327636_1	AW997986
	413382	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	414003	140888_1	AA134472 R76288 AW750262
80	414383	1440279_1	BE279406 BE280100
	415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
	416035	1567254_1	H42314 H43080 H45217 H15384
	416156	1573980_1	Z41922 H23072 T77322
	418162	1725383_1	T11958 T11756 T11816 T20135 T19729 R45874

5	419372	1842942_1	W28781 W26588 W26377
	422731	220507_1	AL138411 AL138412 AA315860
	423593	229955_1	AA328144 AW962385 N30457
	424844	244291_1	D61524 AA347654 AW961758
	429446	304683_1	AI547111 AW973749 AA558007
	430350	316401_1	BE169639 AA476976
	434345	38411_1	AF127772 AF062358 AF060217 AA652270 F23288
	434597	389383_1	AW974668 AA651959 AA649572 AA640401-AA640402
10	435253	403478_1	W91884 W95119 AA676941
	435447	406400_1	AI872932 AA682306 BE220163 W88695 T81307 H91447
	437333	436167_1	AA748898 AW997701 AW997703
	439657	47499_1	W93589 W93487 AF086493
	439780	47673_1	AL109688 R23665 R26578
15	446598	68463_1	AW250546 BE257108 BE251006 BE255957 BE250926 BE513012 AV659318
	447677	732252_1	AM19235 AW055016 BE007490 BE550241
	448643	773566_-1	AI557531
	450736	844652_1	AW970060 AI732366 AI792313 AW839644
	454282	1091035_1	AW296422 H72616 H63825
20	454633	1227504_1	AW811380 AW811385
	454738	1232449_1	BE072139 BE157977 BE157974 AW857974 AW817778
	454790	1234752_1	AW820852 AW820773 AW821088
	455071	1252281_1	BE145826 BE145815 BE145822 AW854707 BE145912
	455308	1278147_1	AW893949 AW893960 AW893966
25	455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
	455391	1288067_1	BE156230 BE156239 AW936260
	455699	1351258_1	BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105
	455743	1354978_1	BE073754 BE073753 BE073755 BE073756 BE073752 BE073795 BE073796 BE073704 BE073791 BE073733 BE073695
	455802	1370828_1	BE141491 BE141016 BE141479
30	455826	1373392_1	BE144228 BE144291
	455968	1391117_1	BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
	456328	1789791_1	T41368 T41369 T41294
	456392	1843059_1	W28766 W26500
	458147	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
35	459233	944881_1	AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

TABLE 47C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
45	400480	8439796	Minus 110553-111119
	401015	8117441	Plus 72260-72369
	401042	8117611	Plus 151364-151606
	401132	8705350	Minus 85679-85795
	401165	9438376	Minus 168244-168423
50	401333	9884881	Plus 13852-14861
	401350	9931226	Plus 14471-14623
	401623	8575907	Plus 163249-163623
	401683	7689961	Plus 2934-3446
	401685	7689961	Minus 8038-8319
55	402015	7417802	Minus 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073
	402243	7690137	Minus 196521-196721
	402319	7582559	Plus 116589-117549
	402750	7210067	Plus 69466-69678,71139-71284,71572-71865
	402758	9213869	Plus 87638-87924
60	402760	9213869	Plus 136829-136952,137336-137521
	402790	4835258	Minus 147744-147861
	403182	9838273	Plus 102163-102345,102545-102725
	403214	7630945	Minus 76723-77027,79317-79484
	403652	8705848	Minus 49991-50129
65	403670	7259739	Minus 88377-88537
	403697	3962501	Minus 102965-103174
	403792	7230192	Minus 149707-149873
	403847	7708844	Plus 317240-317391,317913-318032
	403941	7454203	Plus 114876-115342
70	404097	7770701	Plus 55512-55781
	404145	9863643	Plus 30607-31266
	404187	4481839	Plus 7644-7991
	404269	9711443	Plus 70261-70404,72944-73063
	404364	9964977	Minus 32986-33202
75	404401	7259738	Plus 71066-71326
	404753	7637341	Plus 14770-14931
	404848	8248647	Minus 23955-24034,25143-25264
80	404900	7331453	Plus 22032-22219
	404954	7387327	Plus 131720-132042
	405037	7543748	Minus 127374-127578
	405110	8096888	Minus 118940-119100
	405650	4926905	Minus 71743-72291
	405669	4508140	Plus 14130-14270
	405953	7960374	Minus 65101-65574

5	406242	7417725	Minus	36736-36951
	406291	5686274	Plus	9562-9867
	406293	5686274	Minus	17646-17953
	406333	9213235	Plus	64689-64798
	406560	7711569	Minus	35162-35292
	406589	8224211	Plus	38806-38989
	406597	8248613	Minus	132738-132985, 134266-134425, 135034-135192, 135471-135608, 137345-137478, 138768-138912

10 TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES
Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Key: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Mean of melanoma AIs divided by the mean of normal tissue AIs, where the minimum value for the numerator and denominator was set to 1.0

20	Key	ExAccn	UnigenelD	Unigene Title	R1
	426555	NM 000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	376.61
	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	324.36
	430377	NM 001922	Hs.301865	dopachrome tautomerase (dopachrome delta	231.30
25	453344	BE349075	Hs.44571	ESTs	180.67
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	107.36
	417166	AA431323	Hs.42146	ESTs	97.76
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothesi	96.76
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	94.52
30	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	90.88
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	87.91
	443983	H04482	Hs.163724	ESTs	85.55
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	85.03
	419956	AL137939	Hs.40096	cadherin 19, type 2	84.27
35	423605	AF047826	Hs.129887	cadherin 19, type 2	80.88
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	80.64
	416975	NM 004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	79.09
	421633	AF121860	Hs.106260	sorting nexin 10	71.52
	442064	AI422867	Hs.88594	ESTs	69.88
40	418310	AA814100	Hs.86693	ESTs	67.94
	423799	AW026300	Hs.132906	19A24 protein	67.64
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	63.24
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	63.18
	432882	NM 013257	Hs.279696	serum/glucocorticoid regulated kinase-II	62.33
45	454088	AW062425		gb:CM0-CT0042-090899-018-01 CT0042 Homo	61.62
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	60.52
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	59.73
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	59.33
	450800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	59.00
50	441224	AU076964	Hs.7753	calumenin	58.27
	408418	AW963897	Hs.44743	KIAA1435 protein	56.79
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	56.45
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	56.29
55	420674	NM 000055	Hs.1327	butyrylcholinesterase	56.15
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	55.82
	420552	AK000492	Hs.98806	hypothetical protein	55.39
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	54.97
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	52.85
	410174	AA306007	Hs.59461	DKFZP434C245 protein	52.00
60	437396	BE140396	Hs.21621	hypothetical protein DKFZp762C076	51.97
	409557	BE182896	Hs.3686	ESTs	51.64
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	51.42
	414403	AW969551	Hs.76064	ribosomal protein L27a	50.58
	452958	AA883929	Hs.40527	ESTs	50.21
65	458997	AW937420		ESTs	49.97
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	49.85
	435905	AW997484	Hs.5003	KIAA0456 protein	48.76
	424800	AL035588	Hs.153203	MyoD family inhibitor	48.33
70	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	47.91
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!	47.45
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	46.52
	419465	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	45.79
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	45.52
	430066	AI929659	Hs.237825	signal recognition particle 72kD	45.45
75	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	44.58
	450447	AF212223	Hs.25010	hypothetical protein P15-2	43.36
	446019	AI362520		histone deacetylase 3	43.03
	430015	AW768399		ESTs	42.45
80	446880	AU811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	42.30
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	41.42
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	41.21
	411088	BE247593	Hs.145053	ESTs	40.94
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	40.66
	441590	AI623207	Hs.190537	ESTs	

	457465	AW301344	Hs.122908	DNA replication factor	39.91
	430280	AA361258	Hs.237858	interleukin 7 receptor	38.91
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	38.70
5	421282	AA286914	Hs.40782	ESTs	38.55
	448275	BE514434	Hs.20830	kinesin-like 2	38.00
	453912	AL121031		SWI/SNF related, matrix associated, acti	37.94
	414844	AA296874	Hs.77494	deoxyguanosine kinase	37.88
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	37.70
10	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	37.64
	409078	AW327515		ESTs	37.30
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	37.27
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	37.21
	445819	A1767472	Hs.146290	ESTs, Weakly similar to putative p150 [H	37.21
15	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	37.00
	433226	AW503733	Hs.9414	KIAA1488 protein	36.88
	445784	AJ253155	Hs.146065	ESTs	35.36
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	33.09
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	32.05
20	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	31.00
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	30.76
	429083	Y09397	Hs.227817	BCL2-related protein A1	30.73
	444670	H58373	Hs.332938	hypothetical protein MGC5370	28.45
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	27.62
25	433576	BE080715	Hs.161091	ESTs	27.42
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019 (CEM15)	27.36
	408962	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	26.66
	442757	A1739528	Hs.28345	ESTs	25.94
30	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	25.39
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	24.55
	438461	AW075485	Hs.285049	phosphoserine aminotransferase	22.48
	427581	NM 014788	Hs.179703	KIAA0129 gene product	22.15
	435256	AF193766	Hs.13872	cytokine-like protein C17	20.61
	409588	N27687	Hs.334334	transcription factor AP-2 alpha (activat	19.79
35	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	19.73
	417404	NM 007350	Hs.82101	pleckstrin homology-like domain, family	19.27
	458098	BE550224		metallothionein 1E (functional)	18.09
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	16.95
40	446054	AB014537	Hs.13604	KIAA0637 gene product	15.67
	432606	NM 002104	Hs.3056	granzyme K (serine protease, granzyme 3;	15.54
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	15.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	14.89
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	14.84
45	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	14.61
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	14.12
	421334	BE297729		gb:601175625F1 NIH_MGC_17 Homo sapiens c	13.94
	422423	AF283777	Hs.116481	CD72 antigen	13.77
50	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) nmb	13.33
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	12.76
	427536	BE277141	Hs.115803	gb:601178666F1 NIH_MGC_20 Homo sapiens c	12.76
	423198	M81933	Hs.1634	cell division cycle 25A	12.65
	430770	AA765694	Hs.123296	ESTs	12.58
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	12.09
55	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	11.46
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	10.58
	446950	AA305800	Hs.5672	hypothetical protein AF140225	10.04
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	9.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	9.88
	428799	AJ478619	Hs.104677	ESTs	9.56
60	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp5660134 (fr	9.03
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	9.01
	408393	AW015318	Hs.23165	ESTs	8.99
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	8.99
	450534	AJ570189	Hs.25132	KIAA0470 gene product	8.91
65	410101	AJ338045	Hs.203559	hypothetical protein FLJ12701	8.90
	417129	AJ381800	Hs.300684	calcitonin gene-related peptide-receptor	8.86
	453507	AF083217	Hs.33085	WD repeat domain 3	8.68
	442739	NM 007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	8.46
70	456249	AJ206144	Hs.82508	HRHFB2206 protein	8.38
	437786	BE142681	Hs.155573	polymerase (DNA directed), ela	8.35
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	8.20
	442711	AF151073	Hs.8645	hypothetical protein	8.14
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	7.96
	420208	BE276055	Hs.95972	silver (mouse homolog) like	7.88
75	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	7.79
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	7.66
	451239	H24302	Hs.23127	ESTs	7.50
	442426	AJ373062	Hs.332938	hypothetical protein MGC5370	7.40
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	7.39
80	439574	AJ469788		ESTs	7.13
	431360	NM 000427	Hs.251680	Ionitrin	7.12
	412438	AJ087928	Hs.110741	ESTs	6.96
	452882	AW972990	Hs.196270	folate transporter/carrier	6.87
	436581	AA725726	Hs.180213	ESTs	6.64

	431317	AA502682		gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	6.63
	443264	BE221477	Hs.132137	ESTs, Moderately similar to A47582 B-cel	6.58
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	6.53
5	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	6.52
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	6.50
	453878	AW964440	Hs.19025	DC32	6.48
	424148	BE242274	Hs.1741	integrin, beta 7	6.44
	407876	NM 004519	Hs.40866	potassium voltage-gated channel, KQT-Jik	6.44
10	409512	AW979187	Hs.293591	melanoma differentiation associated prot	6.39
	427951	AJ826125	Hs.43546	ESTs	6.32
	448664	AJ879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	6.03
	416640	BE262478	Hs.79404	neuron-specific protein	6.01
	446830	BE179030		Human DNA sequence from clone RPS-1174N9	5.98
15	452629	W02772	Hs.180178	Homo sapiens, clone IMAGE:3947276, mRNA,	5.93
	427390	AJ432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	5.73
	427853	AI569798	Hs.98260	ESTs	5.55
	434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	5.54
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	5.54
	428524	AA429772		ESTs	5.53
20	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	5.50
	418403	D86978	Hs.84790	KIAA0225 protein	5.50
	411524	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	5.47
	426158	NM 001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	5.40
25	443086	AW977125		sine oculis homeobox (Drosophila) homolo	5.38
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	5.38
	406843	AW196933	Hs.119598	ribosomal protein L3	5.36
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	5.35
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	5.23
30	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.23
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.09
	409264	NM 014937	Hs.52463	KIAA0866 protein	5.03
	414734	AA151712	Hs.82572	ESTs	5.01
	426759	AI590401	Hs.21213	ESTs	4.99
35	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	4.98
	428612	AA770001		ESTs	4.97
	413550	W03011	Hs.306881	MSTP043 protein	4.92
	447349	AI375546		gb:tc23d04.x1 Soares_tetal_fetus_Nb2HF8_	4.86
	403328			Target Exon	4.85
40	452840	AI097393	Hs.43481	hypothetical protein DKFZp564K192	4.83
	439310	AF086120	Hs.102793	ESTs	4.82
	451281	AI768965	Hs.292708	ESTs	4.82
	431183	NM 006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	4.81
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	4.74
45	435963	AF271212	Hs.322901	disrupter of silencing 10	4.67
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.66
	414770	BE257224		Homo sapiens, clone IMAGE:3873720, mRNA	4.66
	419628	H67546	Hs.49768	ESTs	4.64
	420258	AA477514	Hs.96247	translin-associated factor X	4.63
50	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	4.58
	420267	N37030	Hs.173337	ESTs	4.57
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	4.55
	432888	T86823		gb:yd81a08.s1 Soares fetal liver spleen	4.55
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	4.53
55	418340	NM 013286	Hs.84162	chromosome 3p21.1 gene sequence	4.50
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.44
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	4.42
	452036	NM 003966	Hs.27621	sema domain, seven thrombospondin repeat	4.41
	406903	K03121		gb:Human glyceradehyde-3-phosphate dehy	4.40
60	405451			dihydropyrimidinase-like 3	4.34
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.33
	450088	AW292933	Hs.254110	ESTs	4.31
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	4.31
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.30
65	451259	NM 006052	Hs.26146	Down syndrome critical region gene 3	4.29
	452548	AL050321	Hs.301532	CRP2 binding protein	4.28
	432195	AJ243669	Hs.8127	KIAA0144 gene product	4.24
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	4.22
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	4.19
70	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	4.18
	442092	AW578669		hypothetical protein FLJ12439	4.16
	424954	NM 000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	4.05
	427719	AI393122	Hs.134726	ESTs	4.04
	415310	R16313		gb:yf93h09.r1 Soares infant brain 1N1B H	4.04
75	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2	4.03
	427828	AI024471	Hs.98232	ESTs	3.93
	410079	U94362	Hs.58589	glycogenin 2	3.92
	420265	AA766209	Hs.88087	ESTs	3.92
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	3.90
80	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	3.89
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.88
	422150	AI867118		calpastatin	3.87
	429238	NM 002849	Hs.198288	protein tyrosine phosphatase, receptor t	3.86
	418827	BE327311	Hs.47166	HT021	3.84

5	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	3.82
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.81
	410235	AA082977		gb:zn07h10.r1 Stratagene hNT neuron (937	3.79
	408636	BE294925	Hs.46680	CGI-12 protein	3.78
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	3.76
	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (H/	3.74
	458215	AA928160		gb:zn086f10.s1 Soares_NFL_T_GBC_S1 Homo s	3.73
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	3.72
10	442643	U82756		PRP4/STK/WD splicing factor	3.70
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.70
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	3.67
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	3.64
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.64
15	418180	BE618087	Hs.83724	hypothetical protein MGC5466	3.62
	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.62
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HE	3.62
	412156	H29487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	3.61
	417426	NM 002291	Hs.82124	laminin, beta 1	3.61
20	407188	AA457592		gb:aa92f11.s1 Stratagene fetal retina 93	3.61
	426600	NM 003378	Hs.171014	VEGF nerve growth factor inducible	3.61
	440760	AK001145	Hs.284216	hypothetical protein FLJ10283	3.60
	448481	W15284	Hs.74832	ESTs	3.59
	414111	BE047679	Hs.152982	hypothetical protein FLJ13117	3.59
25	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.59
	409703	NM 006187	Hs.56009	Z-5'-oligoadenylate synthetase 3 (100 k	3.59
	406981	S71129		acetylcholinesterase (YT blood group)	3.59
	431586	AW971100	Hs.293189	ESTs	3.58
	415173	AW501735	Hs.180059	ESTs	3.57
30	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	3.57
	446126	AW085909		pleckstrin homology domain interacting p	3.57
	409305	AA070078		gb:zm60f05.r1 Stratagene fibroblast (937	3.57
	433867	AK000596	Hs.3618	hippocampal-like 1	3.56
	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	3.56
35	441412	AI393657	Hs.159750	ESTs	3.55
	416114	AI695549	Hs.183868	glucuronidase, beta	3.55
	454870	AW836081		gb:PM0-LT0019-090300-002-e11 LT0019 Homo	3.54
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.53
	444680	AI186671	Hs.22670	ESTs	3.51
40	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	3.51
	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.50
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	3.49
	437158	AW090198		KIAA1150 protein	3.48
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	3.47
45	440634	AA921767	Hs.132447	ESTs	3.47
	445652	AL117473	Hs.13036	DKFZP727A071 protein	3.46
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.43
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.43
	426141	C05886	Hs.293972	ESTs	3.40
50	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	3.40
	449209	BE616830	Hs.294145	ESTs	3.39
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.37
	416561	D87328	Hs.79375	holocarboxylase synthetase (biotin-prop	3.35
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	3.34
55	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	3.34
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	3.32
	417386	AL037228	Hs.82043	D123 gene product	3.32
	440999	AI951562	Hs.126370	ESTs, Weakly similar to CNE3_HUMAN COPIN	3.31
	407516	X64974		gb:H.sapiens mRNA HTPCRH02 for olfactory	3.31
60	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.31
	416902	AA375634	Hs.288974	hypothetical protein FLJ12528	3.28
	432878	BE386490	Hs.279663	Pirin	3.28
	443296	AI765286	Hs.313342	ESTs	3.27
	429954	AI918130	Hs.21374	ESTs	3.25
65	428044	AA093322	Hs.301404	RNA binding motif protein 3	3.25
	425317	AW205118	Hs.210546	interleukin 21 receptor	3.25
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.25
	432917	NM 014125	Hs.241517	PRO0327 protein	3.24
	447871	BE297946	Hs.239052	ESTs	3.24
70	414829	AA321568	Hs.77436	pleckstrin	3.24
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.23
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	3.22
	429530	AA454191	Hs.99362	Human DNA sequence from clone RP11-530N1	3.21
	445174	AV652850	Hs.172004	titin	3.19
75	459227	AW167599		ESTs	3.19
	439039	AI656707	Hs.48713	ESTs	3.15
	418803	U50079	Hs.88556	histone deacetylase 1	3.15
	420005	AW271106	Hs.133294	ESTs	3.15
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.14
80	452480	AI903526		gb:RC-BT031-090199-063 BT031 Homo sapien	3.14
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	3.14
	410678	BE540516	Hs.293732	hypothetical protein MGC3195	3.14
	458664	AI300427		gb:qo18h07.x1 NCI_CGAP_Lu5 Homo sapiens	3.13
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.13

	430441	BE398091		desmoplakin (DPI, DPII)	3.12
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	3.12
	425606	U52112	Hs.158331	renin-binding protein	3.11
5	432978	AF126743	Hs.279884	DNAJ domain-containing	3.11
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.10
	446627	AJ973016	Hs.15725	hypothetical protein SBB148	3.10
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.09
	417211	T97617	Hs.269092	ESTs	3.08
10	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.08
	448752	AA593867	Hs.300842	KIAA1608 protein	3.07
	416355	H49875	Hs.268906	ESTs	3.07
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	3.07
	410321	Y12860	Hs.62245	solute carrier family 25 (mitochondrial	3.07
15	411395	AA889673	Hs.7542	KIAA1802 protein	3.07
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.06
	432343	NM 002960	Hs.2961	S100 calcium-binding protein A3	3.06
	457991	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	3.05
	433201	AB040896	Hs.21104	KIAA1463 protein	3.03
20	416178	AB808527	Hs.192822	serologically defined breast cancer anti	3.02
	411975	AJ916058	Hs.144583	ESTs	3.01
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	3.00
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.00
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	2.94
25	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	2.93
	453256	AI565587	Hs.32556	KIAA0379 protein	2.81
	436856	AI469355	Hs.127310	ESTs	2.75
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.60
	408209	NM 004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.59
30	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.55
	415314	N88802	Hs.5422	glycoprotein M6B	2.51
	434276	AF123659	Hs.93505	leucine zipper, putative tumor suppresso	2.50
	424085	NM 002914	Hs.139226	replication factor C (activator 1) 2 (40	2.48
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.48
35	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.43
	444809	BE207568	Hs.208219	oculospanin	2.39
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	2.39
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.37
	411358	R47479	Hs.94761	KIAA1691 protein	2.35
40	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	2.34
	426312	AF028939	Hs.181874	interferon-induced protein with tetratri	2.29
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.27
	418661	NM 001949	Hs.1189	E2F transcription factor 3	2.24
45	459373	BE408266	Hs.301406	hypothetical protein PP3501	2.21
	417437	U52682	Hs.82132	interferon regulatory factor 4	2.21
	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.18
	450690	AA296696	Hs.333418	FXD domain-containing ion transport reg	2.15
	432800	BE391046	Hs.278962	AIM-1 protein	2.15
	421773	W69233	Hs.112457	ESTs	2.09
50	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	2.03
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.02
	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.01
	443950	NM 001425	Hs.9999	epithelial membrane protein 3	2.01
	451537	R56631	Hs.26550	retinoid X receptor, gamma	2.00
55	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	1.96
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.94
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.91
	453779	N35187	Hs.43388	28kD interferon responsive protein	1.86
	453107	NM 016113	Hs.279746	vanilloid receptor-like protein 1	1.86
60	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.86
	408561	AI308037	Hs.84120	hypothetical protein MGC13016	1.84
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	1.83
	406016			Target Exon	1.82
	446644	NM 003272	Hs.15791	transmembrane 7 superfamily member 1 (up	1.81
65	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.77
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	1.77
	447604	AW089933	Hs.301342	hypothetical protein MGC4342	1.76
	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.74
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.70
70	416091	AF295370	Hs.283082	defensin, beta 3	1.69
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	1.67
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	1.67
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	1.67
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.67
75	448258	BE386983	Hs.343214	hypothetical protein FLJ20396	1.66
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.66
	425262	D87119	Hs.155418	GS3955 protein	1.65
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64
80	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.63
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.62
	441859	AW194364	Hs.94814	interleukin-4 induced gene-1 protein (FI	1.60
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.58
	412939	AW411491	Hs.75069	eukaryotic translation elongation factor	1.58
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.56

5	412856	BE386745	Hs.74631	basigin (OK blood group)	1.56
	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.54
	409614	BE297412	Hs.55189	hypothetical protein	1.53
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	1.53
	423397	NM 001838	Hs.1652	chemokine (C-C motif) receptor 7	1.49
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.48
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	1.46
	446755	AW451473	Hs.16134	serine/threonine kinase 10	1.46
10	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.46
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.45
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.44
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.43
	436378	AJ227874	Hs.99244	ESTs	1.42
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.42
15	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.42
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.42
	429359	W08482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.42
	427634	AI399745	Hs.18449	hypothetical protein MGC10820	1.40
20	403409			NM_005929:Homo sapiens antigen p97 (meta	1.40
	434262	AF121858	Hs.12169	sorting nexin 8	1.34
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.32
	427730	AW250549	Hs.180577	granulin	1.32
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	1.31
25	450395	BE048545	Hs.161757	ESTs	1.30
	413291	NM 006278	Hs.75268	sialyltransferase 4C (beta-galactosidase	1.26
	442609	AL020996	Hs.8518	selenoprotein N	1.24
	416929	N20535		melastatin 1	1.21
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.21
30	454478	AW805749		superoxide dismutase 2, mitochondrial	1.20
	437723	AI672731	Hs.13256	ESTs	1.18
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.08

TABLE 48B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

40	Pkey	CAT Number	Accession
	430540	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
45			AW062425 AW062411
	454088	1007145_1	BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396
50	458997	11847_4	AW889004 AW937420 AA137082 AA013374 BG619478 BG401839
	446019	658727_1	AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
	430015	713_2	AW362225 AW362228 AL119827
55			BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
60	453912	32562_3	BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893
			AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87967
65			AW327515 AW327774 AW327571
	409078	744783_1	AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224
70	458098	23945_1	AA832519 AF086393 AV733386 BE465409 N29245 W07677 BE503548 H18151 AA461301 W79223 W74510 AI090689 AL600773 AL600781 N46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553
			BG758353 AA287401 BE295646 AL040858
75	421334	267495_1	BG532820 AW246001 AI469788 AI350090 AI446788 BE549330 W84862 AA837988
80	439574	689966_1	AW970601 AW613399 AA503435 AA502682 N91138
	431317	997174_1	

446830	41421_1	BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558 T35055 AW370623 AA339232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237 T25074 C01285 BI489433
5	428524 1382184_1 411524 1089114_1 443086 25669_4 428612 1383189_1 447349 1063443_1 414770 41721_1	AI208080 AA442862 AA429772 AW850587 AW850589 AW850318 AW850303 BE896316 BG819393 AA187888 AW753122 AA770001 AA431112 AA432126 BE743847 AW809603 BM469626 AI375546 AK056926 BG473673 BG482256 AI135566 AW419211 BF949370 AI120313 AV703730 H82569 BG012696 R27084 AA304583 BM452908 BF516419 BF515687 BG036572 BG696740 AW953552 AW859437 AA306038 AI754064 AA608729 AA664163 H65119 AW272606 BF942099 AW130458 BI089467 BG821499 AA152403 BF310450 BF314240 BG830310 BF803223 BG764269 BE542645 BE259142 R26953 BE257224 BG475461 BF677821 R33048
10	432888 2155976_1 425913 4123_2	T86823 AA570737 AI821425 AA569589 AI732232 AV703649 AW959818 AI582119 AI523459 AI674473 AW663543 AA825476 AI935231 BF742805 AA426156 AI253626 AA846477 AI024230 BF221780 AI493027 AW006841 AA814699 H99650 AI088977 AA442691 AI783526 BF207915 AI752847 AA782635 AI978980 AA788634 BG119454 BF678528 AI627829 BG993975 AV701283
15	442092 22756_2 415310 1869807_1 422150 782_1	BM449821 BM069895 BM023170 AW025563 BG152606 BM023452 AI862106 BG959957 R16313 Z45351 R14838 F05290 R14821 R16277 BI086421 BF059136 AW003898 BF446659 AI632891 AI628067 AI703179 AI961149 BF111022 AW614154 BE674215 AA687350 AA779426 BF591963 AW243344 AI356530 AI492508 AI694049 AI090422 AA465307 AI273387 BE674625 AW271971 AA699153 AW468593 AA984014 AI817491 AA970258 AI914450 AI018697 AW577591 AW577616 AA382101 AW954455 AI867266 AI707995 AI337384 BF208406 BF037100 BF223433 BF195517 BE673984 BF224124 BE813387 BG036579 BI553906 AA304995 AW361269 AW754160 AW361276 AW361271 AI867118 AW805555 AW361284 AW954458 AW585551 BG681507 H79011 AW205696 AW134957 AA747667 AW753296 BF939060 AW958549 BF910827 BG573750 BG168639
20	410235 2930253_1 458215 540112_3 442643 2736_1	AA082977 AA082955 BE176902 BE177058 BC001588 BC007424 AF016369 NM_004697 BI756186 BE257019 BG500792 BI862776 AI121371 BG574833 AA703250 AA179511 AW052006 AI280150 AI914000 AI358319 AI081204 AI082594 AA92449 AI470821 AI655744 AW237529 AA678858 AI984430 BF433055 BE467594 BE467573 AA035630 AI289987 AI184802 AI681391 AW592416 AI138377 AI139266 AA961714 AI800163 AA418751 AW451928 AA668676 AI273444 AA494387 BE046912 AI276555 BF196021 AA700055 AA609305 AA772596 AI635758 AI635749 H95459 AW610290 BE464994 AA527136 BF374802 AI800175 AW195227 AI189676 BF802049 AI136332 AL554911 AL538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AI567522 AI745257 AW388641 AW301265 AI141144 AW029280 AU149362 AU152328 AA418960 AL121009 AI890398 AL528748 H13050 T47086 BI000575 BF334914 BF109611 R44450 H13259 T47087 AW388646 BF305834 AL577515 BM041600 BE889299 BF239768
25	446126 610_2	BF946219 BF946218 BF851494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA336407 AA337222 AA319240 BI026817 BI027058 AL536880 AI693827 AA651730 AI701013 BM068789 AW339506 AA293021 BF891108 AI458885 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129587 N52070 AW172361 AA052951 AW085909 AI000008 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008 H40784 BF891112 BE708029 AW043567 AA056762
30	409305 109927_1 454870 2170_9 437158 59575_1	AA071475 AA112236 AA070648 AA071243 AA081725 AA085187 AA070078 AW836081 BF854404 AW578594 AW578581 BF507971 AW196760 AA779923 AA707233 AI655913 AA948295 AW089222 AW291883 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
35	408304 645409_1	AW810279 BE146684 AW810193 AW810515 AW178835 AW810516 BE146689 AW178842 BE146693 BE146694 AW810208 AW810258 AW810447 AW810443 AW810330 AW810211 AW810328 AW810327 AW810288 AW810265 AW810257 AW810263 AW810567 AW178838 AW810323 AW810358 AW810281 AW810321 AW178837 AW810635 BE062400 AW810198 AW810325 AW810513 BE062434 BE146679 AW810441 AW846649 AW810536 AW178857 AW810185 BE146653 AW810636 AW810322 BE146674 AW810359 AW810293 AW810472 AW178852 AW810356 AW810514 AW810289 BE146652 AW810566
40	459227 639802_1 452480 3144986_1 458664 2139033_1 430441 1438_6	AW167599 AI971179 AI934948 AI903574 AI903572 AI903526 AI903571 BF432937 R07053 AI300427 W57876 BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080 R00283 C15236 AW327776 D80759
45	410600 497855_1 452203 2630_1	BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE459623 AI335824 AW408712 BM149172 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569894 AW073296 AI361433 AA554644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AI556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
50	416929 14596_3 454478 4273_16	BC017849 BC005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
55	TABLE 48C: Pkey: Ref: Strand: Nt_position:	Unique number corresponding to an Eos probe set Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.
60	Pkey Ref Strand Nt_position	Pkey Ref Strand Nt_position 403328 8469086 Minus 120428-120703 405451 7622517 Minus 145949-146227 406016 8272661 Plus 41341-41940 403409 9438598 Plus 6860-7054,12573-12771
65		
70		
75		
80		

TABLE 49A: ABOUT 1127 GENES UPREGULATED IN PRIMARY MELANOMA AND/OR MELANOMA METASTASES RELATIVE TO NORMAL BODY TISSUES

Table 49A lists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigeneID:	Unigene number					
	Unigene Title:	Unigene gene title					
	R1:	90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs					
10	R2:	90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator					
	R3:	90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of heart, liver, lung, and kidney AIs					
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
15	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.05	11.83	14.05
	426555	NM_000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	13.15	13.27	13.15
	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	11.77	7.43	11.77
	420208	BE276055	Hs.95972	silver (mouse homolog) like	10.53	19.95	10.27
	431360	NM_000427	Hs.251680	loricrin	9.78	7.09	0.89
20	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	9.40	7.20	8.84
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.03	10.27	12.84
	419628	H67546	Hs.49768	ESTs	7.56	8.92	6.49
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	7.52	5.47	16.47
	430686	NM_001942	Hs.2633	desmoglein 1	6.06	4.13	3.31
25	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	5.86	9.22	0.77
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.84	3.46	5.84
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.82	3.94	5.82
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.81	3.33	6.79
	453344	BE349075	Hs.44571	ESTs	5.78	3.07	5.98
30	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	5.60	3.92	5.60
	402075			ENSP00000251056*-Plasma membrane calcium	5.12	4.22	5.12
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.09	3.33	4.14
	420602	AF060877	Hs.99236	regulator of G-protein signaling 20	5.06	5.78	5.06
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	5.04	6.77	9.42
35	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.03	3.06	5.03
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	4.93	8.13	5.41
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.78	2.93	4.78
	408962	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	4.75	3.28	5.30
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.70	3.11	4.70
40	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	2.27	4.68
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.65	3.21	3.31
	417166	AA431323	Hs.42146	ESTs	4.56	5.23	4.56
	421773	W69233	Hs.112457	ESTs	4.52	11.11	0.96
	442711	AF151073	Hs.8645	hypothetical protein	4.37	3.70	4.30
45	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.37	3.08	6.75
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	4.32	2.61	4.32
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.31	3.13	4.31
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.28	2.89	2.17
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.18	2.68	5.92
50	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specifi	4.16	2.57	4.16
	433447	U29195	Hs.3281	neuronal pentraxin II	4.15	2.26	6.46
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	4.10	4.04	4.64
	408380	AF123050	Hs.44532	diubiquitin	4.02	2.46	5.33
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.02	3.48	3.19
55	421633	AF121850	Hs.106260	sorting nexin 10	4.01	2.61	3.36
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.96	2.68	3.96
	417355	D13168	Hs.82002	endothelin receptor type B	3.95	2.46	3.66
	420267	N37030	Hs.173337	ESTs	3.88	3.87	3.88
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	3.81	3.04	7.94
60	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.79	2.23	3.79
	405451			dihydropyrimidinase-like 3	3.78	3.74	4.06
	449078	AK001256	Hs.22975	KIAA1576 protein	3.76	2.83	3.76
	423799	AW026300	Hs.132906	19A24 protein	3.75	2.36	3.75
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.73	2.59	6.97
65	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	3.72	2.15	3.92
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.69	4.17	1.18
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.64	2.08	3.64
	422423	AF283777	Hs.116481	CD72 antigen	3.64	2.94	3.64
	419956	AL137939	Hs.40096	cadherin 19, type 2	3.56	2.22	4.68
70	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	3.55	2.96	4.70
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.54	1.96	3.54
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.53	2.18	3.27
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.48	2.83	11.00
	449722	BE280074	Hs.23960	cyclin B1	3.48	2.10	4.64
75	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.47	3.90	4.98
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.45	2.38	3.45
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.44	3.83	2.09
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	3.43	2.39	3.43
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wil	3.41	4.33	5.41
80	423605	AF047826	Hs.129887	cadherin 19, type 2	3.40	1.97	4.06
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.38	2.77	5.46
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.36	2.41	3.36
	430770	AA765694	Hs.123296	ESTs	3.36	2.08	3.83
	445784	AI253155	Hs.146065	ESTs	3.32	2.02	3.80

5	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.32	1.87	3.76
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.31	2.10	3.31
	441224	AU076964	Hs.7753	calumenin	3.28	2.04	3.28
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.26	2.43	3.56
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.24	2.94	2.85
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	3.23	1.84	3.87
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.22	3.10	3.13
	442757	AI739528	Hs.28345	ESTs	3.22	3.41	1.45
10	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	3.18	2.50	3.18
	432874	W94322	Hs.279651	melanoma inhibitory activity	3.18	5.31	4.55
	412561	NM_002286	Hs.74011	lymphocyte activation gene 3	3.17	3.09	4.28
	443983	H04482	Hs.163724	ESTs	3.16	2.21	3.16
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.14	1.74	3.25
15	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.14	2.07	3.33
	422424	AI186431	Hs.296638	prostate differentiation factor	3.10	3.20	2.15
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.10	2.23	3.10
	401747			Homo sapiens keratin 17 (KRT17)	3.10	2.10	3.02
20	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.08	3.08	4.00
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.07	3.16	3.07
	432878	BE386490	Hs.279663	Pirin	3.06	2.92	4.20
	401454			NM_014226: Homo sapiens renal tumor anti	3.05	1.96	3.05
	410079	U94362	Hs.58589	glycogenin 2	3.01	2.26	3.27
25	426501	AW043782	Hs.293616	ESTs	3.01	2.00	3.68
	418310	AA814100	Hs.86693	ESTs	3.00	2.35	6.76
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.96	2.31	3.78
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	2.96	2.49	4.74
	408418	AW963897	Hs.44743	KIAA1435 protein	2.94	1.80	2.94
30	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.93	1.74	2.93
	416640	BE262478	Hs.79404	neuron-specific protein	2.93	2.78	3.09
	443264	BE221477	Hs.132137	ESTs, Moderately similar to A47582 B-cel	2.92	2.35	4.27
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.91	2.83	3.84
	405545			Target Exon	2.90	2.44	2.90
35	451537	R56631	Hs.26550	retinoid X receptor, gamma	2.90	4.09	3.40
	439926	AW014875	Hs.137007	ESTs	2.90	2.43	2.90
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.89	3.22	1.44
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.89	3.90	2.89
	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.89	4.40	3.05
40	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	2.88	2.36	4.54
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	2.86	3.23	1.95
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.84	1.84	2.84
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	2.84	1.80	2.92
	424153	AA451737	Hs.141496	MAGE-like 2	2.84	2.26	2.84
45	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.81	2.91	0.83
	431317	AA502682		gb:mg23d01.s1 NCI_CGAP_Ov2 Homo sapiens	2.81	2.17	2.96
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.80	2.06	4.10
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	2.79	1.85	2.42
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.78	2.34	6.53
50	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	2.78	3.75	4.01
	427951	AI826125	Hs.43546	ESTs	2.78	1.99	2.70
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.77	2.28	2.77
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.75	1.98	2.75
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.74	3.18	3.60
55	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.72	2.24	2.72
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.72	2.31	3.59
	420552	AK000492	Hs.98806	hypothetical protein	2.72	1.85	2.72
	409103	AF251237	Hs.112208	XAGE-1 protein	2.72	2.18	2.72
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.71	2.20	4.48
60	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.71	5.74	2.62
	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.71	3.37	3.32
	419098	AA234041	Hs.87271	ESTs	2.70	3.53	1.35
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	2.69	2.48	2.69
	418067	AI127958	Hs.83393	cystatin E/M	2.68	3.04	0.56
65	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.67	2.36	3.16
	437723	AI672731	Hs.13256	ESTs	2.66	2.16	2.66
	411252	AB018549	Hs.69328	MD-2 protein	2.66	1.81	2.66
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.66	2.43	3.92
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	2.65	3.71	2.80
70	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.64	1.85	4.72
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.64	2.07	2.64
	444371	BE540274	Hs.239	forkhead box M1	2.64	2.82	4.46
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.63	1.81	2.95
	439310	AF086120	Hs.102793	ESTs	2.62	2.38	10.12
75	420218	AW958037		ribosomal protein L4	2.62	2.80	2.62
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.60	3.27	2.12
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.60	2.67	3.03
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.59	3.22	2.59
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.58	1.69	2.05
	444809	BE207568	Hs.208219	oculopainin	2.58	2.77	2.88
80	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.58	1.83	2.58
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.55	3.70	3.28
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.55	2.14	1.62
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.55	2.07	2.55
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	2.54	2.17	4.01

5	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	2.53	1.68	3.16
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.53	2.74	3.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.52	1.62	3.17
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.51	2.67	1.88
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	2.51	2.08	4.57
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattractant)	2.51	1.74	2.68
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.51	1.67	2.24
	432800	BE391046	Hs.278962	AIM-1 protein	2.51	5.55	2.42
10	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.50	1.95	2.41
	410326	AI368909	Hs.47650	ESTs	2.50	2.85	2.63
	452833	BE559681	Hs.30736	KIAA0124 protein	2.50	3.14	3.07
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.49	3.38	2.91
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.48	1.85	2.70
15	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.48	2.33	2.99
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.47	1.88	4.14
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.46	2.00	0.98
	401780			NM_005557: Homo sapiens keratin 16 (foca	2.44	2.30	1.39
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.44	1.57	0.88
20	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.42	1.91	2.56
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.42	2.31	4.27
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.41	2.73	2.41
	415752	BE314524	Hs.78776	putative transmembrane protein	2.41	2.07	3.41
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	2.41	2.34	3.26
25	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.40	1.65	2.40
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.40	2.18	8.13
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.40	2.88	2.46
	403328			Target Exon	2.39	2.00	1.95
	427540	R12014	Hs.20976	ESTs	2.39	1.73	3.24
30	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.39	1.96	2.39
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.38	2.45	2.65
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.38	1.85	2.38
	430066	AI929659	Hs.237825	signal recognition particle 72kD	2.38	1.60	2.79
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.37	1.99	6.23
35	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.37	1.72	3.24
	458997	AW937420		ESTs	2.37	1.57	3.27
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	2.35	1.90	2.39
	408838	AI669535	Hs.40369	ESTs	2.35	1.59	2.71
	448275	BE514434	Hs.20830	kinesin-like 2	2.35	2.19	2.35
40	424148	BE242274	Hs.1741	integrin, beta 7	2.35	1.89	3.07
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.35	1.65	2.35
	409105	AW467539	Hs.255877	ESTs	2.35	2.50	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	2.34	2.12	2.90
	425606	U52112	Hs.158331	renin-binding protein	2.34	2.69	1.69
45	433576	BE080715	Hs.161091	ESTs	2.34	3.74	2.34
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	2.34	2.08	4.48
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	2.33	2.43	2.66
	436614	AW104388	Hs.149091	ESTs	2.33	3.37	2.33
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	2.33	1.67	4.28
50	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.33	1.58	0.40
	430015	AW768399		ESTs	2.33	1.76	2.33
	421282	AA286914	Hs.40782	ESTs	2.32	1.65	2.49
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	2.32	2.16	1.48
	432540	AI821517	Hs.105866	ESTs	2.32	1.58	2.35
55	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	2.32	2.46	9.99
	414829	AA321568	Hs.77436	pleckstrin	2.32	1.91	2.32
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.31	1.63	2.31
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.31	2.79	2.41
	428819	AL135623	Hs.193914	KIAA0575 gene product	2.30	1.60	2.95
60	409512	AW979187	Hs.293591	melanoma differentiation associated prot	2.30	1.95	3.66
	425231	AA527161		ESTs	2.28	1.96	2.36
	416091	AF295370	Hs.283082	defensin, beta 3	2.28	2.76	2.18
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.27	2.88	2.46
	427719	AI393122	Hs.134726	ESTs	2.27	1.88	2.29
65	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	2.27	2.16	4.09
	457465	AW301344	Hs.122908	DNA replication factor	2.26	2.23	2.26
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.26	2.13	3.16
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.26	1.75	2.84
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.26	3.38	2.56
70	449317	AW293413	Hs.132906	19A24 protein	2.26	2.04	2.73
	429922	Z97630	Hs.226117	H1 histone family, member D	2.26	1.59	2.38
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Ra	2.25	1.86	3.07
	425388	AA329384	Hs.156110	immunoglobulin kappa constant	2.25	1.91	2.25
	417282	AA195203		RAB5C, member RAS oncogene family	2.25	2.23	3.20
75	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.24	2.69	2.78
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	2.23	2.20	2.51
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.23	4.59	2.47
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.23	3.62	0.85
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.22	1.60	1.69
80	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.22	5.53	2.46
	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	2.21	2.40	4.37
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.21	2.06	2.32
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA sequence	2.20	2.69	2.91
	417366	BE185289	Hs.1076	small proline-rich protein 1B (corniflin)	2.20	2.26	3.79

5	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	2.20	1.96	2.44
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.20	3.28	2.99
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	2.20	1.98	3.40
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.20	1.44	2.31
	409354	N68188	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H	2.18	2.44	2.70
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.18	1.75	2.70
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.18	1.55	2.44
10	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	2.18	1.43	2.37
	452194	AJ694413		Ubiquitin-like protein FAT107?? - diubiq	2.17	3.07	1.76
	417933	X02308	Hs.82962	thymidylate synthetase	2.17	1.86	4.15
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.17	2.38	2.91
	425317	AW205118	Hs.210546	interleukin 21 receptor	2.17	2.02	2.22
15	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.16	1.87	2.49
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.16	1.55	2.26
	452958	AA883929	Hs.40527	ESTs	2.15	1.56	2.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	2.15	1.76	2.97
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.15	1.85	2.74
20	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	2.14	1.88	4.99
	451952	AL120173	Hs.301663	ESTs	2.13	2.08	2.13
	450534	AI570189	Hs.25132	KIAA0470 gene product	2.12	1.67	3.41
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	2.12	1.75	2.27
	432734	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.12	2.14	2.49
25	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.12	2.46	2.67
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	2.12	2.16	2.82
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	2.11	2.01	0.68
	447178	AW594641	Hs.192417	ESTs	2.10	2.52	2.10
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	2.10	1.52	4.01
30	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	2.10	1.53	2.10
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	2.10	1.55	2.41
	453256	AI565587	Hs.32556	KIAA0379 protein	2.09	2.13	2.89
	405547			NM_018833: Homo sapiens transporter 2, A	2.09	2.61	2.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	2.09	1.76	4.10
35	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.09	3.91	2.38
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.09	1.62	1.28
	417576	AA339449	Hs.82285	phosphonobiosylglycinamide formyltransfer	2.08	1.86	2.08
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	2.08	2.83	2.08
	423198	M81933	Hs.1634	cell division cycle 25A	2.08	1.66	2.23
40	433068	NM_006456	Hs.288215	sialyltransferase	2.08	1.94	2.60
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.07	1.91	3.62
	452392	L20815	Hs.507	corneodesmosin	2.07	3.96	0.97
	403532			NM_024638: Homo sapiens hypothetical prot	2.07	1.88	2.68
	439859	AW292872	Hs.124554	ESTs	2.07	1.72	2.22
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.07	2.26	4.22
	442643	U82756		PRP4/STK4WD splicing factor	2.07	1.74	1.90
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	2.06	2.08	1.43
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.06	2.12	2.06
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.06	1.65	2.91
50	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.06	1.97	2.42
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	2.05	2.44	2.05
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.05	2.37	2.05
	450325	AJ935962	Hs.91973	ESTs	2.05	1.67	1.82
	424090	X99699	Hs.139262	XIAP associated factor-1	2.05	1.56	1.99
55	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	2.04	1.52	2.07
	413794	AF234532	Hs.61638	myosin X	2.04	2.02	2.11
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.04	4.57	1.64
	425580	L11144	Hs.1907	galanin	2.04	1.67	2.26
	420052	AA418850	Hs.44410	ESTs	2.03	1.90	2.21
60	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	2.03	1.53	2.31
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.02	1.73	2.02
	426759	AI590401	Hs.21213	ESTs	2.02	1.86	5.47
	432435	BE218886	Hs.282070	ESTs	2.02	1.39	1.67
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	2.02	1.57	2.02
65	421574	AJ000152	Hs.105924	defensin, beta 2	2.02	2.22	2.15
	411358	R47479	Hs.94761	KIAA1691 protein	2.01	2.55	1.75
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.01	2.58	2.39
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.01	1.50	2.01
	400750			Target Exon	2.01	1.73	2.09
70	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.01	2.42	0.78
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.01	1.65	1.72
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.01	1.61	1.03
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.00	2.11	2.33
	436200	R51386	Hs.124881	ESTs	2.00	1.89	2.24
75	414175	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	1.99	1.50	1.99
	420005	AW271106	Hs.133294	ESTs	1.99	2.03	2.59
	417848	AA206581	Hs.116586	ESTs, Weakly similar to JCS314 CDC28cdc	1.99	1.42	2.17
	435545	AA687415	Hs.28107	ESTs	1.99	1.89	1.99
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.99	2.23	3.44
80	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.99	2.05	0.32
	453905	NM_002314	Hs.35566	LIM domain kinase 1	1.98	2.48	2.79
	453884	AA355925	Hs.36232	KIAA0186 gene product	1.98	1.93	1.98
	459373	BE408266	Hs.301406	hypothetical protein PP3501	1.98	2.22	1.91
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.98	1.68	1.98
	452840	AJ097393	Hs.43481	hypothetical protein DKFZp564K192	1.98	1.67	2.18

5	409178	BE393948	Hs.50915	kallikrein 5	1.98	3.76	1.37
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ001111 protein,	1.98	1.90	2.63
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	1.97	1.88	1.23
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	1.97	1.95	5.55
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	1.97	1.77	1.97
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.97	1.73	3.89
	408561	AI308037	Hs.84120	hypothetical protein MGC13016	1.97	2.89	2.08
	421855	M24470	Hs.1435	guanosine monophosphate reductase	1.97	1.95	2.65
	405506			Target Exon	1.96	1.72	2.27
10	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	1.96	1.74	2.35
	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	1.95	2.09	2.77
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.95	1.66	2.58
	453931	AL121278	Hs.25144	ESTs	1.95	2.38	1.95
15	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	1.95	1.63	2.82
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	1.94	2.02	1.35
	442064	AI422867	Hs.88594	ESTs	1.94	1.49	2.21
	400533			ENSP00000209376::PRED65 protein (Fragmen	1.94	1.69	1.94
	448752	AA593867	Hs.300842	KIAA1608 protein	1.94	1.71	2.40
20	408636	BE294925	Hs.46860	CGI-12 protein	1.94	1.69	2.93
	439569	AW602166	Hs.222399	CEGP1 protein	1.93	1.62	3.21
	405779			NM_005367:Homo sapiens melanoma antigen,	1.93	1.83	1.99
	444670	H58373	Hs.332938	hypothetical protein MGC5370	1.93	1.97	1.93
	446950	AA305800	Hs.5672	hypothetical protein AF140225	1.93	1.56	1.61
25	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	1.93	2.12	2.63
	409098	AA132672	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	1.92	2.12	2.51
	413916	N49813	Hs.75615	apolipoprotein C-II	1.92	1.98	0.22
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	1.92	1.65	6.39
	402994			NM_002463::Homo sapiens myxovirus (influ	1.92	2.45	1.89
30	425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.92	2.69	2.30
	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.92	2.10	2.93
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.91	1.57	1.91
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	1.91	1.44	1.68
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.90	1.52	1.14
35	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.90	2.16	1.21
	440773	AA352702	Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	1.90	1.84	2.07
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.90	4.26	1.70
	426470	AA528794	Hs.128644	ESTs	1.90	2.69	2.04
	409557	BE182896	Hs.3686	ESTs	1.90	2.01	1.90
40	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	1.90	2.49	2.52
	428125	AA393071	Hs.182579	leucine aminopeptidase	1.89	1.89	1.49
	427634	AI399745	Hs.18449	hypothetical protein MGC10820	1.89	3.59	1.71
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	1.89	1.67	1.45
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	1.89	2.55	1.39
45	448243	AW369771		integrin, beta 8	1.89	1.96	1.89
	416114	AI695549	Hs.183868	glucuronidase, beta	1.89	1.70	1.10
	425935	Z98200	Hs.163724	HSPC019 protein	1.88	1.86	2.04
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.88	4.16	1.78
50	430171	AF086289	Hs.234766	skin-specific protein	1.87	2.70	0.75
	407366	AF026942	Hs.17518	gb.Homo sapiens cig33 mRNA, partial sequ	1.87	2.25	1.87
	454294	AB000734	Hs.50640	JAK binding protein	1.87	1.98	1.46
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.87	2.73	1.71
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	1.87	1.79	2.72
	401781			Target Exon	1.87	1.88	1.16
55	440590	AI863446	Hs.266308	mosaic serine protease	1.86	1.79	1.13
	428450	NM_014791	Hs.184339	KIAA0175 gene product	1.86	1.72	4.39
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	1.86	1.81	1.86
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.86	1.57	1.86
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.85	1.71	5.82
60	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.85	2.75	1.84
	430441	BE398091		desmoplakin (DPI, DPII)	1.85	1.80	2.79
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	1.85	1.80	1.86
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	1.85	1.94	1.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.85	1.72	2.52
65	414737	AI160386	Hs.125087	ESTs	1.84	1.90	1.84
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	1.84	1.57	1.84
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	1.84	1.41	0.12
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.84	1.70	3.15
	428515	AF030339	Hs.286229	plexin C1	1.84	1.66	1.84
70	427914	AA417350	Hs.20575	ESTs	1.84	2.32	2.17
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	1.84	1.55	1.84
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.83	3.20	1.75
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	1.83	1.62	1.47
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.83	1.58	2.11
75	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	1.83	1.73	2.18
	433029	NM_014322	Hs.279926	opsin 3 (encephalopsin)	1.83	1.96	1.83
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.83	1.61	2.46
	426890	AA393167	Hs.41294	ESTs	1.82	2.44	1.82
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.82	2.24	2.01
80	441859	AW194364	Hs.94814	ESTs, Weakly similar to FIG1 MOUSE FIG-1	1.82	2.72	2.16
	437435	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	1.82	1.50	1.82
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	1.82	2.52	1.76
	420674	NM_000055	Hs.1327	butyrylcholinesterase	1.82	1.43	0.68
	439219	N33883	Hs.41322	ESTs	1.82	1.88	2.43

5	432810	AA863400		ESTs	1.82	1.43	1.82
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	1.82	1.98	1.82
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	1.82	1.63	1.82
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.82	2.80	2.18
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	1.82	2.28	2.00
	424755	AB033094	Hs.152925	KIAA1268 protein	1.82	1.85	1.62
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	1.82	1.74	5.18
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.81	1.87	0.80
10	417105	X60992	Hs.81226	CD6 antigen	1.81	1.88	2.03
	423961	D13666	Hs.136348	periostin (OSF-2os)	1.81	1.73	2.45
	446019	AI362520		histone deacetylase 3	1.81	1.39	2.24
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.81	3.05	1.58
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fs, clone C	1.80	2.00	1.78
15	453684	AK001922	Hs.34578	alpha2,3-sialyltransferase	1.80	1.98	1.22
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.80	1.56	1.71
	453779	N35187	Hs.43388	28kD interferon responsive protein	1.80	2.42	2.04
	434706	AI656291	Hs.116394	ESTs	1.80	1.58	1.80
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	1.80	1.79	2.51
20	453331	AI240665		ESTs	1.79	1.43	2.33
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.79	1.46	4.46
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	1.79	2.30	1.79
	453507	AF083217	Hs.33085	WD repeat domain 3	1.79	1.49	1.51
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.79	1.57	2.00
25	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.79	2.26	2.22
	406672	M26041	Hs.198253	major histocompatibility complex, class	1.79	1.76	1.78
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	1.79	1.43	3.32
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	1.78	1.66	1.29
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	1.78	1.73	2.35
30	436378	AJ227874	Hs.99244	ESTs	1.78	1.84	1.78
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.78	1.66	3.67
	421948	L42583	Hs.334309	keratin 6A	1.78	1.74	3.00
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.77	2.27	2.13
	437317	AA748613	Hs.311977	ESTs, Highly similar to SW/ISNF related,	1.77	1.98	2.32
35	427318	AF186081	Hs.175783	zinc transporter	1.77	1.61	0.92
	418403	D66978	Hs.84790	KIAA0225 protein	1.76	1.49	2.24
	421433	AI829192	Hs.22380	ESTs	1.76	1.49	2.52
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.76	1.74	1.76
40	428655	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	1.76	1.43	1.76
	427536	BE277141	Hs.115803	gb:601178666F1 NIH_MGC_20 Homo sapiens c	1.76	2.12	1.76
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	1.76	1.86	1.48
	401994			Target Exon	1.75	1.44	1.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	1.75	1.69	1.79
45	408633	AW963372	Hs.46677	PRO2000 protein	1.75	1.46	1.88
	429978	AA249027		ribosomal protein S6	1.75	1.60	1.92
	450690	AA296696	Hs.333418	FXYD domain-containing ion transport reg	1.75	2.13	2.03
	456967	AW004056	Hs.168357	T-box 2	1.74	1.95	1.42
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	1.74	2.64	2.01
50	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	1.74	2.82	2.31
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.74	1.51	1.62
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	1.73	1.54	3.15
	412851	AI826502	Hs.97269	ESTs	1.73	1.67	1.05
	453953	AW408337	Hs.36972	CD7 antigen (p41)	1.73	2.22	2.28
55	430413	AW842182	Hs.241392	small inducible cytokine AS (RANTES)	1.73	2.05	1.47
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	1.73	1.71	1.73
	447217	BE465754	Hs.17778	neuropilin 2	1.73	1.62	4.70
	437673	AW665665	Hs.153034	ESTs	1.72	1.55	2.10
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.72	2.50	1.80
60	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	1.72	1.48	3.98
	413313	NM_002047	Hs.283108	glycyl-tRNA synthetase	1.72	2.19	1.82
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.72	2.68	1.68
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	1.71	2.17	2.24
	403969			ENSP00000034663: Zinc finger protein 131	1.71	1.31	1.71
65	450832	AW970602	Hs.105421	ESTs	1.71	1.33	2.38
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	1.71	1.67	1.95
	439783	AI125760	Hs.24835	hypothetical protein FLJ14594	1.71	2.10	2.20
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.71	3.86	1.76
	432259	BE269103	Hs.274201	60S acidic ribosomal protein PO	1.71	1.85	1.94
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (Tti3 com	1.71	2.12	1.98
70	428289	M26301	Hs.2253	complement component 2	1.71	2.46	0.76
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	1.70	1.70	2.78
	440039	Z46188	Hs.6874	KIAA0472 protein	1.70	2.24	1.60
	406646	M33600	Hs.308026	major histocompatibility complex, class	1.70	2.27	1.33
75	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor I	1.70	2.77	2.07
	420286	AI796395	Hs.111377	ESTs	1.70	1.50	3.21
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	1.69	1.44	1.69
	445247	AW274290	Hs.153997	ESTs	1.69	2.57	1.65
	436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	1.69	1.52	3.13
	410257	BE244044	Hs.61469	hypothetical protein	1.69	1.99	1.97
80	424663	NM_002351	Hs.151544	SH2 domain protein 1A, Duncan's disease	1.69	1.76	1.69
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.69	1.98	2.48
	458098	BE550224		metallothionein 1E (functional)	1.68	1.83	1.68
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.68	1.57	4.09
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.68	1.64	0.68

5	421563	NM_006433	Hs.105806	granulysin	1.68	2.24	1.55
	448775	AB025237	Hs.388	nucleoside diphosphate linked moi	1.68	1.98	2.05
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	1.68	1.35	1.68
	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA	1.68	1.88	1.63
	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.67	2.54	1.90
10	401760			Target Exon	1.67	1.93	1.61
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.67	1.85	4.25
	446644	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (up	1.67	1.94	1.48
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	1.67	1.65	0.90
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.67	1.54	1.95
15	412856	BE386745	Hs.74631	basigin (OK blood group)	1.67	2.71	1.47
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.66	1.82	1.19
	424399	AJ905687		AJ905687:IL-BT095-190199-019 BT095 Homo	1.66	3.65	0.44
	432355	AA534416	Hs.162185	ESTs, Weakly similar to S42799 gap prec	1.66	1.98	1.45
	427239	BE270447		ubiquitin carrier protein	1.66	2.94	1.92
20	425262	D87119	Hs.155418	GS3955 protein	1.66	2.36	1.66
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.66	1.86	1.90
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.65	2.05	1.31
	446217	AI651594	Hs.99709	ESTs	1.65	1.98	1.77
	400222			NM_002082: Homo sapiens G protein-couple	1.65	1.74	1.81
25	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.65	2.50	1.77
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.65	2.89	1.57
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, yeast) homo	1.64	2.76	1.26
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	1.64	1.96	1.24
	433867	AK000596	Hs.3618	hippocampin-like 1	1.64	1.47	1.00
30	433671	AW138797	Hs.132906	19A24 protein	1.64	2.17	1.96
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.64	2.18	1.43
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.64	1.47	1.64
	409264	NM_014937	Hs.52463	KIAA0966 protein	1.64	1.46	4.89
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.64	2.58	1.79
35	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	1.63	1.72	1.88
	418117	AJ922013	Hs.83496	linker for activation of T cells	1.63	1.98	1.99
	448304	BE622768	Hs.290356	mesoderm development candidate 1	1.63	1.67	1.86
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.63	2.56	1.97
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.63	1.46	2.43
40	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	1.63	1.34	1.94
	447321	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fs, clone HE	1.63	1.96	1.77
	422192	AA305159	Hs.113019	fts485	1.62	1.45	1.62
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	1.62	2.23	1.53
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	1.62	1.57	2.38
45	424779	AL046851	Hs.153053	CD37 antigen	1.62	1.92	2.10
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	1.62	1.41	1.12
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.62	2.03	2.13
	414159	AW511414	Hs.257352	apolipoprotein L 6	1.62	1.89	1.32
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	1.62	1.81	1.27
50	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	1.62	1.50	2.13
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.61	1.71	2.02
	451708	AI306536	Hs.60975	ESTs	1.61	2.31	1.70
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.61	1.53	2.50
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	1.61	1.83	1.69
55	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	1.61	1.56	1.61
	440201	AL359588	Hs.7041	hypothetical protein DKFZp762B226	1.61	1.58	1.85
	414368	W70171	Hs.75939	uridine monophosphate kinase	1.61	1.59	2.75
	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.61	3.54	1.52
	422257	NM_001716	Hs.113916	Burkitt lymphoma receptor 1, GTP-binding	1.61	2.15	1.54
60	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.60	2.01	1.36
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.60	2.00	1.60
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.60	1.38	2.23
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.60	1.78	2.59
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	1.60	1.78	2.07
65	417324	AW265494		ESTs	1.60	2.48	1.91
	430325	AF004562	Hs.239356	syntaxin binding protein 1	1.60	1.74	2.53
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	1.60	1.46	2.46
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.60	1.81	3.00
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.59	1.88	1.68
70	417437	U52682	Hs.82132	interferon regulatory factor 4	1.59	1.90	2.26
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	1.59	2.14	1.59
	401797			Target Exon	1.59	1.82	1.78
	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	1.59	1.45	4.69
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	1.59	1.82	1.68
75	415474	NM_014252	Hs.78457	solute carrier family 25 (mitochondrial	1.58	1.51	0.30
	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	1.58	1.72	2.46
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.58	1.85	1.94
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	1.58	1.25	2.09
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	1.58	1.72	1.80
80	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA	1.58	2.60	1.58
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	1.58	1.84	1.22
	401151			Target Exon	1.58	2.43	1.60
	441590	AI623207	Hs.190537	ESTs	1.58	1.40	1.58
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	1.58	1.68	1.58
80	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.58	2.28	1.60
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	1.58	2.14	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	1.57	1.46	1.57

	427700	AA262294	Hs.180383	dual specificity phosphatase 6	1.57	1.42	0.88
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.57	1.49	2.69
	404872			ENSP00000243173*:DJ1109J22.1 (novel home	1.57	1.46	1.36
5	408212	AA297567	Hs.43728	hypothetical protein	1.57	1.55	2.73
	414699	AJ815523	Hs.76930	synuclein, alpha (non A4 component of am	1.57	1.36	1.57
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.57	1.70	1.13
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.57	1.75	1.57
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.57	2.26	2.10
10	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	1.57	2.09	1.57
	402876			NM_022161*:Homo sapiens livin inhibitor-	1.56	2.28	1.45
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.56	2.97	1.54
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.56	1.75	1.88
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	1.56	2.76	1.67
15	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.56	2.36	1.83
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.56	1.78	2.06
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.56	1.32	2.70
	453613	F06838		ESTs	1.56	1.76	1.84
	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (TIT3 co	1.56	1.43	1.56
20	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	1.56	1.47	3.15
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	1.56	2.01	1.56
	420842	AJ083668	Hs.50601	hypothetical protein MGC10986	1.55	2.24	1.90
	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	1.55	1.24	3.07
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	1.55	1.79	2.17
25	437669	AJ358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	1.55	1.83	1.96
	439437	AJ207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.55	1.63	2.20
	418835	AL023694	Hs.88977	hypothetical protein dJ511E16.2	1.55	1.73	1.50
	448633	AA311426	Hs.21635	tubulin, gamma 1	1.54	2.02	1.67
	447763	BE199111	Hs.115803	hypothetical protein	1.54	2.52	1.52
30	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	1.54	1.54	3.03
	448258	BE386983	Hs.343214	hypothetical protein FLJ20396	1.54	1.97	1.53
	440165	AW014718	Hs.7753	calumenin	1.54	1.53	2.55
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.54	1.34	1.69
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.54	2.21	1.54
35	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.54	2.50	1.94
	416926	H03109	Hs.263395	HT018 protein	1.54	1.41	2.01
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.54	1.89	1.23
	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.54	1.93	1.79
	420421	AF281133	Hs.343589	exosome component Rrp41	1.53	2.47	1.61
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.53	1.62	1.19
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.53	1.74	1.37
	423420	AJ571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	1.53	2.49	1.59
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.53	2.72	1.54
	429837	NM_003896	Hs.225939	sialyltransferase 9 (CMP-NeuAc: lactosyl	1.53	1.64	2.40
45	412939	AW411491	Hs.75069	eukaryotic translation elongation factor	1.52	1.98	0.98
	410678	BE540516	Hs.293732	hypothetical protein MGC3195	1.52	1.39	2.17
	431186	NM_012249	Hs.250697	ras-like protein	1.52	1.91	1.82
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.52	1.57	1.82
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	1.51	2.08	1.19
50	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	1.51	1.50	0.67
	417308	H60720	Hs.81892	KIAA0101 gene product	1.51	1.42	7.41
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	1.51	2.75	1.51
	405204			NM_002086*:Homo sapiens growth factor re	1.51	1.44	1.53
55	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	1.51	1.92	2.32
	422516	BE258862	Hs.117950	multifunctional polypeptide similar to S	1.50	1.61	1.47
	418827	BE327311	Hs.47166	HT021	1.50	1.35	3.53
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	1.50	1.55	2.09
	432992	BE270472	Hs.279900	HSPCD15 protein	1.50	1.82	0.82
60	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	1.50	1.34	4.87
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.50	3.05	1.51
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	1.50	1.36	0.46
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	1.50	2.05	1.78
	421861	S78798	Hs.108966	phosphatidylinositol-4-phosphate 5-kinas	1.49	1.52	2.62
	422684	BE561617	Hs.119192	H2A histone family, member Z	1.49	1.53	2.02
65	452363	AJ582743	Hs.94953	Homo sapiens, Similar to complement comp	1.49	2.02	1.41
	411825	AK000334		hypothetical protein FLJ20327	1.49	2.55	1.38
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (lk	1.49	1.77	1.49
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.49	1.79	1.75
70	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	1.49	1.57	2.14
	440676	NM_004987	Hs.112378	UM and senescent cell antigen-like doma	1.49	1.42	1.46
	411296	BE207307	Hs.10114	growth suppressor 1	1.49	1.74	1.50
	442894	W02112	Hs.8836	parvin, beta	1.49	2.25	1.51
	416361	AW204907	Hs.6872	ESTs, Weakly similar to CA13_HUMAN COLLA	1.49	2.06	1.89
75	424162	AA336229	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.49	1.59	1.65
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.49	2.00	1.22
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	1.49	2.12	1.41
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.49	1.61	1.67
	417007	AF224741	Hs.80768	chloride channel 7	1.48	1.94	1.71
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.48	1.68	1.67
80	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.48	1.43	2.25
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.48	1.37	3.17
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	1.48	1.35	1.46
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.47	1.58	1.48
	442945	AJ024849	Hs.131853	ESTs	1.47	1.73	1.38

5	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.47	1.89	1.60
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	1.47	2.03	1.47
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.47	1.86	1.93
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.47	2.92	1.49
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	1.47	1.61	1.73
10	447940	D86982	Hs.20060	KIAA0229 protein	1.47	1.93	1.72
	446106	AA377165	Hs.44633	ESTs	1.47	1.56	1.63
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.47	1.78	1.84
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	1.47	2.04	1.47
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.47	1.76	1.83
15	402294			Target Exon	1.47	1.27	1.46
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.46	2.00	1.59
	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	1.46	1.58	2.15
	400270			NM_000026: Homo sapiens adenylosuccinate	1.46	1.42	2.32
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.46	2.07	1.40
20	419625	U91616	Hs.182885	nuclear factor of kappa light polypeptid	1.45	1.78	1.53
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	1.45	1.31	0.90
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.45	2.13	1.46
	453350	AJ917771	Hs.61790	hypothetical protein FLJ23338	1.45	2.00	1.39
	448412	AJ219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	1.45	1.37	3.17
25	411619	AJ418609	Hs.71040	hypothetical protein FLJ20425	1.45	1.39	3.01
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.45	1.82	1.44
	450395	BE048545	Hs.161757	ESTs	1.45	2.40	1.33
	438555	AJ222089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	1.45	1.91	1.65
	422497	D29642	Hs.1528	KIAA0053 gene product	1.45	1.94	1.49
30	400991			Target Exon	1.45	2.10	1.42
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.45	1.53	0.42
	424618	L29472	Hs.1802	major histocompatibility complex, class	1.44	1.96	1.86
	423032	AJ684746	Hs.119274	RAS p21 protein activator (GTPase activa	1.44	1.34	3.36
	424232	AB015982	Hs.143460	protein kinase C, nu	1.44	1.28	2.94
35	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	1.44	1.63	1.45
	445745	AB007924	Hs.13245	KIAA0455 gene product	1.44	1.17	1.52
	449209	BE616830	Hs.294145	ESTs	1.44	1.35	2.48
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.44	2.10	1.79
	401284			Target Exon	1.44	1.71	1.44
40	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.44	1.68	1.45
	433020	AJ375726	Hs.279918	hypothetical protein	1.44	1.37	2.02
	420042	AW015140	Hs.161723	ESTs	1.44	2.02	1.29
	453878	AW964440	Hs.19025	DC32	1.44	1.69	1.44
	427268	X78520	Hs.174139	chloride channel 3	1.44	1.45	1.96
45	417386	AL037228	Hs.82043	D123 gene product	1.43	1.32	2.81
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	1.43	1.80	1.17
	411009	W37572	Hs.285864	ESTs	1.43	1.57	1.72
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.43	1.36	1.49
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	1.43	2.15	1.57
50	407826	AA128423	Hs.40300	calpain 3, (p94)	1.43	1.61	1.69
	439070	AJ733278	Hs.7621	ESTs	1.43	2.10	1.40
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.43	2.09	1.24
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	2.13	1.54
	442591	AW292797		hypothetical protein MGC10772	1.43	2.11	1.61
55	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.43	1.49	1.16
	423639	AB037826	Hs.130411	KIAA1405 protein	1.42	2.08	1.51
	426234	BE314534	Hs.168159	apoptosis regulator	1.42	1.57	1.31
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.42	1.88	1.63
	430294	AJ538226	Hs.32976	guanine nucleotide binding protein 4	1.42	1.46	3.18
60	447126	AW150632	Hs.170307	Raf guanine nucleotide exchange factor R	1.42	1.36	1.38
	432241	AJ937060	Hs.6298	KIAA1151 protein	1.42	1.58	1.98
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	1.41	2.09	1.29
	434262	AF121858	Hs.12169	sorting nexin 8	1.41	3.07	1.41
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	1.41	1.82	1.43
65	402474			NM_004079: Homo sapiens cathepsin S (CTSS	1.41	1.32	1.24
	419897	X90826	Hs.93649	upstream transcription factor 2, c-fos i	1.41	1.69	1.80
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	1.41	1.22	1.74
	424441	X14850	Hs.147097	H2A histone family, member X	1.41	1.74	2.15
	406663	U24683		immunoglobulin heavy constant mu	1.41	1.51	2.03
70	409614	BE297412	Hs.55189	hypothetical protein	1.41	1.54	2.20
	443885	H91806	Hs.15284	ESTs	1.41	1.19	1.41
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.40	1.88	1.24
	425179	AJ224442	Hs.155020	putative methyltransferase	1.40	1.84	1.47
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.40	1.27	2.79
75	432403	AA550815	Hs.124840	ESTs	1.40	1.83	1.44
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.40	1.65	2.51
	422596	AF063611	Hs.118633	Z'-S'-oligoadenylate synthetase-like	1.40	2.57	1.44
	435292	N20514	Hs.172965	ESTs	1.40	1.91	1.43
	419424	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.39	1.57	1.37
80	425068	AL048716	Hs.154387	KIAA0103 gene product	1.39	1.27	3.18
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.39	2.26	1.40
	427740	BE242604	Hs.180616	CD36 antigen (collagen type I receptor,	1.39	1.76	0.99
	402022			C21000178: gi 7341207 gb AA61215.1 JAF22	1.39	1.74	1.36
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (1.39	1.72	1.39
	410103	AW903666		gb:CM4-NN1032-280300-122-b02 NN1032 Homo	1.39	1.46	1.34
	439180	AJ393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.39	1.35	1.79
	414057	AI815559	Hs.75730	signal recognition particle receptor (d	1.39	1.49	1.17

5	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.39	1.52	1.44
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.39	3.02	1.52
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN cDNA 9430	1.38	1.81	1.39
	436856	AI469355	Hs.127310	ESTs	1.38	1.35	0.99
	437179	AA393508		serologically defined colon cancer antig	1.38	1.26	4.14
	437912	BE278594	Hs.5912	F-box only protein 7	1.38	2.03	1.40
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	1.38	1.52	1.38
10	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheri	1.38	1.48	1.38
	432812	AI935412	Hs.50162	ESTs	1.38	1.43	2.18
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.38	1.87	1.28
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	1.38	1.46	2.23
	408787	NM_014784	Hs.47822	Rho guanine exchange factor (GEF) 11	1.38	1.98	1.50
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.38	1.29	2.04
15	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.38	1.52	2.62
	418255	AW135405	Hs.37251	ESTs	1.38	1.44	1.75
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.37	1.51	1.37
	448977	X91809	Hs.22698	regulator of G-protein signalling 19	1.37	1.98	1.45
	422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialidase)	1.37	1.75	1.31
20	435458	F11872	Hs.4892	Homo sapiens clone 24841 mRNA sequence	1.37	1.38	2.80
	429849	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.37	1.61	1.62
	429849	U33053	Hs.2499	protein kinase C-like 1	1.37	1.71	1.45
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.37	1.62	1.82
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.37	1.86	1.37
25	453941	U39817	Hs.36820	Bloom syndrome	1.37	1.59	1.37
	446755	AW451473	Hs.16134	serine/threonine kinase 10	1.37	1.82	1.48
	439755	AW748482	Hs.77873	B7 homolog 3	1.36	2.10	1.35
	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	1.36	1.79	1.67
	413821	AA844126	Hs.55954	ESTs, Weakly similar to C4HU complement	1.36	1.91	1.39
30	445823	AI478563	Hs.145519	FKSG87 protein	1.36	1.29	0.33
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	1.36	1.33	2.01
	402542			Target Exon	1.36	1.66	1.46
	451050	AW937420		ESTs	1.36	2.00	1.36
	444501	AW247624	Hs.11342	ninjurin 1	1.36	1.59	1.14
35	413291	NM_006278	Hs.75268	sialyltransferase 4C (beta-galactosidase	1.36	2.55	1.42
	438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.36	1.46	1.32
	428398	AI243368	Hs.98558	ESTs	1.36	1.25	4.95
	439704	AW020018	Hs.293267	ESTs	1.36	1.84	1.48
	428782	X12830	Hs.193400	interleukin 6 receptor	1.36	1.27	0.58
40	437316	AI683454	Hs.46801	GCN5 (general control of amino-acid synt	1.35	2.10	1.29
	439246	AI498072		membrane-associated tyrosine- and threon	1.35	1.81	1.63
	403409			NM_005929:Homo sapiens antigen p97 (meta	1.35	1.64	1.35
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (tr	1.35	1.37	2.33
	437740	AA810265	Hs.122915	ESTs	1.35	1.91	1.35
45	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	1.35	1.53	1.10
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.35	1.89	1.57
	457760	AA668123	Hs.134170	ESTs	1.35	2.03	1.43
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.35	2.06	1.41
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.35	1.77	1.27
50	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	1.35	1.52	0.51
	421777	BE562088	Hs.108196	HSPC037 protein	1.34	1.65	1.61
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.34	1.77	1.02
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.34	1.77	1.15
	428977	AK001404	Hs.194698	cyclin B2	1.34	1.53	1.82
55	418283	S79895	Hs.83942	cathepsin K (pseudodysostosis)	1.34	1.33	3.45
	425848	BE242709	Hs.159637	valyl-HRNA synthetase 2	1.34	2.11	1.32
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.34	1.27	1.97
	422758	AF152329	Hs.284180	protocadherin gamma subfamily C, 3	1.34	1.61	1.75
	421579	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	1.34	1.75	1.81
60	416374	NM_001154	Hs.300711	annexin A5	1.34	1.68	1.55
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.34	1.87	0.81
	424778	AA251048	Hs.153042	lymphocyte antigen 9	1.34	1.94	1.42
	421703	AI936513	Hs.1416	Fc fragment of IgE, low affinity II, rec	1.33	2.19	1.48
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.33	1.96	1.18
65	425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.33	1.70	1.60
	418803	U50079	Hs.88556	histone deacetylase 1	1.33	1.28	2.65
	427730	AW250549	Hs.180577	granulin	1.33	2.09	1.35
	441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050476, mRNA,	1.33	2.05	1.33
	412738	N34731	Hs.74562	siah binding protein 1; FBP interacting	1.33	1.85	1.35
70	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.33	1.31	2.06
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	1.33	1.77	1.43
	422997	BE018212	Hs.122908	DNA replication factor	1.33	1.91	1.39
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	1.33	1.16	0.60
	409119	AA531133	Hs.4253	hypothetical protein MGC2574	1.33	1.52	1.34
75	419652	AL157485	Hs.91973	hypothetical protein	1.32	2.07	1.29
	415697	AI365603	Hs.198271	DKFZP566I1024 protein	1.32	2.00	1.33
	434359	AF129536	Hs.284226	F-box only protein 6	1.32	2.07	1.39
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	1.32	1.25	1.91
	444029	AW160993	Hs.326292	hypothetical gene DKFZp434A1114	1.32	1.63	1.44
80	456974	M12529	Hs.169401	apoptoprotein E	1.32	1.47	0.85
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.32	2.51	1.23
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	1.31	3.12	1.31
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.31	1.21	1.65
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	1.31	1.68	1.47

5	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.31	1.30	2.14
	407777	AA161071	Hs.71455	squalene epoxidase	1.31	1.45	1.43
	408536	AW381532	Hs.135188	ESTs	1.31	1.38	0.90
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.31	1.81	1.49
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.31	1.63	1.31
10	409154	U72882	Hs.50842	interferon-induced protein 35	1.31	1.69	1.29
	425003	AF119046	Hs.154149	apurinic/apyrimidinic endonuclease(APEX	1.31	1.74	1.39
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	1.31	1.43	0.94
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.30	2.53	1.34
	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.30	1.38	1.38
15	425676	AW410656	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.30	2.11	1.36
	427289	AI097346	Hs.180655	phosphoserine aminotransferase	1.30	2.27	1.48
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.30	1.68	1.79
	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	1.30	1.50	1.30
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.30	1.42	2.13
20	423062	NM_003655	Hs.5637	ESTs	1.30	1.58	1.30
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.30	1.77	1.35
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	1.30	1.57	1.51
	416920	AA176455	Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.30	1.67	1.44
	430451	AA836472	Hs.297939	cathepsin B	1.30	1.49	1.16
25	457400	AF032906	Hs.252549	cathepsin Z	1.30	1.40	1.21
	403506			C3001912:gi5677647[ref NP_033602.1] zin	1.29	1.88	1.26
	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.29	2.64	1.31
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	1.29	1.79	1.36
	416322	BE019494	Hs.79217	pyroline-5-carboxylate reductase 1	1.29	1.59	1.80
30	440795	AA262133	Hs.99741	ESTs, Weakly similar to PNL1_HUMAN PEANU	1.29	2.01	1.43
	421846	AA017707	Hs.1432	protein kinase C substrate 80K-H	1.29	1.70	1.34
	425966	NM_001761	Hs.1973	cyclin F	1.29	1.63	1.50
	446766	AF083208	Hs.16178	apoptosis antagonizing transcription fac	1.29	1.71	1.40
	406827	AA971409		gb:op92cd4.s1 NCI_CGAP_Lu5 Homo sapiens	1.29	2.04	1.35
35	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	1.29	1.41	1.94
	443086	AW977125		sine oculis homeobox (Drosophila) homolo	1.29	1.24	1.29
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.29	1.99	1.36
	434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	1.29	1.18	1.32
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	1.29	1.31	2.19
40	400261			Eos Control	1.29	1.59	1.36
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	1.29	1.67	1.53
	412315	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo	1.28	1.26	1.07
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	1.28	1.85	1.40
	425449	X52056	Hs.157441	spleen focus forming virus (SFFV) provir	1.28	1.45	1.14
45	454478	AW805749		superoxide dismutase 2, mitochondrial	1.28	2.29	1.07
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	1.28	1.20	0.93
	406016			Target Exon	1.28	1.47	1.31
	449609	BE246434	Hs.289026	guanine nucleotide binding protein (G pr	1.28	1.26	3.02
	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.28	1.76	1.23
50	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.28	1.60	1.30
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	1.28	1.51	1.22
	408543	N78098	Hs.44289	ESTs	1.28	2.02	1.08
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	1.27	1.28	3.51
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.27	1.66	1.39
55	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.27	1.47	1.55
	430794	NM_000166	Hs.333303	gap junction protein, beta 2, 26kD (conn	1.27	1.81	0.89
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.27	1.35	1.68
	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	1.27	1.67	1.31
	441598	AI733219	Hs.58262	ESTs	1.27	1.30	1.30
60	431921	N46466	Hs.58879	ESTs	1.27	2.00	1.16
	459345	AW503672		gb:U1-HF-BN0-ald-h-11-0-U1.r1 NIH_MGC_50	1.26	1.44	1.33
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	1.26	1.20	1.45
	426334	BE305081	Hs.169358	hypothetical protein	1.26	1.22	1.89
	414044	BE614194	Hs.75721	profilin 1	1.26	1.48	1.51
65	405268			ENSP00000223174::KIAA0783 PROTEIN.	1.26	1.19	2.25
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	1.26	1.19	4.03
	439529	BE293492	Hs.293984	hypothetical protein MGC13102	1.26	1.83	1.19
	421254	AK001724	Hs.102950	coat protein gamma-cop	1.26	1.61	1.23
	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIA (stero	1.26	1.84	0.68
70	419395	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	1.26	1.66	1.34
	418968	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	1.26	1.42	1.19
	441553	AA281219	Hs.121296	ESTs	1.26	1.29	1.28
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	1.25	1.22	0.65
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	1.25	1.17	2.95
75	450087	BE293180	Hs.24379	MUM2 protein	1.25	1.78	1.28
	429604	AK001851	Hs.210778	hypothetical protein FLJ10989	1.25	1.18	1.25
	429380	AF023268	Hs.200600	secretory carrier membrane protein 3	1.25	2.22	1.25
	440251	AW796016	Hs.332012	Homo sapiens, clone IMAGE:3687782, mRNA,	1.25	1.90	1.39
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	1.24	1.32	1.53
80	435466	BE619165	Hs.29203	G protein beta subunit-like	1.24	1.96	1.32
	450621	AW297288	Hs.55918	hypothetical protein FLJ11354	1.24	1.61	1.27
	400214			NM_007002:Homo sapiens cell membrane gly	1.24	1.88	1.32
	435013	H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.24	1.76	1.25
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.24	1.82	1.42
	406851	AA609784		major histocompatibility complex, class	1.24	1.68	1.19
	448498	AA418276		ESTs	1.24	1.73	1.29
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.24	1.70	1.38

5	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.24	1.61	1.16
	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myosin)	1.24	2.65	1.24
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA	1.24	1.49	1.50
	427390	AA32163	Hs.268231	Homo sapiens cDNA: FLJ23111 fs, clone L	1.24	1.17	2.10
	429954	AI918130	Hs.21374	ESTs	1.23	1.19	4.77
	421178	BE267994	Hs.102419	zinc finger protein	1.23	1.62	1.28
	442609	AL020996	Hs.8518	selenoprotein N	1.23	2.30	1.24
10	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.23	1.18	0.90
	410127	AA354313	Hs.58685	CD5 antigen (p56-62)	1.23	1.68	1.23
	452244	N33530	Hs.176674	ESTs	1.23	2.93	1.23
	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	1.23	1.56	1.29
	436939	AA853680	Hs.5345	arginyl aminopeptidase (aminopeptidase B	1.23	1.68	1.23
	414457	AW514320	Hs.76159	ATPase, H transporting, lysosomal (vacuo	1.23	1.58	1.20
15	416929	N20535		melastatin 1	1.23	1.92	1.20
	401106			Target Exon	1.23	1.82	1.29
	408981	AW500797	Hs.49427	Gem-interacting protein	1.23	1.40	1.59
	413317	U53225	Hs.75283	sorting nexin 1	1.23	1.43	1.44
20	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.23	1.71	1.24
	425455	AL137522	Hs.157777	casein kinase 1, gamma 1	1.23	1.95	1.29
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23	2.07	1.27
	414399	L47345	Hs.155202	transcription elongation factor B (SII)	1.22	1.87	1.19
	422034	AC006486	Hs.333069	Ets2 repressor factor	1.22	1.55	1.21
25	434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	1.22	1.55	1.51
	429574	BE268321	Hs.208912	hypothetical protein MGC861	1.22	1.49	1.46
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	1.22	1.64	1.40
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.22	1.63	1.30
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.22	1.24	0.71
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.22	2.20	1.26
30	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma	1.21	1.55	1.21
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	1.21	1.13	3.29
	404186			NM_019602:Homo sapiens butyrophilin-like	1.21	1.59	1.21
	447604	AW089933	Hs.301342	hypothetical protein MGC4342	1.21	1.25	2.00
35	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	1.21	1.14	1.25
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.21	1.39	1.25
	428468	AA171388	Hs.184482	DKFZP586D0624 protein	1.21	1.66	1.22
	419700	AF084935	Hs.92357	galactokinase 1	1.21	1.63	0.74
	430948	AI347578	Hs.124015	hypothetical protein MGC2605	1.21	1.48	1.21
40	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.20	1.75	1.23
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	1.20	1.54	1.29
	442173	N76101	Hs.8127	KIAA0144 gene product	1.20	1.54	1.31
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	1.20	1.18	1.11
	448230	BE395949	Hs.94814	hypothetical protein MGC2865	1.20	1.83	1.19
45	403817			NM_015271:Homo sapiens tripartite motif,	1.20	1.22	1.61
	411678	AI907114	Hs.71465	squalene epoxidase	1.20	1.15	2.01
	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.20	1.79	1.20
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.20	2.34	1.20
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.20	1.93	1.20
50	422565	BE259035	Hs.118400	Singed (Drosophila)-like (sea urchin fas	1.20	1.32	1.52
	446159	NM_013379	Hs.14089	dipeptidyl peptidase 7	1.19	1.64	1.22
	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	1.19	1.53	1.45
	421541	NM_003942	Hs.105584	ribosomal protein S6 kinase, 90kD, polyp	1.19	1.75	1.27
	450706	AW167578	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.19	1.71	1.22
55	430381	NM_006411	Hs.240534	1-acylglycerol-3-phosphate O-acyltransfe	1.19	1.66	1.21
	426329	AL389951	Hs.271623	nucleoporin 50kD	1.19	1.17	1.55
	421612	AF161254	Hs.106196	BD6 antigen	1.19	1.73	1.30
	410182	NM_001983	Hs.59544	excision repair cross-complementing rode	1.19	1.75	1.18
	434171	BE247688	Hs.347349	KIAA0948 protein	1.18	1.73	1.09
60	424837	BE276113	Hs.333034	N-acetyltransferase, homolog of S. cerev	1.18	2.13	1.22
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.18	1.45	1.30
	453754	AW972580	Hs.172753	ESTs	1.18	1.71	1.35
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	1.18	1.60	1.23
	422256	M64673	Hs.1499	heat shock transcription factor 1	1.18	1.51	1.28
65	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.18	1.89	1.18
	430513	AJ012008	Hs.241586	G6C protein	1.18	2.07	0.81
	427283	AL119798	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	1.18	1.13	3.25
	441648	H05734	Hs.30559	ESTs	1.18	1.56	1.23
	418219	AA731836	Hs.137319	ESTs	1.18	1.77	1.23
70	406422			Target Exon	1.18	1.43	1.31
	414823	AA156531	Hs.103902	ESTs, Weakly similar to A44851 keratin,	1.18	1.66	1.23
	425720	AA362394	Hs.293984	hypothetical protein MGC13102	1.18	1.58	1.15
	419250	AW770185		U5 snRNP-specific protein, 116 kD	1.17	1.74	1.21
	454390	AB020713	Hs.56966	KIAA0906 protein	1.17	1.33	1.35
	428471	X57348	Hs.184510	stratfin	1.17	1.19	1.24
75	430200	BE613337	Hs.234896	geminin	1.17	1.13	1.96
	412965	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	1.17	1.50	1.22
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	1.17	1.69	1.32
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSmb	1.17	1.12	2.44
80	417080	BE392846	Hs.1063	small nuclear ribonucleoprotein polypept	1.17	1.93	1.18
	423102	AW067812	Hs.303025	chromosome 11 open reading frame 24	1.17	1.89	1.17
	408393	AW015318	Hs.23165	ESTs	1.16	1.10	1.91
	424292	AA338432		gb:EST43554 Fetal brain I Homo sapiens c	1.16	1.61	1.21
	446759	R61463	Hs.16165	expressed in activated T/LAK lymphocytes	1.16	1.45	1.23
	427324	AA159587	Hs.285932	hypothetical protein FLJ23322	1.16	1.50	1.23

	446055	AI815981	Hs.12909	muco1ipin 1	1.16	1.49	1.10
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequen	1.16	1.67	1.20
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.16	1.66	1.32
5	411305	BE241596	Hs.69547	myelin basic protein	1.16	1.15	4.29
	438930	AW843633	Hs.343261	hypothetical protein AL110115	1.16	1.37	1.34
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.15	1.82	1.17
	427458	BE208364	Hs.29283	ESTs, Weakly similar to UKHU proteoglyca	1.15	1.46	1.32
	402160			Target Exon	1.14	1.23	1.12
10	416881	N32520	Hs.141358	ESTs	1.14	2.42	1.14
	420223	N27807		ribosomal protein L4	1.14	1.23	1.14
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.14	1.38	1.27
	429538	BE182592	Hs.139322	small proline-rich protein 2A	1.14	1.16	3.52
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	1.13	1.13	1.13
15	436696	AA725678	Hs.120487	ESTs	1.13	1.22	1.13
	448950	AF288687	Hs.9275	CGI-152 protein	1.12	1.52	1.19
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.12	1.31	1.08
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	1.12	1.08	1.20
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.12	2.93	1.12
20	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	1.12	1.11	3.43
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	1.12	1.50	1.12
	450296	AL041949	Hs.24756	hepatocyte growth factor-regulated tyros	1.11	1.48	1.12
	420697	AA827705	Hs.26605	ESTs	1.11	2.19	1.11
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.11	2.73	1.11
25	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.10	1.43	1.14
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.10	1.35	1.19
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), acti	1.10	1.43	1.10
	408801	AI866590	Hs.63405	Homo sapiens, clone IMAGE:3609337, mRNA,	1.10	1.53	1.14
	402622			C1003392":gij12314272jamb CAC00591.1 (A	1.10	1.59	1.06
30	418661	NM_001949	Hs.1189	E2F transcription factor 3	1.09	1.82	1.09
	442680	BE270707	Hs.8583	similar to APOBEC1	1.09	1.49	1.24
	439702	AW085525	Hs.55964	ESTs	1.09	1.68	1.09
	423858	AL137326	Hs.133483	Homo sapiens mRNA: cDNA DKFZp434B0650 (f	1.09	1.10	1.73
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.09	1.23	1.25
35	414396	BE548266	Hs.76057	galactose-4-epimerase, UOP-	1.09	1.07	1.23
	401558			ENSP00000220478":SECRETOGRANIN III.	1.08	1.54	1.08
	428411	AW291464	Hs.10338	ESTs	1.08	1.07	6.19
	422051	AW327546	Hs.111024	solute carrier family 25 (mitochondrial	1.08	1.25	0.93
	414694	NM_015362	Hs.76907	HSPC002 protein	1.08	1.18	1.12
40	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.07	1.15	1.31
	420856	BE513294	Hs.205736	HLA class II region expressed gene KE2	1.06	1.47	1.08
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.06	1.17	1.22
	429259	AA420450	Hs.292911	Plakophilin	1.06	1.08	0.73
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.05	1.04	0.84
45	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	1.05	1.09	1.37
	444438	N32755	Hs.322489	ESTs	1.04	1.13	1.05
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	1.04	1.22	0.78
	404960			eyes absent (Drosophila) homolog 3	1.04	1.06	1.04
50	408972	AL050100	Hs.49378	DKFZP586D0919 protein	1.04	1.09	1.13
	414477	U41635	Hs.76228	amplified in osteosarcoma	1.03	1.11	1.03
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.03	1.02	2.33
	435056	AW023337	Hs.5422	glycoprotein M6B	1.03	1.02	3.56
	415314	N88802	Hs.5422	glycoprotein M6B	1.02	1.02	4.02
	408591	AF015224	Hs.46452	mannanaglobin 1	1.00	1.41	0.05
55	401203			Target Exon	1.00	1.02	0.98
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.00	1.49	0.56
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.00	1.69	0.91
	411388	X72925	Hs.69752	desmocollin 1	1.00	3.12	1.00
	428618	AA885360		Target CAT	1.00	1.77	1.00
60	402860			ENSP00000239210:DJ50024.4 (novel protein	1.00	1.53	1.00
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	1.39	1.00
	409269	AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; HSAR g	1.00	1.46	1.00
	409190	AU076536	Hs.50984	sarcoma amplified sequence	1.00	0.80	1.00
	416143	AI955650		glutamyl-peptide cyclotransferase (glu	1.00	1.96	1.00
65	401588			C15000180":gij544344 sp Q05859 FOR4_MOUS	1.00	2.04	1.00
	419519	AI198719	Hs.176376	ESTs	1.00	1.91	1.00
	448816	AB033052	Hs.22151	KIAA1226 protein	1.00	1.82	1.00
	440270	NM_015986	Hs.7120	cytokine receptor-like molecule 9	1.00	1.15	1.00
70	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.00	1.66	0.74
	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropporin	1.00	2.21	1.00
	452461	N78223	Hs.108106	transcription factor	1.00	1.61	1.00
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	1.00	1.42	1.00
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	1.00	1.81	1.00
	429477	AI275514	Hs.6658	ESTs	1.00	1.67	1.00
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	1.00	1.05	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	1.00	1.79	1.00
	451993	AA765776	Hs.122983	ESTs	1.00	2.15	1.00
	416947	N23282	Hs.184341	ESTs, Weakly similar to B34087 hypothei	1.00	1.67	1.00
	441606	R37263	Hs.21065	ESTs, Moderately similar to PC4259 ferri	1.00	1.87	1.00
80	442590	AI002686	Hs.130313	ESTs	1.00	2.59	1.00
	404831			C1002937":gij7499208 pit T20993 hypothe	1.00	1.44	1.00
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	1.00	1.47	1.00
	419717	H07970	Hs.92458	G protein-coupled receptor 19	1.00	1.78	1.00
	408611	NM_004367	Hs.46458	chemokine (C-C motif) receptor 6	1.00	1.64	1.00

5	421666	AL035250	Hs.1408	endothelin 3	1.00	0.63	1.00
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	1.00	1.60	1.00
	423899	NM_001427	Hs.134989	engrailed homolog 2	1.00	2.91	1.00
	423130	AW897586	Hs.21213	ESTs	1.00	1.65	1.00
	433843	AW021423	Hs.112819	ESTs	1.00	2.08	1.00
	458574	AW384436	Hs.135265	Homo sapiens clone FLB8436 PRO2277 mRNA,	1.00	1.00	1.00
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.00	1.41	1.00
	427335	AA448542	Hs.251677	G antigen 7B	1.00	1.15	1.00
10	439951	AJ347067	Hs.124636	ESTs	1.00	1.80	1.00
	420248	AJ377191	Hs.44714	ESTs	1.00	2.15	1.00
	446259	AA425204	Hs.334721	hypothetical protein FLJ13391	1.00	2.35	1.00
	447164	AF026941	Hs.17518	vipirin, similar to inflammatory respon	1.00	1.53	1.00
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.73	1.00
15	408758	NM_003686	Hs.47504	exonuclease 1	1.00	1.59	1.00
	453745	AA952989	Hs.63908	hypothetical protein MGC14726	1.00	1.73	1.00
	436609	AJ022514	Hs.131380	ESTs	1.00	1.96	1.00
	419308	N40321		gb:yx80g07.r1 Soares melanocyte 2NbHM Ho	1.00	2.28	1.00
	421650	AA781795	Hs.122587	ESTs	1.00	1.74	1.00
20	459578	AW612538	Hs.304491	EST	1.00	2.16	1.00
	446152	AI292036		ESTs	1.00	1.66	1.00
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypothesi	1.00	2.04	1.00
	418673	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog (1.00	1.75	1.00
	415004	AA158925	Hs.240849	ESTs, Weakly similar to GBP1_HUMAN INTER	1.00	1.85	1.00
25	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	1.00	1.92	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	1.00	1.72	1.00
	417791	AW965339	Hs.44269	ESTs	1.00	1.52	1.00
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	2.02	1.00
	416445	AL043004	Hs.79337	KIAA0135 protein	1.00	1.28	1.00
30	408375	AI224520	Hs.40930	ESTs	1.00	1.92	1.00
	406964	M21305		FGENES predicted novel secreted protein	1.00	0.46	1.00
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.00	1.00	2.48
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	0.98	0.98	3.24
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proti	0.95	0.96	3.06
35	446488	AB037782	Hs.15119	KIAA1361 protein	0.94	0.96	1.61
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	0.94	0.94	0.76
	409402	AF208234	Hs.695	cystatin B (stefin B)	0.93	0.91	1.55
	423942	AF209704	Hs.169407	glycolipid transfer protein	0.92	0.93	2.09
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	0.91	0.91	4.08
40	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	0.90	0.81	0.73
	417632	R20855	Hs.5422	glycoprotein M6B	0.90	0.92	3.89
	449092	U91641		alpha2,8-sialyltransferase	0.89	0.79	0.84
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	0.89	0.92	3.70
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	0.88	0.90	2.02
45	408349	BE546947	Hs.44276	homeo box C10	0.88	0.87	0.73
	429345	R11141	Hs.199695	hypothetical protein	0.85	0.84	0.69
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	0.84	0.85	1.32
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	0.84	0.88	3.37
	405885			Target Exon	0.81	0.71	1.00
50	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	0.78	0.78	0.90
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	0.77	0.73	0.71
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	0.75	0.78	4.69
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.74	0.78	5.42
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	0.70	0.75	4.29
55	412719	AW016610	Hs.816	ESTs	0.70	0.77	3.99
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	0.69	0.73	3.79
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.65	0.64	1.11
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	0.61	0.65	3.20
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	0.61	0.22	0.49
60	439659	AW970780	Hs.59482	Homo sapiens cDNA FLJ14471 fis, clone MA	0.49	0.30	0.67
	419092	J05581	Hs.89603	mucin 1, transmembrane	0.41	0.11	0.34
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	0.23	0.30	0.35

TABLE 49B:

65	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

Pkey	CAT Number	Accession
430540	713_2	BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
		BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
		AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA409916 AA59893 AI458188 AI240408 AI191843 AI131029 AW768399
		BE735196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
70		AI702715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
		BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
75		BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
		AJ359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953
		BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
		W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
80		F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114
		AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103
		AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809
		BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
431317	997174_1	AW970601 AW613399 AA503435 AA502682 N91138

	453912	32562_3	BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87967
5	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
	458997	11847_4	BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839
10	430015	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI91843 AI131029 AW768399
15			AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 HM0534 BE301004 AL531791 AI435581 BF931112 AL577303 AA373265 BE746965 BF743630 BE879296
20			AI359459 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AA421728 BG767231 BM462953 BG430524 W52648 AA113434 BE785431 BM041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 W27512 W58732 W85690 BG958989 AI205206 H19721 W10751 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA899120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE079336 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
25	425231	235504_1	AA527161 BG211784 AA527065 AA505489 AW512550
	417282	2142_2	AK025474 U11293 AF141304 BM424202 AL539879 AL554793 AL543707 AL549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347 BI838505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 D31003 AA234218 AJ420466 BM083921 BE856788 BE669957 BF430992 AW614978 AW205958 BF110763 BF222758 AA195232 AI341353 AI698676 AI093230 AI123522 AI656594 AI028758 AA975916 AI089224 AI264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 AL576975 BF687534 W497314 AI680513 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 AI517078 AL546480 AL530507 AL561042 AA024435 W497314 AI680513 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 BM011139 AW675130 BE276045 BF933396 AL517903 AA886367 BI030596 BG477193 BF973867
30	406687	0_0	M31126
	452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
35	442643	2736_1	BC001588 BC007424 AF016369 NM_004697 BI756186 BE257019 BG500792 BI862776 AL121371 BG574833 AA703250 AA179511 AW052006 AI280150 AI914000 AI358319 AI081204 AI082594 AA992449 AI470821 AI655744 AW237529 AA678858 AI984430 BF433055 BE467594 BE467573 AA035630 AI289987 AI184802 AI681391 AW592416 AI138377 AI139266 AA961714 AI800163 AA418751 AW451928 AA668676 AI273444 AI494387 BE046912 AI276555 BF196021 AA700055 AA609305 AA772596 AI635758 AI635749 H95459 AW610290 BE464994 AA527136 BF374802 AI800175 AW195227 AI189676 BF802049 AL513632 AL554911 AL538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AI567522 AI745257 AW388641 AW301265 AI141144 AW029280 AI149362 AU152328 AA418960 AL121009 AI890398 AI528748 H13050 T47086 BI000575 BF334914 BF109661 R44450 H13259 T47087 AW388645 BF305834 AL577516 BM041600 BE889299 BF239768
40	448243	13061_2	BG166513 AA479726 BE622314 AL134913 BE006305 BE006312 BE006298 AA044582 AW994956 AA234175 AA043906 BE006303 BF327669 BE006317 BF326759 BF541959
	430441	1438_6	BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080 R00283 C15236 AW327776 D80759
45	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
50	446019	658727_1	AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
	453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI083329 AI809932 AI808765 AA411449 AI378760 AA976829 AI738620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
55	429978	35194_2	BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI18664 AW963196 C06195 AI678018
60	452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AI556580 AW576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
70	458098	23945_1	AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224 AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W79223 W74510 AI090689 AL600773 AL600781 H46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553
	424399	2196_1	NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853
75	427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI2510913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822
80	400222	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710
	410600	497855_1	BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 AI335824 AW408712 BM149172

4	17324	292720_1	BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
5	453613	10943_2	BG951874 AJ572169 BG121705 BF515413 BE812196 AW173164 AW911266 AI161253 AA006295 AA724987 AA972004 AW085313 B1062611 BG119864 W02997 H80902
10	411825	7891_1	T91294 H09335 H09332 240007 F10399 F02595 F03100 H38987 A101090 H80903 AA913204 F10391 T80640 H24461 RA6234 RS15914 AK000695 AK000489 BC001688 BG325988 AW006329 AJ867644 AJ207230 AI148213 AJ304333 AJ163653 AW662636 A1281247 AA946921 AA424487
15	400270	32329_1	BE277230 AJ305588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 BJ906631 AW083424 AA625199 NM_017767 AK000334 BF984048 AW015634 AJ773992 AA430612 AA928390 AA464447 AW308277 AA424290 AJ927759 BG951502 AW881353 B1765535
20	442591	58995_1	AF067853 NM_000026 X65867 BC018881 S60710 BG686218 BG707897 BF767531 BE742167 BG745544 BG768400 BG323811 AU119991 BG763638 BG330397 BG761706 BF766890 B1457560 BG122629 BF927974 B1194649 BE909022 BG488681 AW328441 AW248366 BF718034 B5985004
25	410103	366775_1	BE264146 AW524840 AA410942 BE256756 AA480227 BF758918 BE251966 A1684330 AW518872 AW264087 AA631137 AT742831 A1990690 A192994 AA417231 AA459341 AA416541 A1652537 A803674 AA631209 A1923786 AW205704 A1354620 A198865 BF593386 AW821194 A1693442 AW977594
30	437179	12239_1	BE893700 BF242879 BE251315 AA534659 AA494551 B1047923 BG949898 BF246869 B1085069 B1007035 AA665981 A1375483 BG221331 A1867580 AA128025 AW612345 R12769 W92325 RA0084 AA191625 D51044 AA599257 BE878335 AA121664 A1146666 B1026299 AJ872356 AA788642
35	438129	497522_1	AA128068 BF819623 A1277591 A1435105 A1354905 AV747031 BC021240 BF430978 BG056212 AW874052 B1856040 A1572156 A1914600 A1002736 BM023413 H191902 AL563177 AL529967 BM023140 BE391587
40	439246	388_5	BG761312 BE277571 B1195388 BE389566 H91851 BE391930 BE391441 BG003993 AW589921 AW892489 AW903666
45	451050	11847_4	AK051509 BC019085 AA187684 BG656226 BM023227 A1932311 AW264381 AA398371 BM021483 A1432433 A1375777 A1129580 AW262782 AA134107 BM023515 AA977504 A1859222 A1348454 R69725 AA975268 BM021207 AL080074 A1129218 AW207842 N90581 A771919 A1092259
50	438129	497522_1	A1028416 A107114 BG656536 BE016777 AW193419 AA917040 W90430 A1342984 A1378957 AL036486 AW020068 B1491093 BF476021 RA1226 R69631 F04125 C02343 AA115589 RS6480 A400988 RS4266 R13422
55	439246	388_5	BM453041 AA760783 BE218582 A1340046 AW166131 BF515854 A1302096 AA461307 A1090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 BF431869 AAD013374 BG619478 BG401839
60	439246	388_5	BE904404 AW778647 BF431869 AW0070999 BG170122 BG191943 BG999184 R42302 AK054564 AF086057 A1869310 BG393141 BE220500 A479459 A1866575 A1361301 A1674602 BF001506 AW004996 A1466292 A1890883 A1608681
65	406827	0_0	A1713194 A1356096 A133040 BG057018 A1696166 AW081428 A1392809 AA985226 AW190187 BE896007 BF714443 AW516382 A1371188 N50847 AA117728 F27148 A1003145 AL520675 AL577680 AL578955 AA316669 BF804796 AA768324 A1285396 BG745142 BG325246 BG475289 AL580501
70	443086	25669_4	AA832445 BG4832168 BF063242 AW251083 BF345614 BE871009 BG698638 BG6978245 BG978247 BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 A1978353 AW327973 AW402425 A1889380 AA686804
75	443086	25669_4	AW612968 AA630644 A1751211 N26980 A1394506 AA474789 BF154928 BF477185 AA469647 R39135 A1750216 T35363 W36278 AW079375 AA612240 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG764222 BG749077 T50662 AA025671 AW815715
80	459345	919706_1	AV703240 H65047 AA485582 R56186 H90385 R55913 B1261497 B1018403 BF376945 T75578 BF933325 BF932853 BG502266 AW686934 AV683504 B1018121 A14953 BF93343 BF932871 H08334 R14012 BF897622 T50816 BG698003 BF340083 Z20199
85	400261	23110_1	AA971409 BE966136 BG819393 AA187888 AW753122
90	412315	1163860_1	BC006097 X03066 NM_002120 M26040 AW469119 AW469127 A1929972 AW518149 A1144556 AW628070 A1629032 A1358810 A180433 A1440472 A1357070 A1865365 AW001479 A1767973 A15518041 AA909398 AW768606
95	454478	4273_16	AW336678 AW936821 AW936683 AW936822 AW936781 AW936817 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812 AW936730 AW936762 AW936682 AW936732
100	459345	919706_1	AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 AW853325 AW503672
105	400214	9255_1	A1659839 BE897640 BE90

Pkey:

Ref:

Step 1

Unique number corresponding to an Eos probe set

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI)

sequence of human chromosome 22^a Dunham, et al. (1999) Nature 402:489-495

Indicates DNA strand from which exons were pred

NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405451	7622517	Minus	145949-146227
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	401454	9186923	Minus	114659-114832
10	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	403328	8469086	Minus	120428-120703
	405547	1054740	Plus	124361-124520,124914-125050
15	403532	8076842	Minus	81750-81901
	400750	8119067	Plus	198991-199168,199316-199548
	405506	6466489	Plus	80014-80401,80593-81125
	400533	6981826	Minus	277132-277595
20	405779	7280331	Minus	33048-33856
	402994	2996643	Minus	4727-4969
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
25	403969	8569909	Plus	31237-31375,32405-32506
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401797	6730720	Plus	6973-7118
	401151	9438288	Plus	30848-31228
30	404872	9650523	Minus	18540-18718
	402876	9864669	Plus	5679-6027,7485-7584
	405204	7230116	Plus	126569-126754
	402294	2282012	Minus	2575-3000
35	400991	8096825	Plus	159197-159320
	401284	9800819	Minus	101307-101421
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	403022	3132351	Plus	92097-92864
40	402542	9801558	Minus	67076-67594
	403409	9438598	Plus	6860-7054,12573-12771
	403506	7596863	Plus	105008-105650
	406016	8272661	Plus	41341-41940
45	405268	4156151	Minus	24404-24521
	401106	8568931	Plus	122694-122893
	404186	4481839	Plus	829-1110
	403817	8962065	Plus	110297-111052
50	406422	9256411	Plus	163003-163311
	402160	8516165	Plus	166063-166354
	402622	9930984	Minus	129861-130099
	401558	7139678	Plus	103510-104090
	404960	7408010	Minus	146186-146377,147747-147943
	401203	9743387	Minus	172961-173056,173868-173928
	402860	9588237	Minus	76423-76560
	401588	7230871	Plus	46412-46561
	404831	6624702	Minus	16833-17020,20007-20120,21605-21799,2333
	405885	7677703	Minus	42574-42998

TABLE 50A: ABOUT 398 GENES UPREGULATED IN PRIMARY MELANOMAS OR MELANOMA METASTASES RELATIVE TO BENIGN NEVI

Table 50A lists about 398 genes upregulated in primary melanoma or melanoma metastases relative to benign nevi. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

55	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
60	R1:	70th percentile of primary melanoma and melanoma metastasis AIs divided by the maximum AI of benign nevi.
	R2:	70th percentile of primary melanoma and melanoma metastasis AIs divided by the maximum AI of benign nevi, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
65	422424	AI186431	Hs.296638	prostate differentiation factor	13.73	16.82
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11.67	11.84
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	9.35	7.59
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.63	7.90
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	8.21	4.09
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	7.13	6.10
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	6.79	6.26
	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	6.36
75	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactadin)	6.43	7.11
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.43	7.51
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.31	4.28
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	6.20	4.32
80	428291	AAS34009	Hs.183487	interferon stimulated gene (20kD)	6.03	4.52
	417308	H60720	Hs.81892	KIAA0101 gene product	6.01	6.78
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.99	7.51
	439310	AF086120	Hs.102793	ESTs	5.95	4.79
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.95	5.55
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.76	4.82
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	5.76	2.19

5	409274	NM_003930	Hs.52644	SKAP55 homologue	5.65	4.63
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.58	3.41
	442711	AF151073	Hs.8645	hypothetical protein	5.45	5.79
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.56
	412918	BE563957		activated RNA polymerase II transcriptio	5.35	4.31
	428125	AA393071	Hs.182579	leucine aminopeptidase	5.33	4.83
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.33	5.13
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.27
10	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.13
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	5.05	13.72
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	5.03	4.93
	436701	AW959032		ESTs, Moderately similar to I78885 serin	5.03	3.42
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.99	3.36
15	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fs, clone C	4.98	5.30
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.98	4.85
	432469	AL080084		CGT-100 protein	4.97	4.46
	404854			Target Exon	4.85	3.49
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.82	4.90
20	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	5.26
	408958	T99607	Hs.49346	signal recognition particle 54kD	4.78	2.34
	453949	AU077146	Hs.36927	heat shock 105kD	4.78	5.18
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	4.13
	440245	AK001913	Hs.7100	hypothetical protein	4.74	3.32
25	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	4.74	1.55
	417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.73	4.25
	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	4.67	4.69
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	4.62	3.02
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.61	5.45
30	452268	NM_003512	Hs.28777	H2A histone family, member L	4.60	2.88
	421311	N71848	Hs.283609	hypothetical protein PRO2032	4.60	3.24
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.34
	425706	AW406678	Hs.122559	hypothetical protein FLJ22570	4.59	3.58
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	4.57	3.82
35	406836	AW514501	Hs.156110	immunoglobulin kappa constant	4.57	9.27
	413441	AJ929374	Hs.75367	Src-like-adaptor	4.53	3.60
	431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434i0812 (f	4.48	4.89
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.47	3.72
	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN	4.47	3.96
40	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig)	4.45	2.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.43	4.27
	448883	BE614989	Hs.7503	hypothetical protein FLJ14153	4.42	3.91
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	4.41	3.80
	419285	D31887	Hs.89868	KIAA0062 protein	4.40	3.20
45	418321	D63477	Hs.84087	KIAA0143 protein	4.38	2.79
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	4.37	3.86
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.36	4.65
	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.36	3.42
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.36	3.31
50	409598	NM_014018	Hs.55097	mitochondrial ribosomal protein S28	4.35	3.10
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.34	5.61
	407047	X65965		gb.H.sapiens SOD-2 gene for manganese su	4.33	3.31
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	4.33	3.57
55	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	4.32	2.20
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ001111 protein,	4.32	3.60
	449722	BE280074	Hs.23960	cyclin B1	4.31	5.79
	408380	AF123050	Hs.44532	drubiquitin	4.30	3.62
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	4.28	4.18
60	417933	X02308	Hs.82962	thymidylate synthetase	4.28	5.06
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	4.25	4.15
	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.24	3.15
	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.23	3.65
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.22	4.21
65	427337	Z46223	Hs.176653	Fc fragment of IgG, low affinity IIb, r	4.20	4.11
	408989	AW361666	Hs.49500	KIAA0746 protein	4.20	4.26
	449626	AA774247	Hs.301637	zinc finger protein 258	4.19	2.65
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	4.18	6.80
	415726	T89844	Hs.78712	aminolevulinic acid, synthase 1	4.16	4.28
	444207	AJ565004		cathepsin D (lysosomal aspartyl protease	4.16	1.89
70	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	4.14	3.32
	438718	AL040058	Hs.6375	uncharacterized hypothalamus protein HT0	4.14	3.02
	437802	AJ475995	Hs.122910	ESTs	4.12	4.18
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	4.12	3.87
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.11	3.80
75	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	4.11	5.71
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	4.10	4.25
	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 fs, clone PL	4.10	2.91
	452882	AW972990	Hs.196270	folate transporter/carrier	4.10	4.25
	414522	AW518944	Hs.76325	immunoglobulin J chain	4.09	3.99
80	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.09	4.60
	405506			Target Exon	4.08	3.64
	444677	AL110212	Hs.301005	purine-rich element binding protein B	4.07	2.43
	417497	AW402482	Hs.82212	CD53 antigen	4.07	6.55
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fs, clone H	4.06	3.27

	421508	NM_004833	Hs.105115	absent in melanoma 2	4.05	4.39
	408688	AI634522	Hs.152925	KIAA1268 protein	4.05	3.32
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.04	3.53
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	4.02	4.20
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	4.01	3.96
	449291	BE176893	Hs.23440	KIAA1105 protein	4.01	2.34
	443071	AL080021	Hs.8986	complement component 1, q subcomponent	4.00	6.97
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.27
10	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	3.98	3.66
	408819	AW163483	Hs.48320	double ring-finger protein, Dorfin	3.98	3.76
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	3.97	2.38
	418942	AI566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	3.97	3.40
	424756	AW504657	Hs.152931	tamin B receptor	3.93	2.67
15	421958	AA357185	Hs.105918	ras homolog gene family, member H	3.89	2.39
	440692	AL031591	Hs.7370	phosphatidylinositol transfer protein, b	3.88	3.23
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.88	4.24
	418255	AW135405	Hs.37251	ESTs	3.87	2.53
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.29
20	450515	AW304226		biphenyl hydrolase-like (serine hydrolase)	3.85	3.73
	416114	AI695549	Hs.183668	glucuronidase, beta	3.85	3.74
	440586	H13032	Hs.103378	hypothetical protein MGC11034	3.84	1.90
	417020	T78413		heterogeneous nuclear ribonucleoprotein	3.82	2.04
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	3.81	3.07
25	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spliced	3.81	3.69
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.80	6.01
	410668	BE379794	Hs.159651	hypothetical protein	3.80	5.22
	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	3.79	3.93
	446071	N51527	Hs.13659	hypothetical protein DKFZp586F2423	3.79	2.74
	419731	S47242	Hs.92909	SON DNA binding protein	3.77	1.85
30	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.98
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	7.42
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.76	3.55
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	3.81
35	423979	AF229181	Hs.136644	CS box-containing WD protein	3.76	3.97
	402474			NM_004079:Homo sapiens cathepsin S (CTSS)	3.76	4.01
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob)	3.75	3.77
	454080	AI199711	Hs.576	fucosidase, alpha-L-1, tissue	3.74	6.15
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	3.74	2.92
40	426096	D87436	Hs.166318	lipin 2	3.72	2.98
	417105	X60992	Hs.81226	CD6 antigen	3.72	2.78
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK)	3.72	3.37
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.70	4.09
	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.79
45	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.69	2.94
	428398	AI249368	Hs.98558	ESTs	3.68	3.82
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	3.67	3.52
	413235	BE243445	Hs.75248	topoisomerase (DNA) II beta (180kD)	3.67	2.79
	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	3.66	3.42
50	409703	NM_006187	Hs.56009	Z'-5-oligoadenylate synthetase 3 (100 k	3.66	6.44
	447225	R62676	Hs.17820	Rho-associated, coiled-coil containing p	3.65	2.93
	414829	AA321568	Hs.77436	pleckstrin	3.65	2.30
	400219			Eos Control	3.64	2.76
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	2.73
55	422445	M23114	Hs.1526	ATPase, Ca transporting, cardiac muscle,	3.62	3.60
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	3.62	3.62
	424460	BE275979	Hs.296014	polymerase (RNA) II (DNA directed) polyp	3.62	3.06
	427609	AK000436	Hs.179791	hypothetical protein FLJ20429	3.62	2.31
	400750			Target Exon	3.61	2.74
60	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	3.61	2.25
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.60	4.20
	433867	AK000596	Hs.3618	hippocampin-like 1	3.59	4.19
	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	3.59	1.58
	414841	H55601	Hs.77490	glutathione S-transferase theta 1	3.58	1.00
65	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.57	3.00
	425204	NM_002436	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.56	3.09
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HE	3.56	3.26
	442043	BE567620	Hs.99210	ESTs	3.55	3.56
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	3.55	3.83
70	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	3.54	3.52
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.54	4.66
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.54	3.25
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fis, clone C	3.54	1.87
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	3.53	3.96
75	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	3.53	3.40
	426643	AA857131	Hs.171595	HIV TAT specific factor 1	3.51	2.21
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	3.51	2.51
	429248	U96759	Hs.198307	von Hippel-Lindau binding protein 1	3.51	2.85
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.51	2.71
80	451791	Z78407	Hs.27023	vesicle transport-related protein	3.49	2.91
	418310	AA814100	Hs.86693	ESTs	3.49	1.45
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.48	6.81
	400200			NM_002788:Homo sapiens proteasome (pros	3.48	2.51
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.94

5	441646	AB023169	Hs.7935	KIAA0952 protein	3.47	3.38
	427968	A1857607	Hs.181301	cathepsin S	3.45	2.71
	440201	AL359588	Hs.7041	hypothetical protein DKFZp762B226	3.45	3.45
	434608	AA805443	Hs.179909	hypothetical protein FLJ22995	3.44	3.68
	427527	A1809057	Hs.153261	immunoglobulin heavy constant mu	3.44	6.70
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	3.44	2.72
	435550	A1224456	Hs.324507	H.sapiens polyA site DNA	3.43	2.76
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.43	3.64
10	423392	AA195037	Hs.169341	HTPAP protein	3.43	2.29
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	3.43	2.78
	453915	AA588721	Hs.286218	ribosomal protein L44	3.41	3.06
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	3.41	4.23
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.40	3.93
15	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	3.40	2.12
	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	4.70
	422545	X02761	Hs.287820	fibronectin 1	3.39	7.58
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.36	4.12
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.34	5.05
20	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.33	4.31
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.33	4.60
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	3.32	4.49
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheri	3.24	4.22
	43623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.23	12.31
25	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23	5.07
	443958	BE241880	Hs.10029	cathepsin C	3.16	4.97
	412577	Z22968	Hs.74076	CD163 antigen	3.14	4.75
	414050	NM_004766	Hs.75724	coatamer protein complex, subunit beta 2	3.13	4.00
	421633	AF121860	Hs.106260	sorting nexin 10	3.12	4.45
30	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	3.11	4.00
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	3.10	4.03
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.06	4.49
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.04	4.98
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.03	4.49
35	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	3.01	4.75
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	2.95	5.55
	422684	BE561617	Hs.119192	H2A histone family, member Z	2.94	4.64
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.93	10.28
40	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.91	5.40
	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.90	4.86
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.89	4.04
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.87	9.61
	423605	AF047826	Hs.129887	cadherin 19, type 2	2.83	4.86
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82	5.02
45	419956	AL137939	Hs.40096	cadherin 19, type 2	2.80	4.30
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.79	5.80
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.21
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	2.78	4.23
	416784	AA334592	Hs.79914	tumican	2.78	4.40
50	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	2.77	4.23
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.77	4.17
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.76	4.43
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.20
	437179	AA393508		serologically defined colon cancer antig	2.74	4.07
55	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72	4.63
	429102	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-i	2.71	4.93
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.15
	426124	A1268389	Hs.250697	phosphatidylinositol glycan, class F	2.68	4.00
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.67	4.72
60	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.65	7.77
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21026 fis, clone C	2.65	4.47
	410341	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	5.61
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.63	4.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62	4.95
65	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.60	6.00
	424779	AL046851	Hs.153053	CD37 antigen	2.60	4.27
	409354	N68188	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H	2.60	4.64
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	2.57	4.27
	426143	BE379836		proteasome (prosome, macropain) subunit,	2.56	4.20
70	421563	NM_006433	Hs.105806	granulysin	2.56	4.13
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	2.55	5.46
	428169	A1928984	Hs.182793	golgi phosphoprotein 2	2.54	5.78
	429800	AA333375	Hs.223014	antizyme inhibitor	2.50	5.15
	407241	M34516		gb:Human omega light chain protein 14.1	2.50	4.98
75	421739	AB004550	Hs.107526	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.45	5.58
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.45	7.20
	412025	A1827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	2.44	4.11
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.67
	445350	AF052112	Hs.12540	lysophospholipase I	2.44	5.44
80	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	2.41	4.31
	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.41	4.25
	400223			Eos Control	2.39	5.68
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	2.39	6.62
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.38	7.22

5	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.21
	415149	X12451	Hs.78056	cathepsin L	2.37	7.71
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.68
	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; poly (ADP-ribose) polymerase 2	2.31	4.89
	426432	AF001601	Hs.169857	paraoxonase 2	2.29	4.83
	430555	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.27	5.03
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	2.25	4.14
	412617	AK001364	Hs.808	heterogeneous nuclear ribonucleoprotein	2.21	4.31
10	447547	NM_007229	Hs.18842	protein kinase C and casein kinase subst	2.19	4.62
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.18	4.84
	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.14	4.22
	411358	R47479	Hs.94761	KIAA1691 protein	2.13	4.65
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.03
15	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.11	4.16
	417331	AW411297	Hs.81972	SHC (Src homology 2 domain-containing) t	2.11	4.25
	450344	AW994032	Hs.8768	hypothetical protein FLJ10849	2.11	4.09
	429642	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (2.11	5.42
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	6.42
20	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	2.10	4.00
	453352	T10446		ESTs	2.09	4.48
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.09	4.98
	414045	NM_002951	Hs.75722	ribophorin II	2.07	4.59
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.09
25	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.06	5.06
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	2.04	11.17
	438393	AA351815	Hs.50740	Homo sapiens cDNA: FLJ22272 fis, clone H	2.03	4.36
	413313	NM_002047	Hs.283108	glycyl-tRNA synthetase	2.02	4.79
	412994	D32257	Hs.75113	general transcription factor IIIA	2.00	4.67
30	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.79
	421897	AW583693	Hs.109253	N-terminal acetyltransferase complex and	1.98	4.17
	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.95	7.53
	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	1.95	4.63
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.95	4.31
35	400203			Eos Control	1.94	5.03
	437317	AA748613	Hs.311977	ESTs, Highly similar to SWI/SNF related,	1.94	4.03
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.93	4.68
	416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.92	4.12
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	1.91	4.23
40	413945	NM_000591	Hs.75627	CD14 antigen	1.90	5.00
	413317	U53225	Hs.75283	sorting nexin 1	1.89	4.20
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.89	4.26
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	1.88	4.15
	427239	BE270447		ubiquitin carrier protein	1.87	5.72
45	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.87	5.81
	433671	AW138797	Hs.132906	19A24 protein	1.85	4.27
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.85	5.19
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.85	4.31
	430040	AW503115	Hs.227823	pM5 protein	1.83	5.57
50	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.82	4.29
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.39
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	1.80	4.20
	428977	AK001404	Hs.194698	cyclin B2	1.79	4.17
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.78	4.30
55	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.78	5.44
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.77	5.11
	422009	AI742845	Hs.110713	DEK oncogene (DNA binding)	1.77	4.37
	424909	S78187	Hs.153752	cell division cycle 25B	1.74	5.00
	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	4.86
60	413892	AI878921	Hs.75607	myristoylated alanine-rich protein kinas	1.73	4.37
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.02
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.70	4.68
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.70	4.59
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.67	5.59
65	413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.39
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4.03
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.24
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	1.64	4.91
	443051	AA333660	Hs.71331	hypothetical protein MGC5350	1.64	4.08
70	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4.41
	446143	BE245342	Hs.306079	sec61 homolog	1.62	4.70
	431142	AA852596	Hs.250641	tropomyosin 4	1.62	4.86
	407752	AA573581	Hs.13328	ESTs	1.62	4.19
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	1.61	4.51
75	414572	AU077174	Hs.288181	cathepsin H	1.60	5.25
	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.56
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.58	5.46
	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	1.58	4.05
	414420	AA043424	Hs.76095	immediate early response 3	1.58	4.00
80	419638	N46504	Hs.91747	profilin 2	1.57	5.57
	422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.57	4.44
	415819	AU077330		transcription elongation factor A (SII),	1.55	4.89
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.66
	425243	N89487	Hs.155291	KIAA0005 gene product	1.54	4.38

5	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-	1.53	4.22
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.53	7.41
	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.51	4.12
	418879	AW162087	Hs.5437	Tax1 (human T-cell leukemia virus type 1	1.50	4.02
	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	1.50	4.18
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.49	4.19
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.49	5.74
	452264	AU077013	Hs.28757	transmembrane 9 superfamily member 2	1.48	4.53
10	415198	AW009480	Hs.943	natural killer cell transcript 4	1.47	4.95
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	1.45	4.61
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H	1.45	4.15
	421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	1.42	4.67
	415089	N25117	Hs.299465	ribosomal protein S26	1.41	5.19
15	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.41	4.03
	400202			NM_002795*:Homo sapiens proteasome (pros	1.41	4.44
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.41	4.57
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase	1.40	4.25
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	4.11
20	447099	AB030656	Hs.17377	coronin, actin-binding protein, 1C	1.39	4.51
	428511	AA019912	Hs.184693	transcription elongation factor B (SIII)	1.38	4.90
	413825	BE299181	Hs.75564	CD151 antigen	1.37	4.44
	441737	X79449	Hs.7957	adenosine deaminase, RNA-specific	1.36	4.29
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.36	4.10
25	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.35	4.50
	413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.35	5.14
	433026	AW160616	Hs.279921	HSPC035 protein	1.35	4.14
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	1.34	4.35
	428289	M26301	Hs.2253	complement component 2	1.33	4.23
30	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.32	4.61
	425299	AW505214	Hs.155560	calnexin	1.31	4.76
	422242	AJ251760	Hs.273385	guanine nucleotide binding protein (G pr	1.30	5.30
	448483	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	1.29	6.09
	407143	C14076	Hs.332329	EST	1.29	4.56
35	413125	BE244589	Hs.75207	glyoxalase 1	1.26	5.56
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.26	4.98
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.25	4.76
	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	1.24	4.56
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.21	8.96
40	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.21	4.02
	425335	BE394327	Hs.296267	folistatin-like 1	1.18	4.29
	446211	AJ021993	Hs.14331	S100 calcium-binding protein A13	1.17	4.32
	428642	NM_014899	Hs.10432	KIAA0878 protein	1.13	4.17
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	1.10	4.00
45	428216	M18468	Hs.183037	protein kinase, cAMP-dependent, regulato	1.09	4.40
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.00	4.70
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	0.98	4.40
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	0.90	4.78
50	TABLE 50B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
55	Pkey	CAT Number	Accession			
	412918	2764_3	BE748583 AL519009 AV755430 AV756363 AV711927 BI523434 AI521453 AA846815 AW024829 AW949702 BG218926 AA626658 AI445621 AI452815			
			AA946555 AA723580 AA612925 BG105326 BG532618 AW513994 AW602165 AI373448 AA907901 AW135104 BG186662 W69205 BG219754			
			BE774875 BG190378 AA483698 BE066066 BE066067 BE066062 AW304207 BE939361 AW795569 BG210592 AW795644 BE939358 AW102886			
			BE065977 BG182971 H97042 D58090 BI046351 H81248 AI750112 AW372079 C05492 D58287 D57835 AA935095 BF700910 BG215802 BG195459			
60	436701	28142_1	AW368467 BG495535 BG533177 BI087962 BE541579 BF130753			
			Z69892 AA210833 BM353155 AI473754 AI147901 AI803109 AA843296 AA418925 AJ478552 AI400067 AI360304 AA418828 AW301673 BE218952			
			AI632804 BF433234 AA394157 BF378047 BE467036 AA319724 AW290940 AJ222671 AI347724 AW001711 AJ028652 AA398130 AI470582 AI515936			
			AA908929 C75102 N36920 H50440 AI919034 AJ004399 AI383862 AI123606 AA648518 AA516258 AI865321 N22865 AA848101 AI589792 AA758196			
			AA214630 AI373911 AW194733 AA213447 AJ290291 BF437165 AA757592 BF086904 AW959032 AW992466 BF446888 AI936337 BE938849			
65	432469	58644_1	AW149064 AI701629 N90021			
			BC016556 BC016365 NM_016040 AF151858 BI561037 AW966873 AW967497 BE219482 BE018650 AW770511 AW469095 AW470133 BM150181			
			BM193977 AI824135 AI632346 AI129838 BM147664 AI292112 BE244667 AA251084 AW503659 BM193866 BM194481 BF446862 AL597435 BF000262			
			AI824386 AI990100 AW087624 AA668793 AL080084 BI335866 BI820940 BG779242 BM069854 AA282620 AA256771 AW964511 AA451623 H00335			
			AW370399 AW954201 BM145846 BG111760 AI750065 BG655794 AA564086 BG494071 BM069606 AI675331 BE302224 AI476466 AI625980			
70			BM147654 AI184602 AI343932 AW135586 AW029464 AI708651 AA824243 BM145917 AA662210 AA825708 AI335858 AI273704 AA662171 N48971			
			AA976614 AI344537 AA609603 AI873901 AI859995 AA833589 AA765811 AI150322 AI926816 BM148634 N98862 AA019347 AA897062 AA831100			
			N69889 BE243185 AA282179 AA831098 AA112676 AI702407 BG621752 BE006492 AA353202 BG674256 N46921 BI048774 AW300233 BF739890			
			AW966879 AA393405 BF115146 AA910851 AA013099 N28878 AA287713 BE348728 BG616446 AL599953 AL599952 BF381073 AW505056 AA094735			
			H03813 AA287714 H27168 R54718 BF792697 AV693603 AV685883 BG619956 BF541504 BF216789 AA319751 BM452652 BF335838 AA280397			
75			BG171509 BF571997 AA490239 AW388161 BE842126 BG165309 N71903 AI955397 AI536898 BE242040 F09718 AA772421 AA450218 M78543			
			BE241414 AA013098 H00297 AW576477 AW150918 AW591371 AI382711 N71926 H72497 AI285602 AA745055 AA281647 BF377670 T65207			
			BE532880 BG721680 AA285143 H27167 AW500235 BG494497 BF668899			
	424571	9758_1	BE379766 AW152643 AI803450 AI564343 AI092711 AI140525 AW152156 AI620740 AI554689 AI161209 AI290242 AI339745 AI374611 AI347388			
			AI858296 AI140529 AI366124 AA493912 AA406235 AA433889 AI057160 AW022264 AI097277 AI144126 AI080051 AA983529 AA860507 N53469			
80			AA843767 N81163 N70628 AA424577 AA983537 BF003004 AA626688 AA235977 AI057152 AI095366 AI095356 AA458646 AW194479 AA150439			
			AI375272 AW571777 AI359198 AA933793 BE614394 BE738239 AA127883 AI034344 T59504 D81608 AA908704 AW051665 AA382785 AA307208			
			N24639 AI370715 BE244980 AA548596 AW449675 AI191008 BF223749 N70752 N22266 AI191012 AA028001 AI419106 BF215661 BF591548			
			BG942356 AI474968 BE858217 BF793358 AV756758 BG483603 AI093724 BF693395 BG545345 AI744294 T59549 AA811773 BG499757			

444207	9172_3	BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AJ470335 AI247243 BGS33994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE066682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299605 AI589870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI087171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI860904 AA876023 AK024824 BI089104 AI596792 AI880004 BF969921 BE349489 AA843097 AI475644 AW576123 AW731676 AI339951 AI128503 AW243903 BG231992 BG057353 AA987811 AA575927 AI889162 N68847 AA464693 AA962541 AA844323 AI969578 AI830997 AW731626 H77926 H77926 AI338984 R24078 AI128953 T88696 AA808038 AA694545 H02091 BF439007 AI189805 AI279912 AA730423 R26552 AA455017 AI264219 AI466015 R19187 D51331 T24484 AI522034 AV721528 BI056340 BG009879 AW371368 Z36733 BE707682 BG501334 BG180238 BE177547 H48381 BF055495 AI948528 AW994256 BF109394 AI817046 W58758 H48807 H01994 T78413 BG750345 R24132 N92060 R25367 BC003552 L10284 NM_001746 AJ271880 BI834281 B597016 AU133331 BI668332 BI463073 BG720694 AL046729 BI460138 BI461052 AV647588 BG623268 AW889757 BE001258 AA312566 AA476446 AU089876 AA312196 BF749977 M94859 AF070646 BG564196 BG623597 AU117332 BG680963 BI667083 AU134542 AU138830 AU761759 BG679882 AA209406 AW512644 AW514813 AI570535 BE547592 BG655418 AI459204 BF725673 BE870032 BF001968 AL047245 BF724470 BF058818 H18415 BE076849 BE076857 BE076848 BE076827 BE076856 AV708887 AA380923 BE076851 F08118 L18887 BF795701 AU128383 BE908383 AW673350 AW500108 BE079837 BE929419 BF686878 AW503373 AW580528 BE005524 BI917505 BI457781 BE883812 BI668159 AA213643 AA374821 BF969974 BM480200 AU136152 BE395635 AV685066 AV693755 AL040984 AA676820 BG896408 BE082272 BE082312 C05287 BE082264 AA379850 AW672902 AI625855 BF033526 AW296557 AA728815 BE077058 AW081700 AA911707 AA362640 BE707179 BG913228 BG116191 BG752367 AA074678 AL036937 BG113760 H03524 BG681802 AI564688 AU149556 BE178600 AI813488 AI452433 AI208989 AA599392 AA580385 AA486274 AA629899 AA565929 AA114046 AA094252 BM450328 BG529968 R68320 BE076792 BE090073 BE076855 BE076859 AA361719 AA379164 AI202712 BG223315 BE122741 BG534531 AA903494 H24978 BF032674 BF085150 BE739158 AA352904 C21593 BG697597 AA134969 AA374612 BE566182 BE871838 BE076911 AW579175 BF966390 BI458494 BG386452 BG913195 BM456787 N40286 T80095 N39642 H42119 BG483861 AW381621 R69347 AW128895 AI367416 AI095285 AA099344 BE568161 AA180109 BF246488 BI561938 AW579170 BG567212 L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 AA430373 AA968771 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AI134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476921 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BMD43599 AL521812 BG705730 BI495545 BI495546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA399446 BG22375 BM019558 BM023382 BG164174 N56909 BI467064 BM023464 AI207475 BM311415 BG758430 BG758807 AI934826 N90351 BG422026 BE910312 AI027778 AI081950 AI360890 BM009115 AI191829 BG759697 AI138728 AA399403 AI355589 AI336427 AA868702 AA393660 AA025127 BG027630 AA962774 AA631224 BG940967 BE791087 AA573315 W81685 AA393525 BG944103 AI339125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA888954 AA975844 AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI601114 AW135664 AI206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI160457 H64512 BG503896 M31126 BG619646 AA367158 BI850421 AW998556 BF107010 BF969630 BF185964 AA361080 AW960026 AA147486 AI807023 AW770262 BI492178 BM145577 AA829932 AW021238 AW629477 AI337862 AI457141 BI712705 BM194542 BI712465 AI380070 N27407 AI609764 AI274152 AI206228 AI076874 AI261827 AI610982 AI469158 AI406990 AI168768 AA491675 C16249 C16232 C16209 C16275 C16274 C16243 R23287 BF246254 R66736 R23212 C14593 NM_002794 D26599 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 AI189162 AI831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133 AA131997 AA284572 AA453009 BF928258 AA152127 AA393918 BF765307 BE247542 BF934697 BF341798 BE253409 AA470620 AI828932 AW379902 AV762678 AV741784 AV760892 AI025755 AA878562 AA630630 AA761708 AA862518 AA855831 AA862947 N53065 AA131821 AA293499 N23342 N26856 AI147346 AW951549 AA772963 BE245986 BG208493 AI831666 BG474873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW276192 AU149842 BG214797 BG198193 AW197923 AW627799 T98663 BG194788 BG214656 BF345258 BG716363 AI066528 BI546220 AA339315 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735966 BG196439 BG216840 BG198438 BG400762 AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA454019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054435 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF178773 BF178645 AW074866 BE857822 BE739429 BM460292 AL549095 BF752457 BE783002 BG035869 AW601528 AI880413 BF593762 AA974415 AA3935318 AA716501 AI936239 AI809486 AI744171 AW804992 BF108747 AW804693 BE219333 AI807707 AA306963 BG012140 BF741621 BF741618 BF741619 AW062543 AA155832 AU151381 AU158043 AU150410 AU145605 AU150252 AA188205 AU153035 AI147293 AA084507 AA868165 AI887120 AI468363 AW023112 H44035 F01513 AA747672 AW779630 AA757298 R77738 AI150931 R38473 AA189022 H96984 AL550490 AW949737 AU150194 AU149258 AI749453 AW172950 AW276160 AI753604 AI421762 AW575512 AI275633 AW516120 AI340167 AI567728 AI797326 AI471532 AI074080 AI633122 AW674646 AW316571 AA258187 AA102780 AA258186 AI363307 AA862862 AI206836 AA629555 AA486287 AI185097 AI872389 BE465687
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TABLE 50C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
404854	7143420	Plus	14260-14537
405506	6466489	Plus	80014-80401,80593-81125
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
400750	8119067	Plus	198991-199168,199316-199548

TABLE 51A: ABOUT 453 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO NORMAL SKIN

Table 51A lists about 453 genes upregulated in primary melanomas relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs

R2: 90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.06	15.56
430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	13.64	11.62
428555	NM_000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	13.50	7.98
438549	BE386801	Hs.21858	trinucleotide repeat containing 3	12.78	13.80
422424	AI186431	Hs.296638	prostate differentiation factor	11.88	15.56
426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	10.14	22.46
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	9.33	7.25
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	8.66	9.62
438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	7.87	9.58
417355	D13168	Hs.82002	endothelin receptor type B	7.66	4.63
447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	7.38	9.04
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.64	7.32
415752	BE314524	Hs.78776	putative transmembrane protein	6.46	4.65
421508	NM_004833	Hs.105115	absent in melanoma 2	6.44	7.00
449644	AW960707	Hs.148324	ESTs	6.43	5.92
426312	AF026939	Hs.181874	interferon-induced protein with tetratri	6.27	6.47
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.17	3.70
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	6.09	3.92
414812	X72755	Hs.77367	monokine induced by gamma interferon	6.04	7.73
452973	H88409	Hs.40527	ESTs	6.04	5.89
402075			ENSP00000251056: Plasma membrane calcium	5.96	2.50
436856	AI469355	Hs.127310	ESTs	5.72	5.29
425088	AA663372	Hs.169395	hypothetical protein FLJ12015	5.68	5.88
439310	AF086120	Hs.102793	ESTs	5.62	6.30
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.62	3.30
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	5.50	4.28
409512	AW979187	Hs.293591	melanoma differentiation associated prot	5.36	4.14
430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	5.36	4.64
436315	BE390513	Hs.27935	hypothetical protein MGC4837	5.35	4.31
442426	AI373062	Hs.332938	hypothetical protein MGC5370	5.28	4.03
435056	AW023337	Hs.5422	glycoprotein M6B	5.23	3.25
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	5.20	5.52
430294	AJ538226	Hs.32976	guanine nucleotide binding protein 4	5.14	4.82
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	5.09	4.35
430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.06	3.68
414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.04	4.23
407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.94	6.29
422192	AA305159	Hs.113019	fts485	4.88	5.62
420208	BE276055	Hs.95972	silver (mouse homolog) like	4.88	6.00
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.77	4.33
440065	W03476	Hs.266331	hypothetical protein MGC4595	4.74	9.85
421574	AJ000152	Hs.105924	defensin, beta 2	4.74	5.75
440274	R24595	Hs.7122	scrapie responsive protein 1	4.72	2.78
417166	AA431323	Hs.42146	ESTs	4.68	4.29
415314	N88802	Hs.5422	glycoprotein M6B	4.65	3.73
443983	H04482	Hs.163724	ESTs	4.64	3.06

5	432642	BE297635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	4.62	2.87
	437179	AA393508		serologically defined colon cancer anti	4.62	5.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.58	3.02
	431620	AA126109	Hs.264981	Z'-5'-oligoadenylate synthetase 2 (69-71	4.50	4.37
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	4.49	16.82
10	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.44	5.95
	409264	NM_014937	Hs.52463	KIAA0966 protein	4.42	2.94
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.42	3.54
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	4.38	3.30
	449722	BE280074	Hs.23960	cyclin B1	4.32	4.07
15	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.30	3.82
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	4.28	4.36
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	4.27	3.05
	413916	N49813	Hs.75615	apolipoprotein C-II	4.25	4.68
	420267	N37030	Hs.173337	ESTs	4.24	4.24
20	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.21	3.00
	433576	BE080715	Hs.161091	ESTs	4.20	6.31
	412652	A1801777		ESTs	4.20	2.73
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	4.20	5.18
	441553	AA281219	Hs.121296	ESTs	4.14	4.94
25	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	4.14	3.14
	439926	AW014875	Hs.137007	ESTs	4.12	4.76
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.12	4.85
	400860			Target Exon	4.10	5.20
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	4.08	6.02
30	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.08	2.42
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	4.06	2.96
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	4.06	2.28
	417632	R20855	Hs.5422	glycoprotein M6B	4.01	2.96
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	4.00	4.62
35	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.00	2.82
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.00	2.90
	451668	Z43948	Hs.326444	cartilage acidic protein 1	3.99	5.17
	430015	AW768399		ESTs	3.96	3.89
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.94	2.91
40	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	3.93	3.89
	433364	AU075407	Hs.296083	ESTs, Moderately similar to I54374 gene	3.93	4.70
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	3.92	7.78
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.87	3.34
	402609			KIAA1209 protein	3.87	3.69
45	408083	BE383668	Hs.42484	hypothetical protein FLJ10618	3.86	4.04
	409703	NM_006187	Hs.56009	Z'-5'-oligoadenylate synthetase 3 (100 k	3.85	3.64
	420218	AW958037		ribosomal protein L4	3.84	3.20
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.84	5.19
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	3.82	5.74
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.82	2.96
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	3.82	4.03
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	3.80	3.56
	432094	AU658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	3.79	3.23
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.77	3.66
55	423605	AF047826	Hs.129887	cadherin 19, type 2	3.72	2.28
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.72	5.34
	442578	AK001643	Hs.8395	hypothetical protein FLJ10781	3.71	3.42
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.68	3.31
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.68	4.24
60	400750			Target Exon	3.68	2.74
	447217	BE465754	Hs.17778	neuropilin 2	3.66	3.60
	459373	BE408266	Hs.301406	hypothetical protein PP3501	3.66	3.48
	419628	H67546	Hs.49768	ESTs	3.62	4.13
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.61	4.40
65	421866	M24470	Hs.1435	guanosine monophosphate reductase	3.59	3.53
	421709	AA159394	Hs.107056	CED-6 protein	3.57	2.63
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	3.54
	408962	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	3.55	2.70
	425139	AW630488	Hs.25338	protease, serine, 23	3.50	2.80
70	428411	AW291464	Hs.10338	ESTs	3.49	2.58
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.48	4.61
	411305	BE241596	Hs.69547	myelin basic protein	3.48	3.37
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	3.47	2.68
	429954	AJ918130	Hs.21374	ESTs	3.47	2.63
75	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3.46	2.34
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.46	2.47
	450534	AJ570189	Hs.25132	KIAA0470 gene product	3.42	3.65
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	3.41	2.63
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	3.40	4.02
80	442711	AF151073	Hs.8645	hypothetical protein	3.39	2.95
	453344	BE349075	Hs.44571	ESTs	3.38	2.38
	436700	AJ693690	Hs.301406	hypothetical protein PP3501	3.36	4.60
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	2.61
	433867	AK000596	Hs.3618	hippocalcin-like 1	3.36	4.26
	408393	AW015318	Hs.23165	ESTs	3.36	2.10
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	3.36	2.49
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.35	2.27

5	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.35	2.58
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	3.34	2.55
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	3.34	5.96
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.34	2.73
	406663	U24683		immunoglobulin heavy constant mu	3.31	5.21
10	427540	R12014	Hs.20976	ESTs	3.30	3.40
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	3.29	2.80
	400282			NM_005313:Homo sapiens glucose regulated	3.29	3.46
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.28	5.20
	416539	Y07909	Hs.79368	epithelial membrane protein 1	3.28	2.79
15	431518	AA743462	Hs.165337	ESTs	3.27	2.51
	402994			NM_002463*:Homo sapiens myxovirus (influ	3.26	6.38
	419956	AL137939	Hs.40096	cadherin 19, type 2	3.26	4.48
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.26	3.71
	444371	BE540274	Hs.239	forkhead box M1	3.25	3.72
20	432874	W94322	Hs.279651	melanoma inhibitory activity	3.25	5.33
	417282	AA195203		RAB3C, member RAS oncogene family	3.24	3.20
	439569	AW602166	Hs.222399	CEGP1 protein	3.24	2.32
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.24	6.20
	403817			NM_015271:Homo sapiens tripartite motif-	3.23	3.70
25	407857	AI928445	Hs.92254	synaptotagmin-like 2	3.22	2.49
	426334	BE305081	Hs.169358	hypothetical protein	3.21	2.46
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	3.19	5.50
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.18	2.04
	437379	AL359575	Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	3.18	3.73
30	424090	X99699	Hs.139262	XIAP associated factor-1	3.18	4.44
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	3.18	3.26
	408418	AW963897	Hs.44743	KIAA1435 protein	3.16	2.21
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.16	4.04
	402829			C1002500.gi6754254[ref]NP_034610.1 hea	3.15	4.57
35	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.15	3.07
	425935	Z98200	Hs.163724	HSPC019 protein	3.14	3.08
	417124	BE122762	Hs.25338	ESTs	3.14	2.73
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.11	2.16
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.10	2.43
40	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.10	2.83
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.10	1.78
	429083	Y09397	Hs.227817	BCL2-related protein A1	3.10	3.17
	437673	AW565665	Hs.153034	ESTs	3.10	3.32
	407813	AL120247	Hs.40109	KIAA0872 protein	3.10	3.90
45	445745	AB007924	Hs.13245	KIAA0455 gene product	3.10	3.35
	451537	R56631	Hs.26550	retinoid X receptor, gamma	3.09	4.45
	408654	BE018882	Hs.46721	UCC1 protein	3.08	3.65
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.08	2.12
	446019	AI362520		histone deacetylase 3	3.08	2.26
50	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	3.08	5.29
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.06	3.36
	403532			NM_024638:Homo sapiens hypothetical prot	3.06	3.37
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.04	3.17
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	3.03	2.98
55	426501	AW043782	Hs.293616	ESTs	3.03	2.01
	450325	AI935962	Hs.91973	ESTs	3.02	2.19
	418941	AA452970	Hs.235527	E1B-55kDa-associated protein 5	3.02	3.29
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.02	2.54
	442064	AI422867	Hs.88594	ESTs	3.00	1.96
60	405451			dihydropyrimidinase-like 3	3.00	2.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.99	6.41
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.98	3.25
	452958	AA883929	Hs.40527	ESTs	2.98	4.14
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.96	3.30
65	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.96	2.47
	428819	AL135623	Hs.193914	KIAA0575 gene product	2.96	4.16
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.96	2.41
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	2.95	2.79
	411358	R47479	Hs.94761	KIAA1691 protein	2.95	4.70
70	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	2.94	2.65
	400222			NM_002082*:Homo sapiens G protein-couple	2.94	2.69
	405785			NM_025184*:Homo sapiens hypothetical pro	2.94	2.55
	409760	AA302840		gb.EST10534 Adipose tissue, white 1 Homo	2.94	2.57
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.93	2.52
75	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.93	2.43
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	2.92	3.20
	459710	AI701596	Hs.121592	ESTs	2.91	4.45
	411395	AA889673	Hs.7542	KIAA1802 protein	2.90	2.72
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.90	2.27
80	406964	M21305		FGENES predicted novel secreted protein	2.90	2.03
	428834	AW899713	Hs.339315	ESTs	2.89	3.55
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.89	3.87
	438619	AB032773		TU12B1-TY protein	2.88	2.37
	442432	BE093589	Hs.38178	hypothetical protein FLJ23458	2.87	2.00
	428782	X12830	Hs.193400	interleukin 6 receptor	2.86	2.51
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.86	3.07
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	2.86	5.58

	414737	AI160386	Hs.125087	ESTs	2.84	2.79
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklins	2.84	3.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	2.83	2.11
	416091	AF295370	Hs.283082	defensin, beta 3	2.83	3.32
5	442445	AA082665	Hs.209561	KIAA1715 protein	2.81	2.17
	408208	BE018717		ESTs	2.81	2.43
	430066	AI929659	Hs.237825	signal recognition particle 72kD	2.80	2.25
	424755	AB033094	Hs.152925	KIAA1268 protein	2.80	2.74
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	2.79	2.01
10	405506			Target Exon	2.78	2.65
	411619	AI418609	Hs.71040	hypothetical protein FLJ20425	2.78	3.10
	400236			Eos Control	2.78	2.21
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.78	3.15
	446488	AB037782	Hs.15119	KIAA1361 protein	2.78	2.80
15	439778	AL109729	Hs.99364	putative transmembrane protein	2.78	3.78
	420005	AW271106	Hs.133294	ESTs	2.78	2.86
	428642	NM_014899	Hs.10432	KIAA0878 protein	2.77	3.07
	453779	N35187	Hs.43388	28kD interferon responsive protein	2.76	4.56
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	2.76	1.83
20	437723	AI672731	Hs.13256	ESTs	2.76	4.23
	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76	2.98
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.76	3.21
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.76	3.97
	421351	AU076667	Hs.103755	receptor-interacting serine-threonine ki	2.74	3.50
25	406673	M34996	Hs.198253	major histocompatibility complex, class	2.74	3.24
	427268	X78520	Hs.174139	chloride channel 3	2.74	2.82
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	2.74	1.95
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.74	2.99
	419705	AW368634	Hs.154331	ESTs	2.74	2.28
30	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.72	3.60
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reductase	2.72	2.43
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.72	4.77
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	2.72	3.67
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.71	12.06
35	424572	M19650	Hs.179600	2',3'-cyclic nucleotide 3' phosphodiester	2.70	2.40
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.70	3.81
	425996	W67330		hypothetical protein AL110115	2.69	3.85
	430441	BE398091		desmoplakin (DPI, DP1)	2.68	2.55
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	2.68	1.67
40	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	2.68	2.94
	437158	AW090198		KIAA1150 protein	2.68	1.89
	412315	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo	2.68	2.80
	432878	BE386490	Hs.279663	Pirin	2.68	2.58
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.68	2.74
45	426759	AI590401	Hs.21213	ESTs	2.68	2.35
	405486			Target Exon	2.67	2.70
	410326	AI368909	Hs.47650	ESTs	2.67	3.33
	434040	AW444613	Hs.288809	hypothetical protein FLJ20159	2.66	2.54
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.66	1.91
50	412719	AW016610	Hs.816	ESTs	2.66	4.21
	451708	AI306536	Hs.60975	ESTs	2.66	5.69
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.66	2.31
	425017	AL119305	Hs.26409	ESTs	2.66	2.73
	400235			NM_005336:Homo sapiens high density lipo	2.66	2.29
55	444809	BE207568	Hs.208219	oculospanin	2.64	2.86
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.64	2.33
	406382			C16001275:gi12698037 dbj BAB21837.1 (2.64	2.48
	432241	AI937060	Hs.6298	KIAA1151 protein	2.63	3.16
	417308	H60720	Hs.81892	KIAA0101 gene product	2.63	2.10
60	429294	AA095971	Hs.198793	Homo sapiens cDNA: FLJ22463 fis, clone H	2.62	2.43
	453935	AI633770	Hs.42572	ESTs	2.62	1.99
	401454			NM_014226*:Homo sapiens renal tumor anti	2.62	3.01
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.62	5.94
65	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.61	3.02
	453256	AI565587	Hs.32556	KIAA0379 protein	2.60	2.68
	451622	AW139587	Hs.30579	Homo sapiens cDNA: FLJ23070 fis, clone L	2.60	2.51
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.60	2.56
	409354	N58188	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H	2.59	3.00
	425392	N39725	Hs.15220	zinc finger protein 106	2.58	3.52
70	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	2.58	1.86
	418166	AI754416		Cdc42 effector protein 3	2.58	2.15
	413794	AF234532	Hs.61638	myosin X	2.58	2.54
	445707	AI248720	Hs.114390	ESTs	2.58	1.95
	416640	BE262478	Hs.79404	neuron-specific protein	2.57	2.46
75	427982	NM_016156	Hs.181326	KIAA1073 protein	2.56	1.74
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.56	2.22
	455839	BE145814		gb:MR0-HT0208-101299-202-a04 HT0208 Homo	2.55	2.34
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	2.55	2.31
	423799	AW026300	Hs.132906	19A24 protein	2.54	2.11
80	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.54	2.47
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.54	3.99
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54	2.96
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.53	6.98

5	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1		
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2.53	3.06
	458997	AW937420		ESTs	2.53	3.13
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.53	1.63
	414807	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.52	2.30
10	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.52	1.80
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.52	3.02
	407260	L09095		gb:Homo sapiens mRNA fragment	2.52	3.05
	431186	NM_012249	Hs.250697	ras-like protein	2.50	5.00
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	2.49	6.16
15	419556	U29615	Hs.91093	chitinase 1 (chito/hiosidase)	2.49	4.71
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.48	5.77
	405885			Target Exon	2.48	3.77
	406837	R70292	Hs.156110	immunoglobulin kappa constant	2.46	3.11
	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.44	3.10
20	421633	AF121860	Hs.106260	sorting nexin 10	2.44	4.90
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.44	4.31
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.42	3.19
	406621	X57809	Hs.8997	immunoglobulin lambda locus	2.37	3.57
	414142	AW368397	Hs.334485	hemocentin (fibrin 6)	2.36	5.87
25	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.36	3.04
	414283	AW960011	Hs.154993	ESTs	2.36	3.66
	453931	AL121278	Hs.25144	ESTs	2.34	4.95
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.34	4.18
	435292	N20514	Hs.172965	ESTs	2.32	3.45
30	412926	AJ879076	Hs.75061	macrophage myristoylated alanine-rich C	2.32	4.94
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	2.31	3.78
	425262	D87119	Hs.155418	GS3955 protein	2.30	3.95
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.29	5.08
	403969			ENSP00000034663:Zinc finger protein 131	2.28	4.05
35	421686	AB011156	Hs.106794	KIAA0584 protein	2.28	3.64
	432800	BE391046	Hs.278962	AJM-1 protein	2.26	3.31
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.24	4.08
	415539	AJ733881	Hs.72472	BMP-R1B	2.24	3.47
	447523	BE613328	Hs.21938	hypothetical protein FLJ12492	2.22	3.66
40	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipper-like pr	2.20	3.43
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	2.20	3.52
	407241	M34516		gb:Human omega light chain protein 14.1	2.19	3.76
	422243	AW803733	Hs.23585	hypothetical protein MGC12250	2.18	3.17
	417324	AW265494		ESTs	2.18	3.28
45	412819	T25829	Hs.24048	FK506 binding protein precursor	2.16	5.85
	432342	AL036128	Hs.274404	plasminogen activator, tissue	2.14	3.49
	427923	AW274357	Hs.301406	hypothetical protein PP3501	2.13	4.39
	417437	U52682	Hs.82132	interferon regulatory factor 4	2.13	5.48
	425535	AB007937	Hs.158287	KIAA0468 gene product	2.13	3.08
50	429638	AJ916662	Hs.211577	kinectin 1 (kinesin receptor)	2.13	8.66
	409154	U72882	Hs.50842	interferon-induced protein 35	2.12	3.01
	429951	AL040521	Hs.15220	zinc finger protein 106	2.12	4.66
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	3.71
	419200	AW966405		EST	2.11	4.27
55	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.11	3.58
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	2.10	5.34
	445133	AW157646	Hs.198689	ESTs	2.07	7.86
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.06	3.68
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.04	3.36
60	424412	H15512	Hs.10043	hypothetical protein FLJ13074	2.03	3.41
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypothei	2.03	3.82
	427536	BE277141	Hs.115803	gb:G01178666F1 NIH_MGC_20 Homo sapiens c	2.02	3.03
	400533			ENSP00000209376::PREDE65 protein (Fragmen	2.02	3.09
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	2.00	3.29
65	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.99	3.07
	417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (1.97	4.52
	423952	AW877787	Hs.136102	KIAA0853 protein	1.97	3.26
	455705	AW161061		ESTs, Weakly similar to zinc finger prot	1.94	3.79
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	1.93	3.16
70	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.93	3.11
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	1.93	3.47
	400292	AA250737	Hs.72472	BMP-R1B	1.92	3.00
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	1.92	4.07
	406851	AA609784		major histocompatibility complex, class	1.90	3.04
75	428437	AV656017	Hs.184325	CGI-76 protein	1.90	6.53
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.89	3.39
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.89	4.04
	426322	J05068	Hs.2012	transcobalamin 1 (vitamin B12 binding pr	1.87	3.64
	425221	AV649864	Hs.155188	TATA box binding protein (TBP)-associate	1.85	4.21
80	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.85	3.13
	443530	BE563088	Hs.9552	bindin of Ar1 Two	1.85	3.04
	433671	AW138797	Hs.132906	19A24 protein	1.85	3.20
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.84	3.39
	400991			Target Exon	1.82	3.22
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	1.82	4.11
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	3.43
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.81	3.12
					1.79	5.31

5	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.79	3.40
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	1.78	3.38
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.77	3.69
	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.77	3.12
	401591			Target Exon	1.75	4.30
	425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.75	3.68
	412844	AJ828045	Hs.18016	Homo sapiens mRNA; cDNA DKFZp586H0324 (f	1.74	3.53
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.73	3.06
10	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	1.72	4.38
	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.72	4.38
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.72	3.61
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	1.72	3.06
	430148	BE387620	Hs.234489	lactate dehydrogenase B	1.71	4.38
15	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myosin)	1.70	3.13
	413317	U53225	Hs.75283	sorting nexin 1	1.70	3.08
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.68	3.15
	407222	H96850		gb:yu03b12.s1 Soares melanocyte 2NtHM Ho	1.68	4.19
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.67	5.74
	404067			Target Exon	1.67	4.73
20	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	1.66	3.22
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	1.65	3.17
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.64	3.35
	437912	BE278594	Hs.5912	F-box only protein 7	1.64	3.24
	404140			NM_006510:Homo sapiens ret finger protei	1.64	3.10
25	414214	D49958	Hs.75819	glycoprotein M6A	1.64	3.45
	427239	BE270447		ubiquitin carrier protein	1.62	3.58
	427289	AJ097346		phosphoserine aminotransferase	1.62	5.89
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.62	3.23
30	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.62	4.00
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.61	5.00
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	1.60	3.06
	414699	AJ815523	Hs.76930	synuclein, alpha (non A4 component of am	1.58	3.34
	411825	AK000334		hypothetical protein FLJ20327	1.56	3.18
35	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.56	3.23
	428081	AA421048	Hs.95011	syntrophin, beta 1 (dystrophin-associate	1.55	3.10
	401914			Target Exon	1.54	3.33
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	1.54	3.15
	441648	H05734	Hs.30559	ESTs	1.52	3.36
40	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.52	3.17
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.52	4.93
	413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.52	3.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.52	3.83
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	1.50	3.04
45	421851	R18586	Hs.108896	lambda-crystallin	1.47	3.10
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	1.44	3.07
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.44	3.00
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	1.42	3.66
	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.42	4.16
50	413291	NM_006278	Hs.75268	sialyltransferase 4C (beta-galactosidase	1.41	3.30
	435968	AW161481	Hs.111577	integral membrane protein 3	1.41	3.30
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.40	3.01
	443759	BE390832	Hs.134729	FXD domain-containing ion transport reg	1.39	3.82
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	1.39	3.43
55	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.36	3.32
	406827	AA971409		gb:op92c04.s1 NCL CGAP_Lu5 Homo sapiens	1.35	3.03
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.34	6.25
	426890	AA393167	Hs.41294	ESTs	1.34	3.66
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.34	3.18
60	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.33	3.19
	421612	AF161254	Hs.106196	BDG antigen	1.33	3.03
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.32	3.68
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	1.32	3.10
	449444	AW818436		salute carrier family 16 (monocarboxylic	1.30	3.30
65	404700			Target Exon	1.30	3.14
	403043			Target Exon	1.30	4.22
	409858	NM_006586	Hs.56828	trinucleotide repeat containing 5	1.29	3.09
	424679	AL117477	Hs.119960	DKFZP727G051 protein	1.27	3.13
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.27	3.66
70	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.26	3.09
	423130	AW897586	Hs.21213	ESTs	1.24	3.34
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	1.24	3.15
	442680	BE270707	Hs.8583	similar to APOBEC1	1.22	3.94
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	1.21	3.36
75	402408			NM_030920*:Homo sapiens hypothetical pro	1.04	3.37
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	3.02

TABLE 51B:

80	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

Pkey CAT Number Accession

430540	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AA459893 AA58188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AU243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AI134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AA459893 AA58188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AU243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE459623 AI335824 AW408712 BM149172 BC014433 Z49835 D16234 U42068 D83485 NM_005311 AL535156 AL533202 AL533596 AL531770 AL542767 AL551050 AL548510 AL542531 AL548618 BE799237 AL547374 AL560312 AL543505 AL540727 AL541255 BG765697 AI126498 BI289574 BG576125 AL519304 AL548821 AL542983 BI596431 BI829284 AL045490 BE407984 BI668702 BI713725 BE547233 BM312673 BG822625 AW239512 BM312685 BE296719 BM312059 BI712618 BF724689 AA353713 BF477104 BI838605 BG170854 BE612762 BF917301 BF332271 BI049186 BE715514 AW392181 BE768470 AI912855 AW991405 BG739837 AA287804 AW801855 AL568814 AW384099 AW384058 AW754178 AI001019 R33917 BE814037 AI557164 AK025474 U11293 AF141304 BM442402 AL539879 AL554793 AL543707 AL549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347 BI838505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 D31003 AA234218 AJ420466 BM083921 BE856788 BE669957 BF430992 AW614978 AW205958 BF110763 BF222758 AA195232 AI341353 AI698676 AJ093230 AI123522 AI656594 AI208758 AA975916 AI089224 AI264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 AL576975 BF689524 AL563130 BI858155 AA417889 AL513995 AL568815 AI160693 AA836028 H84388 AL517078 AL546480 AL530507 AL561042 AA024435 W47314 AI680513 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 BM011139 AW675130 BE276045 BF933396 AL517903 AA886367 BI030596 BG477193 BF973867 AI382520 D25917 AI670784 AI742347 AW269789 AI270700 AW610641 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827 NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710 AA302840 T93016 T92950 AU184997 AA077551 NM_016575 AB032773 AI765521 BF593742 AI497757 AJ761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 AI147248 AI086795 AA151317 T95298 AW083548 AA058371 N27951 AI769860 AI784548 AW205506 AI800679 AI041733 AI459902 BE327641 AI865829 AI254736 AI302433 AI744176 AI241825 AA027842 AL524933 AL524932 BF947764 BF340737 BF948700 BG996393 N53455 N21027 AI127616 N35901 AA682443 AA678249 AA719371 AA132582 T15981 H99958 N40717 AW959402 AI267251 BF909329 AI142035 T95379 H29420 RS9632 H17318 H17331 H29327 R40829 R43395 R59573 AI749561 R56599 H16755 AI694500 AA027907 BI757837 AW439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387 M80359 NM_002376 AU132239 AU120606 AU124963 AI055116 BE900808 BF968374 AI066648 BG774205 AW250728 BE265845 AA290719 AU125196 BG428863 AA333580 AA604551 W73300 AI932646 AA082201 AA627618 BF038887 BF337051 BI021159 AW057581 AI983156 AI268004 T71931 T90093 AW194009 H93969 AI742843 AI935080 BE041751 H93970 AW797399 W05032 T87824 T82912 AW129639 AI221821 AI911810 AA703093 AA160135 AW779124 AA102559 AA969546 D29560 BI915937 AA707716 BI085679 AA700887 AA081085 H80564 T99937 T70802 BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AA431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 NS0122 BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D10684 AW380068 AW380080 R00283 C15236 AW327776 D80759 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW223536 BM021837 AA911956 AI860606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847 AW936678 AW936821 AW936822 AW936781 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812 AW936730 AW936762 AW936682 AW936732 BC001179 NM_005336 M64098 BC014305 BI827845 BI918183 AU124191 AU125604 AU140930 AL043307 BG763670 BG824279 AI125959 BI518466 BE271867 BM264138 BE314823 BM090633 BE273657 BG419830 BM048338 AU134368 BE163486 BE163483 BG421980 BG768130 AW500482 AI910107 AW868323 BF083170 AW450290 BM466817 BG255224 BE394282 AU140278 BE887464 AL042675 BI195986 BE883385 BE544751 BE270148 BM011334 AI093482 AA029903 AI610705 BE386809 F06628 AW408605 BF814085 BC007961 BM451548 BG768053 BM452948 AU140330 BG489566 BI870474 BM014013 AU131264 BG679824 BI225752 BI457400 BE410173 BM044254 BG763690 BE251495 BG179862 BE513489
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5			BM005937 AI064815 BF569858 BI712614 BG655891 BG424940 BE175180 BM313160 BG471936 BM091124 BF885884 BF870522 BE004490 BE712976 BE712862 AA01033 BF569477 BE712936 BF353839 BE713042 AA316561 BE712974 BE712977 BE712938 BE712937 BE712867 BE713043 BE713023 N42463 BE712901 BE713041 BE712904 BE712895 BE713012 BE713049 BE713025 BE712998 BE712988 BE712897 BE712986 BE712984 BE712982 BE712975 BE712970 BE712953 BE712929 BE712922 BE712875 BE712866 BE712861 BE712860 BE712854 BE712853 BE712902 BE712897 BE712912 BG984910 BE712903 BE764759 BE715723 BE715745 BE712915 AA441839 BE713040 BE715755 BF872528 BF060840 BG395104 BG744878 AU124081 AI889823 AI801072 AI633102 AI678670 AI493608 AW194294 AI354559 AI686736 AW152477 AI419496 AI720319 AI866190 AA047013 AA039625 BE049622 AA369065 AA025686 AI570198 AA706304 AW439251 H64553 AW168006 AI983753 AW081999 AW082909 AI951490 BF886341 AW591246 AI190143 AI151074 AI499541 AI050934 AA402167 AA382049 T16207 T03299 AI932691 AW571663 BG479797 BE408436 BI450153 BG386046 BE616601 AW151629 BG236164 BF852743 BF852046 T57801 W37981 AA482668 H43740 W58142 W25087 BM459852 AU125403 BG767992 BE258516 AI114509 BE394494 BE386905 AA450315 BG750593 AA557855 BG766487 BG766998 BF948864 BE279327 BE870900 AA577098 BF365851 AA745058 N29867 AI625038 AA641801 AA846174 H26395 AA025568 BF690282 R67845 R72666 H39554 T78959 W01317 H45860 W80837 N53985 BG757202 BE838055 BE072895 BE072668 BE867012 BM042833 AA083591 BG745462 AW374086 BG831326 BE715757 BG767243 BG763272 AA113402 AI024044 BF818501 BE081938 BF353818 AA746336 BM019086 BE712894 H16977 H45012 R10793 BE708619 BF570432 AA593938 AA064637 T28082 AA852845 T78907 AA346590 F00017 BE966368 N58726 AA732431 T54379 W80749 BF238314 BE279768 AA325106 T19241 BE409939 BF852119 W23803 T54011 AW392638 BI465185 AW516784 AA211335 BI159846 AA064680 N80615 W49676 BF851406 R88120 AA434028 H44546 T61029 N44804 AA114948 H26960 BI261965 AA582599 BG469385 BF818172 BF923672 BI024270 AW362633 BE883122 BM470779 BE935760 AW856056 AW856103 BE828607 AW381799 AI121058 BE828618 BE769545 AA102142 BG749978 BI770417 BI862544 AI110687 AF083562 BE740347 BE874864 AI305113 BE513675 BE091369 BI046660 BE091453 BI046548 AI673786 BF868704 AI025179 BF358640 BF886357 BF886313 BG951884 AI347880 AW627563 BF932536 AW820377 BF739372 BF831620 BE068264 BE613627 AA641745 W01130 H28252	418166	18858_1
10			AK055915 BE867252 AI523348 AA765350 BF468558 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI000361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732	455839	1518842_1
15			BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 AA430373 AA968771	458997	11847_4
20			BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059 BG951874 AI572169	406782	0_0
25			BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AI118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861585 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AI118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BF971018 BE513812 AA133359 AW581719 BF434402 AL600619 BG669973 BI551395 AW027136 AW055130 BF939512 AI076048 H18584 AW161061 AA864334 AI616101 BE049456 AW044012 AA954079 AI274682 AI370526 AW131990 AA853195 AA853191 BG118295 AA761620 BG705371 BF355591 BF335596 AA360497 H28072 BG198352 AW364709 H40926 H44214 AA836538 BI059563 AA609784 R97304	419200	9531_1
30			AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI340734 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI005372 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF178773 BF178645 AW074866 BE857822 BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 AI889380 AA868504 AW612968 AA630644 AI751211 N26980 AI394506 AA747849 BF154926 BF477185 AA649647 R39135 AI750216 T35363 W36278 AW079375 AW612240 AA505495 AA515380 BG760793 AW370651 BG768029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 AV703420 H65047 AA485582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504 BI018121 AA1953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199 AK000695 AK000489 BC001688 BG235988 AW006329 AI887644 AI207230 AI148213 AI304333 AI634653 AW662636 AI281247 AA946921 AA424487 BE272330 AI830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 BI906631 AW083424 AA625199 NM_017767 AK000334 BF984048 AW815634 AL573992 AA430612 AA928390 AA464447 AW340827 AA424290 AI927759 BG951502 AW881353 BF765535 AA971409	406851	0_0
35			AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI895971 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW265313 AA913892 AI693486 AW263502 AI06164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166	427289	1820_2
40			U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU135895 AU158158 AU155762 R73608 R65751 R23756 N14630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258	411825	7891_1
45			BG165971 BE143233 AL577712 AI400326 AA769318 AA427866 AW088714 AI150755 AI924874 AI186243 AA804195 AA768972 AW574769 AW341643 AW204520 AA235326 AI005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 AW514133 AI690331 AI673409 AA627727 AI923685 AA931499 AI249783 AI810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840 AA810885	406827	0_0
50			TABLE 51C: Pkey: Unique number corresponding to an Eos probe set Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NI_position: Indicates nucleotide positions of predicted exons.	428342	6712_1
55			Pkey Ref Strand NI_position 402075 8117407 Plus 121907-122035,122804-122921,124019-12416		
60					
65					
70					
75					
80					

5	400860	9757499	Minus	151830-152104,152649-152744
	402609	9926446	Minus	113464-113633,114264-114654
	400750	8119067	Plus	198991-199168,199316-199548
	402994	2996643	Minus	4727-4969
	403817	8962065	Plus	110297-111052
	402829	8918414	Plus	101532-101852,102006-102263
	403532	8076842	Minus	81750-81901
	405451	7622517	Minus	145949-146227
10	405785	9581533	Minus	98702-98925
	405506	6466489	Plus	80014-80401,80593-81125
	405486	6651379	Plus	179441-179598
	406382	9256148	Plus	122336-122851
	401454	9186923	Minus	114659-114832
15	405885	7677703	Minus	42574-42998
	403969	8569909	Plus	31237-31375,32405-32506
	400533	6981826	Minus	277132-277595
	400991	8096825	Plus	159197-159320
	401591	9966977	Minus	55410-55835
20	404067	3282162	Plus	1415-2071
	404140	9843520	Plus	37761-38147
	401914	9369520	Plus	62537-62945,63155-63308
	404700	9800123	Minus	159621-160203
25	403043	7768753	Minus	314423-316252
	402408	9796239	Minus	110326-110491

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES

Table 52A lists about 204 genes upregulated in primary melanomas relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Key:
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs

R2: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
40	421948	L42583	Hs.334309	keratin 6A	21.90	16.66
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)	21.36	43.65
	401781			Target Exon	18.70	18.58
	401780			NM_005557:Homo sapiens keratin 16 (foca	15.34	16.00
45	431360	NM_000427	Hs.251680	loricin	12.34	9.86
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	11.24	8.73
	412636	NM_004415		desmoplakin (DPI, DPII)	11.20	6.62
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	10.46	12.75
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	10.41	25.49
50	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	9.20	8.63
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	8.11	11.14
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	7.90	8.92
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	7.14	22.14
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	7.03	8.90
55	430686	NM_001942	Hs.2633	desmoglein 1	6.88	5.39
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (6.60	12.79
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.44	6.19
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	6.34	7.77
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.15	8.91
60	418067	AI127958	Hs.83393	cystatin E/M	6.08	9.24
	408536	AW381532	Hs.135188	ESTs	6.04	17.40
	402075			ENSP00000251056:Plasma membrane calcium	5.96	8.41
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.46	3.32
	410001	AB041036	Hs.57771	kalikrein 11	5.38	5.36
65	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fs, clone C	5.32	3.84
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.19	5.30
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	5.03	7.94
	429504	X99133	Hs.204238	tipocalin 2 (oncogene 24p3) (NGAL)	4.86	5.22
	421773	W69233	Hs.112457	ESTs	4.82	12.41
70	442577	AA292998	Hs.163900	ESTs	4.82	4.40
	401760			Target Exon	4.60	11.03
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	4.50	11.35
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.47	12.43
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.45	2.99
75	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.39	4.23
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.38	4.55
	418663	AK001100	Hs.41690	desmocollin 3	4.36	5.16
	424620	AA101043	Hs.151254	kalikrein 7 (chymotryptic, stratum com	4.29	5.19
	401747			Homo sapiens keratin 17 (KRT17)	4.28	5.41
80	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	4.24	2.30
	411274	NM_002776	Hs.69423	kalikrein 10	4.22	4.82
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.21	8.26
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.18	4.73
	429538	BE182592	Hs.139322	small proline-rich protein 2A	4.16	7.30

	418686	Z36830	Hs.87268	annexin A8	4.12	4.09
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.08	2.13
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	4.08	4.38
5	416091	AF295370	Hs.283082	defensin, beta 3	4.05	5.38
	442757	A1739528	Hs.28345	ESTs	3.94	4.28
	427318	AF186081	Hs.175783	zinc transporter	3.92	3.07
	453309	A1791809	Hs.32949	defensin, beta 1	3.90	4.30
	422192	AA305159	Hs.113019	fts485	3.88	2.81
10	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.86	5.03
	429365	AA451798	Hs.99249	ESTs	3.76	4.05
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.72	6.35
	425580	L11144	Hs.1907	galanin	3.68	3.65
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.68	2.75
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.59	5.72
15	408591	AF015224	Hs.46452	mammaglobin 1	3.58	4.73
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.58	2.62
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	2.61
	421574	AJ000152	Hs.105924	defensin, beta 2	3.56	4.04
20	402294			Target Exon	3.48	4.38
	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.44	2.95
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.42	4.92
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	4.24
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.31	5.42
25	452392	L20815	Hs.507	corneodesmosin	3.30	8.56
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.30	2.35
	433124	U51712	Hs.13775	hypothetical protein SMAP31	3.26	2.15
	419098	AA234041	Hs.87271	ESTs	3.25	4.34
	421978	AJ243662	Hs.110196	NICE-1 protein	3.17	5.86
30	445493	AJ915771		metallothionein 1E (functional)	3.16	2.98
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	3.14	2.07
	445745	AB007924	Hs.13245	KIAA0455 gene product	3.10	2.39
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.06	2.71
	407839	AA045144	Hs.161566	ESTs	3.06	3.54
35	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.04	4.64
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	3.04	2.78
	452240	AJ591147	Hs.61232	ESTs	3.00	4.79
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.96	3.05
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.94	10.53
40	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.91	3.01
	406964	M21305		FGENES predicted novel secreted protein	2.90	5.34
	451541	BE279383	Hs.26557	plakophilin 3	2.89	6.64
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.86	2.81
	414737	AI160386	Hs.125087	ESTs	2.84	1.76
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.82	1.83
	405542			Target Exon	2.80	2.77
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.78	5.17
	402970			C20000886:gij9280563[gb]AAF86472.1) (AF	2.78	3.37
50	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76	2.76
	433435	BE545277	Hs.340959	Ts translation elongation factor, miloch	2.75	2.76
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.72	2.86
	409453	AI885516	Hs.95612	ESTs	2.70	6.68
	428824	W23624	Hs.173059	ESTs	2.67	2.75
55	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.65	3.07
	430630	AW269920	Hs.2621	cystatin A (stefin A)	2.63	2.38
	433339	AF019226	Hs.8036	glioblastoma overexpressed	2.61	2.44
	444670	H58373	Hs.332938	hypothetical protein MGCS370	2.57	1.74
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	2.54	3.66
60	400995			C11000295:gij12737279[ref]XP_012163.1)	2.54	2.93
	423515	AA327017	Hs.176594	ESTs	2.53	7.36
	417359	T99264	Hs.191117	ESTs	2.53	2.54
	432426	AW973152	Hs.31050	ESTs	2.52	2.15
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.52	3.05
65	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.52	3.85
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.48	1.76
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.47	1.92
	413392	AW021404	Hs.13021	ESTs	2.47	2.56
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.46	1.90
70	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.46	7.90
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.46	2.66
	420568	F09247	Hs.247735	protocadherin alpha 10	2.46	3.01
	405885			Target Exon	2.46	2.82
	412633	AF001691	Hs.74304	periplakin	2.46	5.01
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.45	3.35
75	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	2.44	2.33
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.44	2.11
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.43	3.66
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	2.42	3.12
	430168	AW968343	Hs.145582	DKFZP43411735 protein	2.41	2.75
80	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	2.40	3.67
	404049			NM_018937*:Homo sapiens protocadherin be	2.39	1.89
	433576	BE080715	Hs.161091	ESTs	2.39	1.59
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.38	2.59
	408208	BE018717		ESTs	2.37	2.12

5	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	2.36	2.23
	453931	AL121278	Hs.25144	ESTs	2.34	1.99
	452308	A167560	Hs.61297	ESTs	2.31	3.82
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	2.31	2.18
	403752			NM_002753*:Homo sapiens mitogen-activate	2.30	2.38
10	402525			NM_002699*:Homo sapiens POU domain, clas	2.30	2.36
	420223	N27807		ribosomal protein L4	2.30	1.73
	452023	AB032999	Hs.27566	KIAA1173 protein	2.29	4.54
	443172	AW662964	Hs.199061	p300/CBP-associated factor	2.28	2.02
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	1.71
15	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.27	1.81
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.26	2.17
	436895	AF037335	Hs.5338	carbonic anhydrase XII	2.26	2.51
	404029			NM_018936*:Homo sapiens protocadherin be	2.26	2.19
	424049	AB014524	Hs.138380	KIAA0624 protein	2.26	2.99
20	442423	BE326264	Hs.246842	ESTs	2.26	1.75
	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.26	2.29
	428471	X57348	Hs.184510	stratfin	2.25	2.40
	410541	AA050003	Hs.64179	syntenin-2 protein	2.24	2.46
	415539	AI733881	Hs.72472	BMP-R1B	2.22	1.64
25	425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	2.22	3.04
	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	2.22	3.24
	409178	BE393948	Hs.50915	kallikrein 5	2.19	4.74
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.19	7.96
	430171	AF086289	Hs.234766	skin-specific protein	2.17	3.56
30	401994			Target Exon	2.14	3.34
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.11	5.52
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.11	5.78
	426150	NM_003658	Hs.167218	BarH-like homeobox 2	2.05	2.96
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.04	4.17
35	443162	T49951	Hs.9029	DKFZP434G032 protein	1.98	3.20
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.94	3.20
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.92	3.24
	412507	L36645	Hs.73964	EphA4	1.92	3.06
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	1.90	3.18
40	425415	M13903	Hs.157091	involucrin	1.89	5.26
	417324	AW265494		ESTs	1.88	3.82
	412446	AI768015		ESTs	1.88	3.36
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.87	3.75
	444726	NM_006147		interferon regulatory factor 6	1.86	4.11
45	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	1.85	4.20
	434346	AA630445		ESTs	1.84	3.08
	446051	BE048061	Hs.37054	ephrin-A3	1.83	3.44
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	1.78	3.45
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.76	2.99
50	411908	L27943	Hs.72924	cytidine deaminase	1.74	3.60
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.71	3.56
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.71	3.38
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.70	3.92
	425650	NM_001944	Hs.1925	desmoglein 3 (permpigus vulgaris antigen	1.68	3.25
55	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.67	2.92
	429002	AW248439	Hs.2340	junction plakoglobin	1.66	3.35
	421335	X99977	Hs.103505	ARS component B	1.66	4.31
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.65	3.55
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.64	4.04
60	414214	D49958	Hs.75819	glycoprotein M6A	1.64	3.59
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	1.62	3.13
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	1.62	2.92
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	1.57	3.09
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.53	3.39
65	427751	AF000152		conserved gene amplified in osteosarcoma	1.52	3.53
	416881	N32520	Hs.141358	ESTs	1.52	3.06
	435013	H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.49	2.91
	434574	AJ424458	Hs.33470	ESTs	1.48	3.05
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.48	3.54
70	447330	BE279949	Hs.18141	ladinin 1	1.46	4.48
	414583	AA362907	Hs.76494	proline arginine-rich end leucine-rich r	1.41	2.99
	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.40	3.71
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.36	2.98
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.36	3.14
75	450796	NM_001988	Hs.25482	envoplakin	1.34	3.74
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	1.30	3.26
	430513	AJ012008	Hs.241586	G6C protein	1.28	3.26
	411388	X72925	Hs.69752	desmocollin 1	1.22	3.64
	431089	BE041395		ESTs, Weakly similar to unknown protein	1.14	3.71
80	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.00	3.20
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.00	3.26

TABLE 52B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG688865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 A951766 AI434518 AW804674 BF752969 BE837009 BE825826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BC005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142892 AA039975 AA946936 AA644381 BM314884 AA702424 AI176112 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 AI665588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AI128330 BG681425 BE706078 R20904 BG680058 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AI131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BG931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 AV711317 AI809938 AI808768 AI240593 AI915771 H80564 T99937 T70802 BI836699 AI123195 BI757837 AW439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387 N27807 AA256634 BE276324 BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059 BG951874 AI572169 BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE69424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F07221 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AI159045 AI693500 AW293668 AW371408 BE856107 AI338042 AW188320 AI698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327 AW664668 AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF178731 BF178413 AA877495 BF001575 AI824693 AW849604 AW849405 AW849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 AI140849 T67412 AI889885 AW104647 AI912495 AI889874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853 AK056896 AI924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AI274929 AI281211 AI821178 BC020841 BF352476 BF843140 BF917041 W80832 AA630445 BF350167 BE162052 BE931808 AI572329 BG536379 BE875818 AW751975 W39241 BF808798 W22600 BF082190 AG031290 R42801 H98235 H17925 AI631236 AI933786 H42736 AF000152 AU123911 AW140526 BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 U81556 AI422831 AU154008 AA147822 AA873109 AI089244 AI360868 AW168024 AI819848 AA811327 AI355616 AA281629 AI880578 AI274316 AW014622 AI268660 AI270283 AA171981 AI349410 AA402469 AI421985 AI004864 AI423497 AI361503 AI363096 AW805345 AL539979 AA553967 AW502264 AI290698 N22420 AI281054 AI500699 AW342095 C75122 AW504577 AI130811 AI423567 R79086 AI860451 BE222885 AI697830 AI279575 BF438693 AW576277 BE218210 AI952376 AA506609 AI145766 AI391690 AA991622 AI696368 AI784664 AA741555 AI002681 AW474554 AW474508 D25623 AI493929 AA179800 W73566 AW411368 AA147971 AA088581 BF804510 AU145809 AU148108 AA232319 AU157840 AW169577 AI537862 N42341 AI128667 AW327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 AI905211 BF802713 N40338 AA249397 BF752939 BE250441 H64761 BF853011 H81877 H96088 AL576453 W73585 H39990 AW438965 BF899684 AI040299 AL561879 AA293821 H27760 BC018922 AL533396 BE513580 BF432649 AI884985 AA404264 AW024396 AW167863 AW027036 AI302177 AI660487 AW026086 BF432564 BF091011 AI193156 AA744623 AI859510 BI063081 BI061541 AA777036 BG058486 BI063555 AI349411 BF874521 AW139801 AI268585 AA401267 AI905209 R64276 N72043 AF022231 BI256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697 AI857745 AW192840 AW410527 AI697435 AW006631 AW504124 AL048926 AI085476 AW327855 AA459344 AW207516 AW204875 BM142514 BF436650 AA960980 AW242609 BI012363 AW837102 BE703126 BE814612 BE837981 BE703141 BF343101 R47375 AA031413 N40264 BG027363 BF526360 BE391263 AA280192 BE294042 BE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603 BE857292 AI719393 AU155418 BG770385 AA339673 BG337748 H42694 BE834346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280 AW957721 BF304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629 AW796921 AW798102 AW805749 AW805872 BF895060 AW794380 BF380449 AW794466 AW794538 AF005081 BG193848 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

TABLE 52C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

80	Pkey	Ref	Strand	Nt_position
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287

401747	9789672	Minus	118596-118816,119119-119244,119609-11976
402294	2282012	Minus	2575-3000
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
405542	9857564	Plus	71331-72183
402970	9650703	Minus	124891-125049
400995	8099094	Plus	141186-141601
405885	7677703	Minus	42574-42998
404049	3688074	Minus	75765-78155
403752	7678857	Plus	33704-33828
402525	9800048	Minus	19748-20683
404029	7671252	Plus	108716-111112
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519

TABLE 53A: ABOUT 298 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO PRIMARY MELANOMAS
 Table 53A lists about 298 genes upregulated in melanoma metastases relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Key:
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of primary melanoma AIs
 R2: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of primary melanoma AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
407245	X90568	Hs.172004	titin	10.56	11.32
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	9.22	6.14
426752	X69490	Hs.172004	titin	8.78	10.44
418310	AA814100	Hs.86693	ESTs	8.85	6.49
414522	AW518944	Hs.76325	immunoglobulin J chain	8.37	4.39
433447	U29195	Hs.3281	neuronal pentraxin II	8.27	7.25
456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	7.78	6.70
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	7.49	9.02
428087	AA100573	Hs.182421	tropoin C2, fast	7.45	7.65
436485	X59135	Hs.156110	immunoglobulin kappa constant	7.35	6.18
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	6.97	5.75
412519	AA196241	Hs.73980	tropoin T1, skeletal, slow	6.15	6.33
430280	AA361258	Hs.237868	interleukin 7 receptor	6.07	3.11
449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	6.03	5.36
412561	NM_002286	Hs.74011	lymphocyte activation gene 3	5.85	5.57
431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	5.74	6.40
458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	4.76
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	5.71	5.00
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	3.84
420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17333, mRNA, com	5.37	4.12
430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	6.02
428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.29	7.97
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.26	2.93
445784	AI253155	Hs.146065	ESTs	5.12	3.10
409461	AA382169	Hs.54483	N-myc (and STAT) interactor	5.05	3.41
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.59	4.00
420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.47	3.92
453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.46	3.61
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.37	3.22
414829	AA321568	Hs.77436	pleckstrin	4.35	3.35
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fs, clone H	4.35	2.68
422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.27	2.67
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.27	3.67
441623	AA315805		desmoglein 2	4.24	3.66
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor I	4.22	3.60
417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	4.20	2.58
426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.82
430770	AA765694	Hs.123296	ESTs	4.15	5.10
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.12	5.06
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	4.11	3.82
444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	4.10	2.68
432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.04	4.10
417105	X60992	Hs.81226	CD6 antigen	4.03	4.51
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.02	3.72
432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.99	4.87
415165	AW887604	Hs.78065	complement component 7	3.97	3.98
421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	3.96	3.19
421712	AK000140	Hs.107139	hypothetical protein	3.95	7.34
408380	AF123050	Hs.44532	diubiquitin	3.94	2.45
422423	AF283777	Hs.116481	CD72 antigen	3.93	3.29
408989	AW361666	Hs.49500	KIAA0746 protein	3.90	3.02
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	3.84	3.40
420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	3.84	4.84
424922	BE386547	Hs.217112	hypothetical protein MGC10825	3.78	3.04
400440	X83957	Hs.83870	nebulin	3.77	4.89

	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	3.74	3.91
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.74	2.89
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.72	2.65
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!	3.72	2.43
5	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.71	2.23
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.70	2.36
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.67	3.30
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	3.67	6.72
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.66	2.49
10	424153	AA451737	Hs.141496	MAGE-like 2	3.64	2.65
	421666	AL035250	Hs.1408	endothelin 3	3.64	5.92
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.61	2.69
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60	1.95
	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	3.59	3.08
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	3.57	11.26
	42379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	3.56	4.91
	439859	AW292872	Hs.124554	ESTs	3.53	4.15
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.51	2.88
	411252	AB018549	Hs.69328	MD-2 protein	3.46	1.82
20	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.45	4.65
	420286	AI796395	Hs.111377	ESTs	3.42	2.47
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	3.42	3.09
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.41	2.22
	405545			Target Exon	3.40	2.46
25	416373	AA195845		ESTs, Weakly similar to S12658 cysteine-	3.40	5.64
	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	3.37	4.27
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.33	2.37
	433470	AW960564		transmembrane 4 superfamily member 1	3.33	3.13
30	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.32	2.51
	442149	AB014550	Hs.8118	KIAA0650 protein	3.30	2.29
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.29	3.85
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.24	2.79
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.23	1.78
	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	3.22	2.90
35	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.16
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.17	3.59
	424148	BE242274	Hs.1741	integrin, beta 7	3.14	2.29
	406648	AA563730	Hs.277477	major histocompatibility complex, class	3.13	3.05
40	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	3.13	2.36
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.12	2.55
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.12	5.54
	443885	H91806	Hs.15284	ESTs	3.08	3.55
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.08	2.20
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	3.06	3.21
45	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	3.05	3.36
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04	2.07
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.04	2.24
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.03	1.91
	444666	BE293347	Hs.11638	long-chain fatty acid coenzyme A ligase	3.01	3.43
50	425295	AA431366	Hs.37251	ESTs	3.01	3.07
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.99	2.55
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (TiT3 com	2.98	5.98
	418968	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	2.97	2.68
	438914	N93892	Hs.10727	ESTs	2.97	2.19
55	418391	NM_003281	Hs.84673	troponin I, skeletal, slow	2.96	2.68
	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	2.96	3.94
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.96	4.02
	450847	NM_003155	Hs.25590	stanniocalcin 1	2.96	3.24
60	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.95	2.73
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.94	2.36
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	2.93	2.17
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	2.93	2.70
	408633	AW963372	Hs.46677	PRO2000 protein	2.92	2.16
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	2.92	2.92
65	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.90	2.09
	437802	AI475995	Hs.122910	ESTs	2.90	3.71
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	2.90	3.56
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	2.90	2.60
70	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	2.87	2.07
	421958	AA357185	Hs.109918	ras homolog gene family, member H	2.87	3.48
	420224	M84371	Hs.96023	CD19 antigen	2.86	4.77
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.85	5.44
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	2.84	2.55
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	2.84	4.16
75	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	2.83	2.97
	408838	AI669535	Hs.40369	ESTs	2.82	1.82
	429124	AW505086	Hs.196914	minor histocompatibility antigen HA-1	2.82	4.21
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.79	4.00
	425388	AA329384	Hs.156110	immunoglobulin kappa constant	2.79	2.28
80	414290	AI568801	Hs.71721	ESTs	2.78	3.19
	418255	AW135405	Hs.37251	ESTs	2.76	3.27
	451952	AL120173	Hs.301663	ESTs	2.75	1.74
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.75	3.10

	409245	AA361037		IRNA isopentenylpyrophosphate transferase	2.74	2.12
	453920	AI133148	Hs.36602	I factor (complement)	2.74	3.08
	443968	AA287702	Hs.10031	KIAA0955 protein	2.74	2.34
5	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.73	1.67
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.72	1.70
	428398	AI249368	Hs.98558	ESTs	2.72	2.06
	417141	U22662		nuclear receptor subfamily 1, group H, m	2.70	2.55
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.69	3.15
10	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.69	1.99
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	2.69	1.70
	443998	AI620661	Hs.296276	ESTs	2.69	2.30
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	2.68	3.23
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.68	3.01
	448861	AL049951	Hs.22370	Homo sapiens mRNA: cDNA DKFZp56400122 (f	2.66	2.51
15	432435	BE218886	Hs.282070	ESTs	2.65	3.28
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	2.65	3.04
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	2.64	3.82
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.64	1.94
20	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ001111 protein,	2.64	2.51
	401566			NM_005159:Homo sapiens actin, alpha, car	2.63	3.74
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26886 hypotheti	2.63	2.13
	425231	AA527161		ESTs	2.61	2.95
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.61	1.90
25	437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.60	4.45
	413856	D13639	Hs.75586	cyclin D2	2.60	5.71
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfam	2.59	2.68
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.58	2.77
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.58	9.28
30	443021	AA368546	Hs.8904	Ig superfamily protein	2.58	4.49
	424779	AL046851	Hs.153053	CD37 antigen	2.58	3.88
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.57	2.09
	424265	AF173901	Hs.144287	hair/eyenhancer-of-split related with YRP	2.57	3.57
	426780	BE242284	Hs.172199	adenylate cyclase 7	2.57	1.86
35	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.56	2.90
	442904	AW575008	Hs.11355	thymopoietin	2.56	3.39
	433646	AA603319	Hs.155195	ESTs	2.54	2.19
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.53	4.56
	422640	M37984	Hs.118845	troponin C, slow	2.53	5.38
40	448413	AI745379	Hs.42911	ESTs	2.53	2.08
	429536	AA873016	Hs.206097	oncogene TC21	2.52	2.49
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.52	3.46
	424378	W28020	Hs.167988	neural cell adhesion molecule 1	2.52	2.91
	410257	BE244044	Hs.61469	hypothetical protein	2.51	3.67
45	427609	AK000436	Hs.179791	hypothetical protein FLJ20429	2.51	3.11
	424868	AI568170	Hs.96886	ESTs	2.51	2.30
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.50	2.64
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.50	3.04
	413441	AI929374	Hs.75367	Src-like-adaptor	2.49	2.37
50	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.49	1.82
	429493	AL134708	Hs.145998	ESTs	2.49	2.40
	419631	AW188117		popeye protein 3	2.48	1.85
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.48	2.32
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	2.47	4.17
55	420158	AI791905	Hs.95549	hypothetical protein	2.47	2.62
	453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.47	2.49
	429640	U83508	Hs.2463	angiopoietin 1	2.47	2.57
	437330	AL353944	Hs.50115	Homo sapiens mRNA: cDNA DKFZp761J1112 (f	2.46	2.42
	426969	AI936504		CDC-like kinase 1	2.46	2.41
60	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.46	2.17
	405547			NM_018833*:Homo sapiens transporter 2, A	2.46	2.84
	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	2.45	2.89
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	2.45	3.40
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.43	6.25
65	453953	AW408337	Hs.36972	CD7 antigen (p41)	2.39	4.01
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.39	4.56
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.39	3.31
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.38	3.15
	440596	H13032	Hs.103378	hypothetical protein MGC11034	2.37	3.68
70	452651	AI218918	Hs.30209	KIAA0854 protein	2.36	4.08
	421563	NM_006433	Hs.105806	granulysin	2.34	3.25
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	2.33	3.38
	449092	U91641		alpha2,8-sialyltransferase	2.32	3.53
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	2.32	7.02
75	418117	AI922013	Hs.83496	linker for activation of T cells	2.30	3.56
	425795	AJ000479	Hs.159543	EDG-6 (endothelial differentiation, G-p	2.26	3.42
	428111	S76617	Hs.2243	B lymphoid tyrosine kinase	2.25	3.69
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	2.25	4.05
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.25	3.44
80	436648	R18656		ESTs	2.24	3.23
	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	2.23	3.08
	441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	2.23	3.30
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.22	3.25
	449626	AA774247	Hs.301637	zinc finger protein 258	2.21	3.14

5	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, S	2.18	3.41
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.15	3.62
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2 (ICAM	2.09	5.21
	436420	AA443966	Hs.31595	ESTs	2.07	3.81
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	2.05	3.14
	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.01	4.42
	428289	M26301	Hs.2253	complement component 2	2.00	3.33
	429683	AF148213	Hs.211604	a disintegrin-like and metalloprotease (2.00	3.75
10	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.96	3.68
	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	1.91	4.84
	416445	AL043004	Hs.79337	KIAA0135 protein	1.91	3.41
	409817	BE295464	Hs.56607	Williams-Beuren syndrome chromosome regi	1.87	3.53
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.86	3.55
15	437740	AA810265	Hs.122915	ESTs	1.86	3.79
	437938	AI950087		gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapien	1.83	3.42
	425240	AA306495	Hs.1869	phosphoglucomutase 1	1.83	3.75
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.80	4.03
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	1.78	3.53
20	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	1.78	3.39
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.78	5.48
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	1.78	4.88
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.77	5.79
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.74	3.41
25	427278	AL031428	Hs.174174	KIAA0601 protein	1.74	3.80
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.73	4.21
	420397	NM_007018	Hs.97437	centrosomal protein 1	1.73	3.21
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.73	3.77
	459245	BE242623	Hs.31939	manic fringe (Drosophila) homolog	1.72	3.12
30	425356	BE244879	Hs.155339	inositol polyphosphate-5-phosphatase, 14	1.71	3.55
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.70	7.70
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.70	3.10
	451579	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.68	4.19
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	1.68	5.76
35	416819	U77735	Hs.80205	pim-2 oncogene	1.67	3.17
	409896	AW205479	Hs.279780	NY-REN-18 antigen	1.67	3.74
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.66	3.62
	426666	AW500131	Hs.171763	CD22 antigen	1.65	4.67
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.65	3.43
40	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.64	3.66
	430449	AA352723	Hs.241471	RN86	1.62	3.09
	424661	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	1.61	3.37
	453027	AI879341	Hs.539	ribosomal protein S29	1.61	11.60
	410068	AK633888	Hs.58435	FYN-binding protein (FYN-120/130)	1.60	3.28
45	440446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and coiled/coi	1.59	3.14
	453657	W23237	Hs.296162	AD037 protein	1.59	3.12
	418102	R58958	Hs.26608	hypothetical protein MGC15880	1.58	3.55
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.58	3.07
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.55	5.06
50	421703	AI936513	Hs.1416	Fc fragment of IgE, low affinity II, rec	1.53	3.59
	421859	AA356620	Hs.108947	KIAA0050 gene product	1.52	3.41
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	1.52	3.28
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.47	3.34
	425783	AI026740	Hs.1948	ribosomal protein S21	1.46	4.95
55	407682	AL035858	Hs.3807	FXFD domain-containing ion transport reg	1.46	3.48
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	1.45	3.25
	435624	AF218942	Hs.24889	formin 2	1.45	3.11
	413969	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidyl	1.45	3.33
	426530	U24578	Hs.278625	complement component 4A	1.44	4.27
60	425928	SS5736	Hs.238852	ESTs, Weakly similar to hypothetical pro	1.44	3.65
	418219	AA731836	Hs.137319	ESTs	1.43	4.01
	429071	AW794126	Hs.195453	ribosomal protein S27 (metalloproteinstimuli	1.41	4.23
	418473	AA243335	Hs.309943	nuclear body protein Sp140	1.41	3.29
	423766	AA303799	Hs.300141	ribosomal protein L39	1.40	3.22
65	430150	L05148	Hs.234569	zeta-chain (TCR) associated protein kina	1.39	3.29
	416370	N90470	Hs.203697	CD38 antigen (p45)	1.36	3.08
	406758	AA552326	Hs.77039	ATP synthase, H transporting, mitochondr	1.32	3.29
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	1.31	3.85
	444674	BE562200	Hs.244	amino-terminal enhancer of split	1.30	3.10
70	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.30	3.91
	427349	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	1.28	3.59
	419032	W81330	Hs.99877	ESTs, Highly similar to JAK3B [H.sapiens	1.28	3.21
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.27	4.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.24	3.25
	406623	X69392		ribosomal protein L26	1.24	3.31
75	437895	AB014568	Hs.5898	KIAA0668 protein	1.21	3.33
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing le	1.18	3.35

TABLE 53B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89355 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BC496559 BF248373 BG494800
416373	3442_1	AK056582 AW755252 AL596757 BF827376 BF827373 BF827375 BF827369 BF826900 F01252 BC022888 BI850312 AA159845 BF825671 BF574821 Z21696 F32854 AA211780 F21569 AI288453 AI803678 AA180309 AI074627 AA192950 AA661688 F36698 F32290 F28773 F22692 AA424993 AW340328 AA192247 BF672229 BF575143 BF673106 BF693623
433470	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW529505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AI103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z27771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AI136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AJ377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 AI344943 AI348877 AI348860 BE621857 BE156280 AA45099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27522 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BC400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF327070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AI458715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA331835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA059911 BE222062 D56772 AW372265 BM054985 DI2465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
409245	3199_2	AI391712 U22662 NM_005693 AW166878 BF339795 AI970974 AI521157 AI336082 AW339789 AI288682 BF477594 BF477593 AI703008 AI290961 AI049684 AW770753 AI208561 AI699406 F33996 AA630563 AI985346 AI927058 AA533982 AW204589 AI206938 AW590068 AI263769 AA991550 AI192005 AL558946 AI524337 AL516239 AL580848 AL580658 AI719135 AW026500 AI698217 AI872977 AI670983 AI654870 AA493407 AA548525 AI016420 AA843563 W15576 H61726 AA913245 BF438146 AL524338 BI762380 AU136488 BI759892 AV655930 T78977 BI524075 BE538944 AA527161 BG211784 AA527065 AA505489 AW512550 BC022323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA861832 H84897 AI382294 AA662874 AW993380 BE813742 H84368 AI188074 N20482 H84369
426969	12113_1	M59287 AI936504 AI694705 AI679216 AI679235 BF110184 AW518110 AI679811 AW054981 BE465531 BE327409 AW339105 BI714787 AI871568 AW129115 AU145080 AI223299 AW129986 AW780771 BG654629 AU144657 BF437422 AI478374 AA492513 AU157562 AI826962 AU145528 AI951093 AW513819 AA042856 AA725690 AW733176 AI028702 AI251890 AI811729 AW975208 AW339589 AI147868 AU157862 AA629327 BF476670 BE464796 AW510511 AA399098 AA398210 AI291998 AI160296 AU158075 N34811 BE326407 AI270552 AA496923 AA508002 AI270284 AI139504 BF437009 AI354626 AI936336 AA287250 AA491855 BF445818 AA688026 AA284510 AW151564 AA412072 AA709241 H89332 BF445769 BF989466 BF989472 AA631105 AI129915 W96362 AA515277 AA541513 L29222 AV758119 D82109 AL040956 BE244413 AV645640 BE246321 BE246314 D82116 AL036176 AA331779 AU100106 BE243857 AU076865 AW972327 AA497087 AI687039 AW072798 AI174455 AU156788 AA044401 AA046086 BE244986 AI634456 BE242945 BE242089 AU156034 BE244982 AL567955 BI005141 AA040426 AW630506 BF155668 AU118544 BG573573 W96436 AA373395 BE710347 AI564154 AI708332 AA729530 N92729 AI573015 T29655 H89333 H85847 AI886473 AW189980 H02905 AI811986 AU157753 W86829 AA020844 AU158204 AA057356 AA283466 AA405504 AA017027 W94754 AA226498 W72391 H66461 C00442 H01925 BI912232 U77534 U77537
406678	0_0	AK056270 AV706896 AK692935 AI681140 AW162481 AW087114 AW157019 AI689795 AW251085 AW206911 BF438207 AW134945 BE041668 BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AI929731 AW161524 R43753 BE779688
449092	4406_1	AJ002788 AL118666 AI381600 BE672862 AW500520 BF223709 AW593740 AA262174 AA810597 AA810596 AA810595 F09382 BF976590 AW968002 AA262288 BF931698 AW968014 R18656 BM459356 AW794189 BF954184 Z42558 BF891641 BF963380 Z45874 F05187 X93079 BF742651 BF742649 R51324 D80031 BI457883 F06613 Z43128 F12243 BF950830 H19040 BF950829 F06439 R14947 F06702 R61037 R52173 R14953 R12174 R13610 H10426 R11851 T65264 R18737
437938	66997_1	U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 AI653832 W87891 AI961530 T85904 H59397 R97278 W01059 AI820532 T82391 AI820501 T63226 R66056 R67840 AW961101 AA337499 W37181 AA180009 AW205862 AA988777 AA866975 BF172457 BG751124 AI741346 AI950344 AI689062 AI872193 AW102898 AW173586 AI763273 AI890387 AW150329 AI762688 AA488892 AI356394 AI539642 AA642789 AI950087 BF589902 N07020 AA283144 AA488964 H60052 R97040 BF886630 AW967677 AW971573 AW967671 AI308119 AA251875 AA908598 AI819225 AI564269 AA908741 AA293273 AA969759 AW276905 AA044209 H83488 T92487 X69392 T24055

TABLE 53C:
Pkey:

Unique number corresponding to an Eos probelet

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
401566	8469090	Minus	96277-96420,96979-97160
405547	1054740	Plus	124361-124520,124914-125050

TABLE 54A: ABOUT 161 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER

Table 54A lists about 161 genes upregulated in primary melanomas from tumors that later metastasized relative to primary melanomas that did not metastasize later. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of AIs for primary melanomas that later metastasized divided by the 90th percentile of AIs for primary melanomas that did not metastasize later

R2: 90th percentile of AIs for primary melanomas that later metastasized divided by the 90th percentile of AIs for primary melanomas that did not metastasize later, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.15	3.41
413916	N49813	Hs.75615	apolipoprotein C-II	5.93	6.55
414807	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	5.64	2.98
415668	AW957684	Hs.306814	hypothetical protein FLJ21889	5.03	4.56
440274	R24595	Hs.7122	scrapie responsive protein 1	4.98	4.83
417542	J04129	Hs.82269	progesterone-associated endometrial prote	4.96	7.07
427882	AA640987	Hs.193767	ESTs	4.68	4.68
452744	A1267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.29	3.06
407907	A1752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	3.94	3.86
424410	W79027	Hs.271762	ESTs	3.67	3.19
429083	Y09397	Hs.227817	BCL2-related protein A1	3.46	2.49
407951	W77762	Hs.79015	antigen identified by monoclonal antibod	3.31	3.06
426330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.27	2.12
440099	AL080058	Hs.6909	DKFZP564G202 protein	3.22	2.69
428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.20	1.85
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.18	4.61
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.13	2.11
430643	AW970065	Hs.287425	MEGF10 protein	3.10	3.31
412262	W26406		seven in absentia (Drosophila) homolog 1	3.06	3.94
438328	A1492261	Hs.32450	ESTs	3.05	3.09
409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	3.01	2.65
453912	AL121031		SWI/SNF related, matrix associated, acti	2.94	1.86
416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.91	3.70
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	2.88	2.53
453935	A1633770	Hs.42572	ESTs	2.88	2.00
452689	F33868	Hs.284176	transferrin	2.84	6.47
449550	AA353125	Hs.184721	ESTs	2.83	4.74
409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.82	2.43
438898	A1819863	Hs.106243	ESTs	2.81	2.08
430191	A1149880	Hs.188809	ESTs	2.80	2.69
408418	AW963897	Hs.44743	KIAA1435 protein	2.79	1.75
450157	AW961576	Hs.60178	ESTs	2.77	3.40
420380	AA640891	Hs.102406	ESTs	2.77	4.28
443172	AW662964	Hs.199061	p300/CBP-associated factor	2.75	2.88
456629	AW891965		histone deacetylase 3	2.72	2.24
407857	A1928445	Hs.92254	synaptotagmin-like 2	2.72	1.93
421097	A1280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.68	2.59
436280	A1690734		Homo sapiens cDNA: FLJ22562 fis, clone H	2.67	2.79
407550	Y10515		gb:H.sapiens mRNA for CD58 T7 protein.	2.65	1.98
427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.64	1.76
427899	AA829286	Hs.332053	serum amyloid A1	2.59	3.01
442793	AJ017798		ESTs, Weakly similar to T147_HUMAN CARGO	2.58	1.60
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.57	1.91
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.57	2.13
458247	R14439	Hs.209194	ESTs	2.56	2.61
451668	Z43948	Hs.326444	cartilage acidic protein 1	2.52	2.74
433980	AA137152	Hs.286049	phosphoserine aminotransferase	2.51	1.88
412719	AW016610	Hs.816	ESTs	2.50	1.68
441789	D52059	Hs.7972	KIAA0871 protein	2.50	3.11
405885			Target Exon	2.50	3.15
453464	A1884911	Hs.32989	receptor (calcitonin) activity modifying	2.48	3.33
417821	BE245149	Hs.82643	protein tyrosine kinase 9	2.48	1.66
450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	2.47	2.79
436825	AW341123	Hs.120275	ESTs	2.47	2.55
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.42	2.28
432426	AW973152	Hs.31050	ESTs	2.42	1.76
409095	AW337272	Hs.293656	ESTs, Moderately similar to S72481 proba	2.41	2.41
403752			NM_002753: Homo sapiens mitogen-activate	2.41	2.87

	404489		Target Exon		
	411690	AA669253	RNA, U2 small nuclear	2.39	1.97
	439195	H89360	gb:Yw28008.s1 Morton Fetal Cochlea Homo	2.37	2.54
5	453582	AW854339	hypothetical protein FLJ11937	2.37	2.27
	438461	AW075485	phosphoserine aminotransferase	2.36	2.81
	432878	BE386490	Purin	2.35	2.91
	416647	BE297139	replication protein A2 (32kD)	2.35	2.28
	428666	AL080190	Homo sapiens mRNA: cDNA DKFZp434A202 (fr	2.33	1.97
10	413645	AA130992	gb:zo15e02.s1 Stratagene colon (937204)	2.32	2.92
	421282	AA286914	ESTs	2.31	2.63
	434418	AF134707	a disintegrin and metalloproteinase doma	2.31	1.85
	413204	BE071603	gb:QV3-BT0510-161299-032-03 BT0510 Homo	2.31	2.21
	449720	AA311152	hypothetical protein FLJ21562	2.31	1.49
15	451838	AW005866	ESTs	2.30	1.78
	410943	AW968322	low molecular mass ubiquinone-binding pr	2.28	2.05
	459711	BE386801	trinucleotide repeat containing 3	2.28	2.39
	429489	AF008203	aristatless-like homeobox 3	2.27	2.39
	429493	AL134708	ESTs	2.26	1.97
20	422283	AW411307	ESTs	2.26	2.77
	441989	AA306207	CDC45 (cell division cycle 45, S.cerevis	2.26	1.78
	419352	AI675008	protein kinase, cAMP-dependent, regulato	2.26	1.84
	427393	AB029018	ESTs	2.25	1.47
	418522	AA605038	KIAA1095 protein	2.25	1.83
25	433458	AA832055	Homo sapiens cDNA: FLJ21950 fis, clone H	2.24	2.42
	452782	AA028166	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.24	1.76
	443910	AW051711	ESTs	2.24	2.34
	408832	AW085690	ESTs	2.24	1.79
30	407283	TS1008	ESTs, Weakly similar to Z195_HUMAN ZINC	2.22	1.52
	437376	AA749400	gb:yb55e08.s1 Stratagene ovary (937217)	2.22	1.31
	450712	AI732130	ESTs	2.22	2.44
	421362	AK000050	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.22	1.62
	445183	AB007877	hypothetical protein FLJ20043	2.22	2.36
	438501	Z44110	KIAA0417 gene product	2.20	1.84
35	432882	NM_013257	phosphoinositol 3-phosphate-binding prot	2.20	1.76
	414900	AW452420	serum/glucocorticoid regulated kinase-li	2.19	1.59
	427704	AW971063	ESTs	2.18	1.89
	404942		ESTs	2.17	1.86
40	448019	AW947164	splicing factor, arginine/serine-rich 9	2.17	1.86
	459254	AA694386	ESTs, Moderately similar to I38022 hypot	2.17	1.64
	418965	AI002238	ESTs	2.16	1.61
	443357	AW016773	splicing factor, arginine/serine-rich 11	2.16	1.79
	412432	AA126311	low molecular mass ubiquinone-binding pr	2.16	2.32
45	449567	AI990790	ESTs	2.15	2.73
	433179	AW362945	ESTs	2.08	2.85
	408243	Y00787	ESTs	2.07	4.77
	435294	T84084	interleukin 8	2.05	3.12
	449656	AA002008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.97	2.89
50	412649	NM_002206	ESTs	1.94	3.60
	445162	AB011131	integrin, alpha 7	1.93	2.76
	419356	AI656166	piccolo (presynaptic cytomatrix protein)	1.93	2.66
	424263	M77640	hypothetical protein FLJ22316	1.92	3.39
	414694	NM_015362	L1 cell adhesion molecule (hydrocephalus	1.89	3.10
55	415825	Y18024	HSPC002 protein	1.88	4.25
	409105	AW467539	inositol 1,4,5-trisphosphate 3-kinase B	1.87	2.66
	444784	D12485	ESTs	1.87	2.96
	404149		ectonucleotide pyrophosphatase/phosphodi	1.85	2.80
	406387		C6002509*gi 5031885 ref NP_005568.1 li	1.84	2.93
60	420871	AA702972	Target Exon	1.82	2.96
	455797	BE091833	ESTs	1.76	3.12
	418751	BE389014	gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.75	3.12
	412347	AW970026	phosphoinositide-3-kinase, regulatory su	1.70	3.20
	413211	AW967107	ubiquinol-cytochrome c reductase hinge p	1.67	3.65
	459317	BRCA1b	hypothetical protein MGC4365	1.66	2.89
65	425525	AA358883	Eos Control	1.61	7.34
	436823	AW749865	ESTs	1.59	2.67
	433669	AL047879	ESTs, Weakly similar to I38022 hypothi	1.56	2.76
	424389	AA339786	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.55	2.76
	426672	AW270555	lymphocyte-specific protein 1	1.53	2.95
70	415977	AL037622	hypothetical protein	1.51	3.39
	404780		methionine aminopeptidase; eIF-2-associa	1.47	2.65
	436476	AA326108	Target Exon	1.43	2.77
	428284	AA535762	bHLH protein DEC2	1.41	3.04
75	448571	AA486794	NM_004545:Homo sapiens NADH dehydrogenas	1.38	2.94
	428156	BE269388	ESTs, Weakly similar to 16.7Kd protein [1.37	2.80
	447752	M73700	mitochondrial ribosomal protein L20	1.36	3.29
	447455	H38335	lactotransferrin	1.35	2.70
	453281	W46280	Homo sapiens mRNA for FLJ00058 protein,	1.35	3.03
	413142	M81740	ESTs, Weakly similar to A25704 synapsin	1.34	2.69
80	407194	AA621644	ornithine decarboxylase 1	1.33	2.96
	444107	T46839	gb:af54a01.s1 Soares_total_fetus_Nb2HF8_	1.32	2.70
	406797	AI432224	UDP glycosyltransferase 2 family, polype	1.26	3.27
	406711	N25514	ribosomal protein L6	1.26	2.72
	414608	BE396215	myosin, light polypeptide 6, alkali, smo	1.25	7.10
			ATP synthase, H transporting, mitochondr	1.24	2.72

401846			NM_000988*: Homo sapiens ribosomal protein	1.24	2.82
432982	AA531058	Hs.182248	truncated calcium binding protein	1.23	3.10
428578	BE391797	Hs.343588	ribosomal protein S12	1.23	2.74
400199			Eos Control	1.21	3.58
400079			Eos Control	1.20	2.99
412623	R28898	Hs.74170	metallothionein 1E (functional)	1.19	2.63
406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.19	4.15
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	4.75
442492	AA528489	Hs.234518	ribosomal protein L23	1.17	2.74
431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.17	3.15
436398	H87136	Hs.5174	ribosomal protein S17	1.16	3.22
432205	AI806583	Hs.125291	ESTs	1.15	2.76
406859	AI581134	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.09	2.66
401254			Target Exon	1.00	3.08
405752			Target Exon	1.00	2.87
445772	AI733941	Hs.145493	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.00	2.70
452916	AA642831	Hs.31016	putative DNA binding protein	1.00	2.62
451411	AA017492	Hs.135655	EST	1.00	2.64
415658	BE501921	Hs.270471	ESTs	1.00	2.82
448610	NM_006157	Hs.21602	nel (chicken)-like 1	1.00	3.30

TABLE 54B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

412262	4362_1	Accession	AK056051 AI971258 AI681134 AU146134 AI803300 AA917325 AA923663 BF895068 AI304442 AI167464 AI284188 AA054272 AA829262 AI351910 T90300 AI886230 U70056 AU119916 BF446537 BE503207 BE502849 AI698102 AA258553 AV719917 BF72133 BI438668 AI804000 B349103 AI912294 BE645117 AA227954 AA446520 AA879147 AA281770 AW136872 AA807907 AI435989 AI339626 AI383274 AA418512 BE771804 BF894509 AA455093 AI379061 AI150855 BF769906 R17298 AU138740 BF808607 BE674633 AV700132 AA227789 AA253099 AW975199 AA935418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810 R42784 R44804 R41278
409760	865166_1	AA302840 T93016 T92950 AU184997 AA077551	
453912	32562_3	BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BC460936 AW388482 AW388420 BF374777 W01360 N94710 H87967	
456629	207_22	AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548 AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200 AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420 AI695314 BE083790 AW858568 AW545550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW877775 AW838449 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717 AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW388713 AW062593 AW176663 AW842064 AW842089 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577 AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484 BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999878 AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL36722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972 AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945 AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781	
436280	36296_1	AK026215 AI201248 BE671206 AA860436 AA730787 AA834507 D79304 D79806 AW961628 AI017068 BE044373 AA322458 AA987927 AA385869 BI492783 AW021853 R79299 N73208 AI016622 N24609 AW192569 AA707819 AI690734 R79189 AI535900 AW589301 AI128434 BE838011 BE837891 BF894555 H95408	
442793	417820_2	BG741247 BG741022 AI017798 AI953594 AW445065 AI245087	
411690	53926_1	AK027091 BF514593 BF768430 BI037830 BE175161 BG000114 BG897171 AA745391 AA669569 AA669253 BI049453 BE304449 BG010136 BG830874 BF091358 BF762561 T56173 BC003629 BF091330 BE697323 BF091340 BE843330 AA744150 AA745471 W26276 BI037837	
439195	21979_1	AF086037 H89360 H89546	
413645	1234345_1	AA130992 AW969537 AA503835	
413204	1494523_1	BE071616 BE071613 BE071603 BE071587 BE071607 BE071615 BE071636	
443357	427117_1	AV715934 BG654600 AI052778 BG057892 AW016773 AI452937 AW085293	
455797	1511159_1	BE091833 BE091874 BE091871	
418751	21393_1	BF690141 BE159368 AI937311 AU151256 AW341542 AW274231 AW341609 AW450447 AA843698 AW188066 AW007171 AW007027 AI075008 AL520351 AA608992 AW151842 AA622181 AI273454 AI005661 AA205946 AA677899 AW473512 AW296620 AA872899 AI094216 AI025188 AA256998 AI539154 AI500192 AI289493 AI040740 BE167841 AW151374 BE167754 BF036108 AA299181 N23237 T62967 W96060 AA574412 AW606697 W96059 R51303 R09158 R59113 T48473 T59023 AA122066 AW606643 R38386 R06567	
424389	1059_4	BG190758 AW961118 W77994 AA339877 AW845121 AW845129 BG181820 BE716719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786 BE838286 BE838282 BE716636 AA777158 W94063 BE716628 BE716625 BE838371 BF371044 BE716631 BE716402	
406797	0_0	AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640	

TABLE 54C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NI_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	405885	7677703	Minus	42574-42998
	403752	7678857	Plus	33704-33828
5	404489	8113772	Plus	98183-98480
	404942	7382153	Plus	92095-92252
	404149	7534008	Plus	121831-121951,124044-124150
	406387	9256180	Plus	116229-116371,117512-117651
	404780	9887810	Minus	175708-175871
10	401846	7712190	Minus	82775-82823,82912-83022
	401254	9796309	Plus	152209-152383
	405752	9212305	Plus	91392-91528

15	TABLE 55A: ABOUT 201 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT DID NOT METASTASIZE RELATIVE TO PRIMARY MELANOMAS THAT LATER METASTASIZED			
	Table 55A lists about 201 genes upregulated in primary melanomas from tumors that did not metastasize relative to primary melanomas that metastasized later. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.			
20	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
25	R1:	90th percentile of AIs for primary melanomas that did not metastasize divided by the 90th percentile of AIs from primary melanomas that metastasized later		
	R2:	90th percentile of AIs for primary melanomas that did not metastasize divided by the 90th percentile of AIs from primary melanomas that metastasized later, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator		

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.08	5.48
30	404854			Target Exon	5.18	8.18
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	4.89	4.95
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	4.83	4.86
	408471	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	4.71	4.70
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.71	3.85
35	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	3.98	4.01
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	3.92	3.35
	400417	X72475		Target	3.83	2.78
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.67	2.29
	409190	AU076536	Hs.50984	sarcoma amplified sequence	3.62	3.68
40	408692	AL040127	Hs.34074	dipeptidylpeptidase VI	3.61	3.89
	423619	T48691	Hs.249159	adrenergic, alpha-2A-, receptor	3.56	3.61
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.55	2.85
	445745	AB007924	Hs.13245	KJAA0455 gene product	3.38	2.55
	406663	U24683		immunoglobulin heavy constant mu	3.34	6.16
45	414522	AW518944	Hs.76325	Immunoglobulin J chain	3.32	2.75
	419235	AW470411	Hs.288433	neurotrimin	3.32	2.74
	441598	AI733219	Hs.58262	ESTs	3.31	3.71
	402294			Target Exon	3.24	2.35
	402737			Target Exon	3.22	2.87
50	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.20	3.04
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.18	2.81
	427335	AA448542	Hs.251677	G antigen 7B	3.17	4.62
	404955			ENSP00000251890:Monocytic leukemia zinc	3.13	2.34
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	3.12	2.21
55	430015	AW768399		ESTs	3.12	1.93
	414340	AI022656	Hs.296272	ESTs	3.09	2.87
	400072			Eos Control	3.08	3.16
	422567	AF111178	Hs.118407	glypican 6	3.06	2.73
	401284			Target Exon	3.04	2.56
60	455839	BE145814		gb:MR0-HT0208-101299-202-a04 HT0208 Homo	3.02	2.76
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.00	3.15
	437258	AL041243	Hs.174104	ESTs	2.99	2.44
	445612	N94126	Hs.12969	hypothetical protein	2.98	2.40
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.97	2.13
65	437723	AI672731	Hs.13256	ESTs	2.95	2.46
	439658	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	2.95	2.77
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.94	2.68
	424761	AA534528	Hs.152944	loss of heterozygosity, 11, chromosomal	2.92	3.81
	405757			Target Exon	2.92	3.00
70	406621	X57809	Hs.8997	immunoglobulin lambda locus	2.92	6.71
	409060	AI815867	Hs.50130	necdin (mouse) homolog	2.86	2.16
	431712	R26584	Hs.267993	hypothetical protein FLJ10143	2.82	2.50
	413441	AI929374	Hs.75367	Src-like-adaptor	2.82	2.48
	452651	AI218918	Hs.30209	KIAA0854 protein	2.82	1.13
75	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.78	2.77
	439778	AL109729	Hs.99364	putative transmembrane protein	2.77	1.92
	434293	NM_004445	Hs.3796	EphB6	2.75	2.89
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.70	2.03
	406638	M13861		gb:Human T-cell receptor active beta-cha	2.69	2.67
80	432331	W37862	Hs.274368	MSTP032 protein	2.68	3.08
	408989	AW361666	Hs.49500	KIAA0746 protein	2.68	2.58
	401731			NM_017990: Homo sapiens hypothetical pro	2.68	2.53
	401979			C17000767.gil11990770[emb]CAC19651.1[1] (A	2.68	3.42
	415539	AI733881	Hs.72472	BMP-R1B	2.68	2.51

	425032	NM_001186	Hs.154276	BTB and CNC homology 1, basic leucine zi	2.67	2.13
	406837	R70292	Hs.156110	immunoglobulin kappa constant	2.66	3.25
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	2.66	2.74
	425100	AF051850	Hs.154567	supervillin	2.65	2.80
5	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	2.65	2.63
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.64	1.84
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.63	2.63
	425580	L11144	Hs.1907	galanin	2.62	2.00
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.61	1.80
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	2.61	1.82
	433470	AW960564		transmembrane 4 superfamily member 1	2.60	2.44
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	2.60	2.47
	401112			NM_024997:Homo sapiens hypothetical pro	2.60	2.58
15	411802	AA733204		nuclear transcription factor Y, gamma	2.59	2.32
	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.59	1.88
	425209	AL049761	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.58	2.81
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.56	2.10
	442560	AA365042	Hs.325531	ESTs, Weakly similar to 2004399A chromos	2.55	3.97
20	408491	AI088063	Hs.7882	ESTs	2.54	2.74
	420223	N27807		ribosomal protein L4	2.54	2.02
	444467	AI150368	Hs.143844	ESTs	2.54	2.59
	436729	BE621807		transmembrane 4 superfamily member 1	2.53	2.29
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	2.53	1.80
25	453507	AF083217	Hs.33085	WD repeat domain 3	2.52	1.99
	420315	NM_006299	Hs.96448	zinc finger protein 193	2.52	2.50
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	2.50	2.35
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	2.50	2.44
	402692			Target Exon	2.50	1.73
30	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	2.50	4.55
	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.49	2.95
	420568	F09247	Hs.247735	protocadherin alpha 10	2.49	3.55
	444115	AW954585	Hs.271920	ESTs, Weakly similar to Z195_HUMAN ZINC	2.49	2.52
	404049			NM_018937:Homo sapiens protocadherin be	2.48	2.67
35	417694	R09486	Hs.193118	ESTs	2.48	2.09
	420600	BE011657	Hs.165695	ESTs, Weakly similar to unnamed protein	2.48	2.00
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.47	2.01
	404752			NM_024778:Homo sapiens hypothetical prot	2.47	3.07
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-i	2.47	2.46
40	436378	AJ227874	Hs.99244	ESTs	2.46	1.88
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.44	2.98
	431190	AL134172	Hs.120852	ESTs	2.44	2.48
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.44	2.96
	436608	AA628990	Hs.192371	down syndrome critical region protein DS	2.44	3.16
45	445547	D86181	Hs.273	galactosylceramidase (Krabbe disease)	2.43	3.33
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	2.43	2.07
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	2.43	3.36
	405782	AAA30373		gb:zw20111.s1 Soares ovary tumor NbhOT H	2.40	3.38
	407260	L09095		gb:Homo sapiens mRNA fragment	2.38	3.78
50	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.36	3.56
	431365	AA504080	Hs.191958	immunoglobulin superfamily receptor tran	2.34	2.84
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	2.33	3.21
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.31	2.94
	403632			Target Exon	2.27	2.80
55	434232	AW297064	Hs.131862	ESTs	2.24	2.98
	428114	AI821548	Hs.98363	ESTs, Weakly similar to I38022 hypotheti	2.23	2.81
	403294			Target Exon	2.19	2.81
	429249	X81479	Hs.2375	egl-like module containing, mucin-like,	2.16	3.13
	403295			Target Exon	2.15	2.95
60	427817	AA503373	Hs.186678	ESTs	2.13	2.80
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.08	3.28
	443176	AI696081	Hs.223770	ESTs	2.04	3.50
	401770			C17001739:gi 2327052 gb AAC48759.1 (U9	2.04	5.39
	407124	R08160		gb:yf18a07.s1 Soares fetal liver spleen	2.03	2.95
65	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	2.03	2.97
	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA1399 pro	2.01	3.42
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.01	3.05
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.01	3.58
	401673			C16001416:gi 12743112 ref XP_010131.2	1.99	4.99
70	420983	W95228	Hs.100764	cathepsin G	1.95	5.47
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	1.94	4.58
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	1.93	2.82
	405121			mitogen-activated protein kinase 8 inter	1.92	2.82
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.92	2.80
75	450852	AI983354	Hs.7740	oxysterol binding protein-like 1	1.91	5.08
	432902	U75697		histone deacetylase 3	1.90	2.84
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	1.89	3.04
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.87	2.85
	424398	BE397787	Hs.146393	homocysteine-inducible, endoplasmic reti	1.85	3.71
80	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	1.85	3.38
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	1.85	3.57
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.82	6.17
	421563	NM_006433	Hs.105806	granulysin	1.80	3.50
	453804	AA300204	Hs.35276	KIAA0852 protein	1.78	2.87

429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.78	3.54
437866	AA156781		metallothionein 1E (functional)	1.77	2.97
427751	AF000152		conserved gene amplified in osteosarcoma	1.75	6.89
400442			DKFZP586G1722 protein	1.74	3.60
456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.74	3.45
414477	U41635	Hs.76228	amplified in osteosarcoma	1.71	4.99
432870	AW974124		gb:EST386227 MAGE resequences, MAGM Homo	1.68	2.86
456642	AW451623	Hs.109752	putative c-Myc-responsive	1.68	3.09
456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fls, clone H	1.66	2.83
430449	AA352723	Hs.241471	RNB6	1.65	2.84
401029			v-myc avian myelocytomatosis viral relat	1.65	2.88
402742			NM_002508:Homo sapiens nidogen (enactin)	1.64	3.37
402559			Rho GTPase activating protein 1	1.63	3.07
418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	1.62	3.11
406851	AA609784		major histocompatibility complex, class	1.62	2.86
450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.60	3.94
447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	1.60	3.75
417739	Z43995		gb:HSC1QB121 normalized infant brain cDN	1.59	2.96
452950	AA428123	Hs.302766	tyrosine 3-monooxygenase/tryptophan 5-mo	1.58	2.95
427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.58	4.11
444182	AW160432	Hs.296460	craniofacial development protein 1	1.57	2.98
407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.57	3.88
452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.56	2.88
416819	U77735	Hs.80205	pim-2 oncogene	1.56	3.59
414583	AA362907	Hs.76494	proline arginine-rich end leucine-rich r	1.55	4.38
426104	AI204418	Hs.190080	ESTs	1.55	3.47
441591	AF055992	Hs.183	Duffy blood group	1.52	4.28
446406	AI553681		Arg/Abi-interacting protein ArgBP2	1.49	2.87
427343	AI880044	Hs.176977	protein kinase C binding protein 2	1.49	2.88
415550	L13720	Hs.78501	growth arrest-specific 6	1.47	4.82
411961	AI478432	Hs.72956	hypermethylated in cancer 1	1.46	3.48
406213			ENSP00000246202:DJ63M2.2 (similar to AC	1.42	3.19
400847			NM_003105:Homo sapiens sortilin-related	1.41	2.97
404642			NM_021965:Homo sapiens phosphoglucomuta	1.40	3.02
452650	AW270150	Hs.254516	ESTs	1.40	2.86
432894	AW167668	Hs.279772	brain specific protein	1.37	5.52
404030			NM_015669:Homo sapiens protocadherin be	1.37	3.03
422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	1.35	3.15
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.34	3.09
425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.32	3.29
415198	AW009480	Hs.943	natural killer cell transcript 4	1.32	2.89
406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.31	2.89
423959	AA333025		gb:EST37122 Embryo, 8 week I Homo sapien	1.31	2.88
408135	AA317248	Hs.42957	methyltransferase-like 1	1.29	3.81
427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.29	3.25
415512	Y16270	Hs.78482	paralemnin	1.29	2.85
413531	AL036958	Hs.75416	DAZ associated protein 2	1.28	3.06
419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	1.27	2.80
424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibitor	1.26	2.90
422934	BE244189	Hs.122492	hypothetical protein	1.25	3.41
450935	BE514743		tumor suppressor deleted in oral cancer-	1.25	3.63
416630	H69392	Hs.174051	small nuclear ribonucleoprotein 70kD pol	1.24	2.93
416950	AL049798	Hs.80552	dermatopontin	1.22	2.81
412558	AW962019		gb:EST374092 MAGE resequences, MAGG Homo	1.21	3.02
419593	W73092	Hs.58282	ESTs	1.19	2.84
403470			Target Exon	1.14	2.82
402230			Fgenesh predicted: CYTOCHROME P450 4F5 (1.12	2.96
400559			Target Exon	1.00	2.90
412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	1.00	2.84
427072	H38046	Hs.293981	ESTs	1.00	2.89
430439	AL133561		DKFZP4348061 protein	1.00	3.09
418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.00	2.93

TABLE 558:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	406636	0_0	L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080
	430540	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
75			BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
			AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
			BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
			BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
			BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
			AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953
80			BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
			W58732 W56990 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
			F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114
			AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103

			AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 B1860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW766399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AJ914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AJ205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 B1860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 AJ245210 AJ245212 AJ245211 AJ245213 M13861
430015	713_2		
5			
10			
15			
		455839 1518842_1 406642 0_0 406638 0_0 433470 6624_1	
20			
25			
30			
35			
40			
45			
		411802 609_6	
50			
		420223 191648_1 436729 6624_1	
55			
60			
65			
70			
75			
80		406782 0_0 432902 35601_1	

5	437866	34267_1				
10	427751	15028_1				
15						
20						
25						
30	432870	1238170_1				
	406851	0_0				
	417739	2145372_1				
	445406	11004_1				
35	423959	887999_1				
	450935	4469_1				
40						
	412558	1227364_1				
	412695	1243394_1				
	430439	6750_2				
45						
50						
55						
60						
65						
70						
75						
80						

TABLE 55C:

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probe set

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404854	7143420	Plus	14260-14537
402294	2282012	Minus	2575-3000
402737	9212184	Minus	13358-13552
404995	6006247	Minus	154015-154123
401284	9800819	Minus	101307-101421
405757	3334694	Minus	66825-70466
401731	9690317	Plus	43830-43963,44787-44935,45698-45810,4741
401979	2826778	Minus	75693-75851,76977-77112
401112	9966198	Minus	60628-61041
402692	8468956	Plus	124606-125387
404049	3688074	Minus	75765-78155
404752	7109522	Minus	120168-120326
403632	8572864	Minus	35197-35358
403294	8096496	Plus	41565-41881
403295	8096528	Plus	22386-22708
401770	9958312	Plus	183424-183576
401673	7689903	Minus	122587-122705,122765-123047
405121	8102330	Minus	35816-36004,36587-36684
400442	9887672	Plus	59362-59574
401029	8117523	Plus	41999-42172
402742	9212200	Minus	23487-23613
402559	9864273	Plus	33539-33715
406213	7342019	Plus	25921-26612,34539-35161
400847	9188605	Plus	44643-44835
404642	9796810	Plus	102999-103145
404030	7671252	Plus	149362-151749
403470	9929739	Minus	8376-8552
402230	9966312	Minus	29782-29932
400559	9843598	Plus	75483-75584

TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI

Table 56A lists about 277 genes upregulated in melanoma metastases relative to benign nevi. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
10	R1:	70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs
	R2:	70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
422424	A1186431	Hs.296638	prostate differentiation factor	13.73	17.18
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11.67	13.25
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	9.35	8.75
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	8.63	6.22
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	8.21	8.65
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	7.13	5.04
447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	6.79	7.12
417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	5.94
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	6.43	3.46
414812	X72755	Hs.77367	monokine induced by gamma interferon	6.43	5.44
451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.31	6.08
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	6.20	6.04
428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	6.03	4.72
417308	H50720	Hs.81892	KIAA0101 gene product	6.01	7.07
448569	BE382657	Hs.21486	signal transducer and activator of trans	5.99	8.88
439310	AF086120	Hs.102793	ESTs	5.95	6.63
452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.95	3.77
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.76	6.37
442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	5.76	3.14
409274	NM_003930	Hs.52644	SKAP55 homologue	5.65	5.01
442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.58	3.50
442711	AF151073	Hs.8645	hypothetical protein	5.45	5.84
425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.75
412918	BE563957		activated RNA polymerase II transcrip	5.35	4.94
428125	AA393071	Hs.182579	leucine aminopeptidase	5.33	5.34
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.33	4.98
431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.25
414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.33
426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.05	8.77
415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	5.03	5.17
436701	AW959032		ESTs, Moderately similar to I78885 serin	5.03	4.17
406648	AA563730	Hs.277477	major histocompatibility complex, class	4.99	5.08
410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ121425 fis, clone C	4.98	4.71
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.98	4.08
432469	AL080084		CGI-100 protein	4.97	4.70
404854			Target Exon	4.85	4.07
415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.82	4.90
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	3.45
408958	T99607	Hs.49346	signal recognition particle 54kD	4.78	2.34
453949	AU077146	Hs.36927	heat shock 105kD	4.78	6.32
458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	6.57
440245	AK001913	Hs.7100	hypothetical protein	4.74	3.83
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	4.74	5.53
417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.73	4.35
451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	4.67	4.60
424571	BE379766		polymerase (RNA) II (DNA directed) polyp	4.62	3.50
434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.61	5.67
452268	NM_003512	Hs.28777	H2A histone family, member L	4.60	3.79
421311	N71848	Hs.283609	hypothetical protein PRO2032	4.60	3.58
410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.68
425706	AW406678	Hs.122559	hypothetical protein FLJ22570	4.59	3.83
450293	N36754	Hs.171118	hypothetical protein FLJ00026	4.57	5.40
406836	AW514501	Hs.156110	immunoglobulin kappa constant	4.57	6.33
413441	AJ929374	Hs.75367	Src-like-adaptor	4.53	4.77
431129	AL137751	Hs.263671	Homo sapiens mRNA: cDNA DKFZp434I0812 (f	4.48	4.89
418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.47	4.17
411060	NM_005074	Hs.318501	Homo sapiens mRNA full length insert cDN	4.47	4.33
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	4.45	3.32
437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.43	4.43
448883	BE614989	Hs.7503	hypothetical protein FLJ14153	4.42	3.91
417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	4.41	4.09
419285	D31887	Hs.89868	KIAA0062 protein	4.40	3.56
418321	D63477	Hs.84087	KIAA0143 protein	4.38	3.00
430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	4.37	4.26
428450	NM_014791	Hs.184339	KIAA0175 gene product	4.36	4.90
428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.36	3.57
447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.36	4.07
409598	NM_014018	Hs.55097	mitochondrial ribosomal protein S28	4.35	3.29
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.34	5.80
407047	XG5965		gb:H.sapiens SOD-2 gene for manganese su	4.33	3.51

5	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	4.33	4.23
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	4.32	2.68
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	4.32	4.54
	449722	BE280074	Hs.23960	cyclin B1	4.31	3.73
	408380	AF123050	Hs.44532	diubiquitin	4.30	5.74
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	4.28	4.80
	417933	X02308	Hs.82962	thymidylate synthetase	4.28	3.59
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	4.25	4.15
10	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.24	3.15
	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.23	4.12
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.22	4.64
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.20	4.62
	408989	AW361666	Hs.49500	KIAA0746 protein	4.20	4.92
15	449626	AA774247	Hs.301637	zinc finger protein 258	4.19	3.17
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	4.18	8.91
	415726	T89844	Hs.78712	aminolevulinatase, delta-, synthase 1	4.16	4.21
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	4.16	1.89
	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	4.14	3.30
20	438718	AL040058	Hs.6375	uncharacterized hypothalamus protein HT0	4.14	3.04
	437802	AI475995	Hs.122910	ESTs	4.12	5.13
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	4.12	3.87
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.11	4.96
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	4.11	6.37
25	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	4.10	4.16
	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 fis, clone PL	4.10	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	4.10	4.50
	414522	AW518944	Hs.76325	immunoglobulin J chain	4.09	6.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.09	5.03
30	405506			Target Exon	4.08	3.71
	417497	AW402482	Hs.82212	CD53 antigen	4.07	8.61
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	4.05
	421508	NM_004833	Hs.105115	absent in melanoma 2	4.05	4.61
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	4.02	4.56
35	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	4.00	8.91
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.15
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.58
	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	3.85	4.26
40	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.81	4.06
	410668	BE379794	Hs.159651	hypothetical protein	3.80	6.84
	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.46
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	6.44
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	4.00
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	3.76	4.67
45	454080	AI199711	Hs.576	fucosidase, alpha-L-1, tissue	3.74	6.22
	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.36
	428398	AI249368	Hs.98558	ESTs	3.68	5.18
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	3.67	4.12
	414829	AA321568	Hs.77436	pleckstrin	3.65	4.45
50	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	4.84
	433867	AK000596	Hs.3618	hippocalcin-like 1	3.59	4.49
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.54	5.31
	418310	AA814100	Hs.86693	ESTs	3.49	4.57
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.48	4.33
55	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.87
	427527	AI809067	Hs.153261	immunoglobulin heavy constant mu	3.44	10.42
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	3.41	4.60
	432606	NM_002104	Hs.3086	granzyme K (serine protease, granzyme 3;	3.40	4.50
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	3.40	4.22
60	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	5.03
	422545	X02761	Hs.287820	fibronectin 1	3.39	7.32
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.36	4.47
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.34	5.02
65	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.34	4.24
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.33	4.29
	432642	BE297635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	3.32	4.48
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	3.24	4.64
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.23	13.58
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23	4.20
70	443958	BE241880	Hs.10029	cathepsin C	3.16	5.05
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	3.15	4.04
	412577	Z22968	Hs.74076	CD163 antigen	3.14	5.32
	414050	NM_004766	Hs.75724	coatomer protein complex, subunit beta 2	3.13	4.65
75	442904	AW575008	Hs.11355	thymopoietin	3.13	4.34
	421633	AF121860	Hs.106260	sorting nexin 10	3.12	4.99
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibitor	3.11	5.47
	428797	AA496205	Hs.193700	Homo sapiens mRNA: cDNA DKFZp586I0324 (f	3.10	4.30
	408515	AI289507	Hs.295883	hypothetical protein FLJ23399	3.10	4.03
	409442	AA310162	Hs.169248	cytochrome c	3.07	4.00
80	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.04	4.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.04	5.53
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.03	4.97
	452139	AA099959	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	3.01	4.87
	430478	NM_014349	Hs.241535	apolipoprotein L 3	2.98	4.44

	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	2.95	7.45
	406782	AA430373		gb:zw20111.s1 Soares ovary tumor NbHOT H	2.93	8.49
	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.90	5.08
5	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.87	7.07
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.87	4.29
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82	5.53
	419956	AL137939	Hs.40096	cadherin 19, type 2	2.80	4.26
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.79	5.55
10	421712	AK000140	Hs.107139	hypothetical protein	2.79	6.29
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.74
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	2.78	4.69
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	2.77	5.18
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.90
15	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019 (CEM15)	2.75	4.33
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.72	4.19
	429402	AF116571	Hs.201671	SRV (sex determining region Y)-box 13	2.72	5.15
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-f	2.71	4.82
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	2.71	4.61
20	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.69	4.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.89
	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	2.68	4.25
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.67	5.00
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.65	9.54
25	445784	AI253155	Hs.146065	ESTs	2.65	4.11
	410341	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	4.50
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.63	4.17
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62	5.80
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.61	5.57
30	424779	AL046851	Hs.153053	CD37 antigen	2.60	5.72
	420224	M84371	Hs.96023	CD19 antigen	2.60	4.02
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	2.57	4.83
	426143	BE379836		proteasome (prosome, macropain) subunit,	2.56	4.50
	421563	NM_006433	Hs.105806	granulysin	2.56	5.35
35	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	2.55	4.32
	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.54	5.78
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	2.54	4.09
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.53	4.41
	429800	AA333375	Hs.223014	antizyme inhibitor	2.50	5.68
40	407241	M34516		gb:Human omega light chain protein 14.1	2.50	4.69
	421739	AB004550	Hs.107526	UDP-Gal:betaGlcNAc beta 1,4-galactosylt	2.45	4.35
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.45	4.66
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.91
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.41	4.80
45	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (TIT3 com	2.41	4.00
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	2.41	4.77
	417370	T26651	Hs.82030	tryptophanyl-tRNA synthetase	2.41	4.04
	400223			Eos Control	2.39	5.47
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.38	7.67
50	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.32
	415149	X12451	Hs.78056	cathepsin L	2.37	8.07
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.23
	454390	AB020713	Hs.56966	KIAA0906 protein	2.35	4.57
	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; poly (ADP-r	2.31	5.48
55	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	2.24	4.08
	438956	W00847	Hs.135056	Human DNA sequence from clone RPS-850E9	2.23	4.02
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.23	4.90
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.18	4.97
	436692	AW243158	Hs.5297	DKFZP564A2416 protein	2.17	4.13
60	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.14	5.14
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.43
	429642	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (2.11	5.42
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	6.36
	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	2.10	4.06
65	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.09	4.67
	414045	NM_002951	Hs.75722	ribophorin II	2.07	4.32
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.24
	441211	AW946155	Hs.7750	hypothetical protein AL133206	2.06	4.64
	434692	H06586	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.05	4.33
70	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	2.04	13.36
	438393	AA351815	Hs.50740	Homo sapiens cDNA: FLJ22272 fis, clone H	2.03	4.52
	413313	NM_002047	Hs.283108	glycyl-tRNA synthetase	2.02	4.11
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.00	4.04
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.99	4.35
75	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.52
	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	1.95	5.60
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.95	5.38
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.93	4.69
	418917	X02994	Hs.1217	adenosine deaminase	1.91	4.32
80	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	1.91	4.48
	413945	NM_000591	Hs.75627	CD14 antigen	1.90	6.03
	429119	AV660012	Hs.196437	hypothetical protein FLJ10788	1.90	4.08
	413317	U53225	Hs.75283	sorting nexin 1	1.89	4.06
	427239	BE270447		ubiquitin carrier protein	1.87	5.98

5	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.87	6.33
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.85	4.21
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarro	1.84	5.07
	430040	AW503115	Hs.227823	pMS protein	1.83	5.57
	416819	U77735	Hs.80205	pim-2 oncogene	1.83	4.12
	425356	BE244879	Hs.155939	inositol polyphosphate-5-phosphatase, 14	1.82	5.71
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.73
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	1.80	4.71
10	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.78	5.16
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor I	1.78	7.00
	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	5.10
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.15
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.70	4.43
15	428385	AF112213	Hs.184062	putative Rab5-interacting protein	1.69	4.06
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.67	5.68
	413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.56
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4.40
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.02
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4.49
	446143	BE245342	Hs.306079	sec61 homolog	1.62	4.73
	413511	AI627178	Hs.75412	arginine-rich, mutated in early stage tu	1.60	4.19
	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.61
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	1.59	4.26
25	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.56	4.10
	419489	AW411280	Hs.90693	replication initiation region protein (6	1.55	4.30
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.54
	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	1.53	4.00
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.53	4.79
30	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.51	4.12
	418879	AW162087	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.50	4.93
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (Hv	1.45	4.15
	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.45	4.03
	432805	X94630	Hs.3107	CD97 antigen	1.43	4.11
35	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	1.43	4.08
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.41	4.36
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU proteoglyca	1.41	4.10
	412968	AW500508	Hs.75102	alanine-tRNA synthetase	1.40	4.25
	428511	AA019912	Hs.184693	transcription elongation factor B (SIII)	1.38	4.91
40	413825	BE299181	Hs.75564	CD151 antigen	1.37	4.46
	427496	D21260	Hs.178710	clathrin, heavy polypeptide (Hc)	1.30	4.04
	407143	CA1076	Hs.332329	EST	1.29	4.37

45	TABLE 56B:		
	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	

50	Pkey	CAT Number	Accession
	412918	2764_3	BE784583 AL519009 AV755430 AV756363 AV711927 BI523434 AI521453 AA846815 AW024829 AW949702 BG218926 AA626658 AI445621 AI452815 AA946555 AA723580 AA612925 BG105326 BG532618 AW513994 AW602165 AI373448 AA907901 AW135104 BG186662 W69205 BG219754 BE774875 BG190378 AA483698 BE066066 BE066067 BE066068 AW304207 BE939361 AW795569 BG210592 AW795644 BE939358 AW102886 BE065977 BG182971 H97042 D58090 BI046351 H81248 AI750112 AW372079 C05492 D58287 D57835 AA935095 BF700910 BG215802 BG195459 AW368467 BG495535 BG533177 BI087962 BE541579 BF130753 Z69892 AA210833 BM353155 AI473754 AI147901 AI803109 AA843296 AA418925 AI478552 AI400067 AI360304 AA418828 AW301673 BE218952 AI632804 BF433234 AA394157 BF378047 BE467036 AA319724 AW290940 AI222671 AI347724 AW001711 AI028652 AA398130 AI470582 AI915936 AA908929 C75102 N36920 H50440 AI919034 AI004399 AI383862 AI123606 AA648518 AA516258 AI855321 N22865 AA848101 AI589792 AA758196 AA214630 AI373911 AW194733 AA213447 AI290291 BF437165 AA757592 BF086904 AW959032 AW992466 BF446888 AI936337 BE938849 AW149064 AI701629 N90021 BC016556 BC016365 NM_016040 AF151858 BI561037 AW966873 AW967497 BE219482 BE018650 AW770511 AW469095 AW470133 BM150181 BM193977 AI824135 AI632346 AI129838 BM147664 AI292112 BE244667 AA251084 AW503659 BM193866 BM194481 BF446862 AL597435 BF000262 AI824386 AI990100 AW087624 AA668793 AL080084 BI335866 BI820940 BG779242 BM069854 AA282620 AA256771 AW964511 AA451623 H00335 AW370399 AW954201 BM145846 BG111760 AI750065 BG655794 AA564086 BG494071 BM069606 AI675331 BE302224 AI476466 AI625980 BM144854 AI184602 AI343932 AW136586 AW029464 AI708651 AA824243 BM145917 AA662210 AA825708 AI335858 AI273704 AA662171 N48971 AA976614 AI344537 AA609603 AI873901 AI859995 AA833589 AA765811 AI150322 AI926816 BM148634 N98862 AA019347 AA897062 AA831100 N69889 BE243185 AA282179 AA831098 AA112676 AI702407 BG621752 BE006492 AA353202 BG674256 N46921 BI048774 AW300233 BF739890 AW966879 AA393405 BF115146 AA910851 AA013099 N28878 AA287713 BE348728 BG616446 AL599953 AL599952 BF381073 AW505056 AA094735 H03613 AA287714 H27168 R54718 BF792697 AV693603 AV685883 BG619956 BF541504 BF216789 AA319751 BM452652 BF335838 AA280397 BG171509 BF571997 AA490239 AW388161 BE842126 BG165309 N71903 AI955397 AI536898 BE242040 F09718 AA772421 AA450218 M78543 BE241414 AA013098 H00297 AW576477 AW150918 AW591371 AI382711 N71926 H72497 AI285602 AA745055 AI281647 BF377670 T65207 BG532880 BG721680 AA285143 H27167 AW500235 BG494497 BF668899 BE379766 AW152643 AI803450 AI564343 AI092711 AI140525 AW152156 AI620740 AI554689 AI161209 AI290242 AI339745 AI374611 AI347388 AI858296 AI140529 AI366124 AA493912 AA406235 AA493889 AI057160 AW022264 AI097277 AI144126 AI080051 AA983529 AA860507 N53469 AA843767 N81163 N70628 AA424577 AA583537 BF003004 AA626688 AA235977 AI057152 AI095366 AI095356 AA458646 AW194479 AA150439 AI375272 AW571777 AI359198 AA953793 BE514394 BE738239 AA127883 AI034344 T59504 D81608 AA908704 AW051665 AA382785 AA307208 N24639 AI370715 BE244980 AA548596 AW449675 AI91008 BF223749 N70752 N22266 AI91012 AA028001 AI419106 BF215661 BF591548 BG942356 AI474968 BE858217 BF793358 AV756758 BG483603 AI093724 BF693395 BG545345 AI744294 T59549 AA811773 BG499757 BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317

			AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299605 AJ589870 AA847598 AI470122 BF938896 AI304356 BE223045 BF435800 AI394207 AI708171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI860904 AA876023 AA430373 AA968771 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI707743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599 AL521812 BG705730 BI495545 BI495546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375 BM019558 BM023382 BG164174 N56909 BI467064 BM023464 AI207475 BM311415 BG758430 BG758807 AI934826 N90351 BG422026 BE910312 AI027778 AI081950 AI360890 BM009115 AI191829 BG759697 AI138728 AA399403 AI355589 AI336427 AA868702 AA393660 AA025127 BG027630 AA962774 AA631224 BG940967 BE791087 AA573315 W81685 AA393525 BG944103 AI339125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA889544 AA975844 AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI601114 AW135664 AI206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI160457 H64512 BG503896 427239 20459_2 AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF118773 BF718645 AW074866 BE857822			
5	450515	13638_2				
	406782	0_0				
	426143	3806_1				
10						
15	400223	2368_1				
20						
25						
30	TABLE 56C:					
	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. *Dunham, et al.* refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
35	NL_position:	Indicates nucleotide positions of predicted exons.				
	Pkey	Ref	Strand	NL_position		
	404854	7143420	Plus	14260-14537		
	405506	6466489	Plus	80014-80401,80593-81125		
40	402474	7547175	Minus	53526-53628,55755-55920,57530-57757		

45	TABLE 57A: ABOUT 304 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO NORMAL SKIN					
	Table 57A lists about 304 genes upregulated in melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.					
	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
50	UnigenelD:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	90th percentile of melanoma metastasis AIs divided by the 90th percentile of normal skin AIs				
	R2:	90th percentile of melanoma metastasis AIs divided by the 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator				
55	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	422424	AI186431	Hs.296638	prostate differentiation factor	18.94	25.00
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	17.45	18.47
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	14.05	11.15
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	13.91	15.41
60	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	13.41	9.73
	426555	NM_000372	Hs.2053	tyrosinase (ocutaneous albinism IA)	12.24	7.33
	439310	AF086120	Hs.102793	ESTs	10.12	10.80
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	9.74	10.16
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	9.43	11.69
65	414812	X72755	Hs.77367	monokine induced by gamma interferon	9.28	10.97
	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	9.07	7.96
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	9.06	19.93
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	8.66	5.87
	418310	AA814100	Hs.86693	ESTs	8.65	6.62
70	433447	U29195	Hs.3281	neuronal pentraxin II	8.27	4.68
	430280	AA361258	Hs.237868	interleukin 7 receptor	8.01	6.37
	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	7.80	6.10
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	7.78	7.60
	415752	BE314524	Hs.78776	putative transmembrane protein	7.68	5.41
75	419628	H67546	Hs.49768	ESTs	7.66	8.96
	417355	D13168	Hs.82002	endothelin receptor type B	7.56	4.59
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	7.48	5.77
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.43	4.93
80	436485	X59135	Hs.156110	immunoglobulin kappa constant	7.35	7.98
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	6.97	5.06
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	6.83	5.20
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	6.67	3.77
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	6.67	15.22

5	428398	AI249368	Hs.98558	ESTs		
	409899	AW361666	Hs.49500	KIAA0746 protein	6.57	3.60
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.48	4.93
	449644	AW560707	Hs.148324	ESTs	6.38	3.65
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.35	5.84
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.30	7.18
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	6.25	7.21
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	6.25	5.36
10	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	6.18	6.01
	449078	AK001256	Hs.22975	KIAA1576 protein	6.12	6.51
	436856	AI469355	Hs.127310	ESTs	6.05	8.55
	433658	L03678	Hs.156110	immunoglobulin kappa constant	6.00	5.54
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.92	7.18
15	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	5.89	4.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	5.86	6.07
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.74	6.03
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.72	5.92
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	3.22
20	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	5.69	5.17
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	5.68	3.35
	452973	H88409	Hs.40527	ESTs	5.67	4.56
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	5.63	5.50
	406663	U24683		immunoglobulin heavy constant mu	5.62	3.09
25	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.54	9.68
	408380	AF123050	Hs.44532	diubiquitin	5.52	6.42
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.51	4.49
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	5.43	4.50
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	5.42	3.54
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	5.41	5.29
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	5.40	4.35
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.38	4.16
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.37	5.77
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.31	5.32
35	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	5.29	4.80
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.29	3.61
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.27	5.35
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.26	6.00
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	5.26	5.04
40	400750			Target Exon	5.23	3.60
	417933	X02308	Hs.82962	thymidylate synthetase	5.18	3.62
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.14	3.33
	445784	AI253155	Hs.146085	ESTs	5.12	5.36
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	5.12	4.06
45	421508	NM_004833	Hs.105115	absent in melanoma 2	5.06	7.68
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.03	5.59
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	4.96	6.25
	400417	X72475		Target	4.95	5.13
50	420137	AA306478	Hs.95327	CD30 antigen, delta polypeptide (TIT3 co	4.90	3.93
	409264	NM_014937	Hs.52463	KIAA0966 protein	4.88	6.81
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	4.88	3.18
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.87	4.20
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	4.85	5.86
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	4.83	5.94
55	405506			Target Exon	4.82	5.19
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.74	4.09
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	4.74	3.72
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.73	3.50
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.72	3.66
60	447217	BE465754	Hs.17778	neuropilin 2	4.71	5.16
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	4.70	4.52
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.69	3.51
	419956	AL137939	Hs.40096	cadherin 19, type 2	4.68	3.69
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	5.83
65	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.68	5.29
	449722	BE280074	Hs.23960	cyclin B1	4.66	3.84
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	4.64	4.29
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.62	4.54
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.62	6.78
70	406673	M34996	Hs.198253	major histocompatibility complex, class	4.59	5.81
	431620	AA126109	Hs.264981	Z'-5'-oligoadenylate synthetase 2 (69-71	4.57	5.60
	441224	AU076964	Hs.7753	calumenin	4.56	4.44
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.56	3.75
	444371	BE540274	Hs.239	forkhead box M1	4.56	3.22
75	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	4.53	5.28
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.48	9.08
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.47	5.61
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	4.43	4.11
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.41	4.43
80	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	4.39	3.99
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholenergic	4.38	5.50
	421633	AF121850	Hs.105260	sorting nexin 10	4.37	3.25
	414829	AA321568	Hs.77436	pleckstrin	4.36	6.23
	417166	AA431323	Hs.42146	ESTs	4.35	2.91
					4.35	4.08

	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	4.34	5.35
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	4.34	3.72
	411305	BE241596	Hs.69547	myelin basic protein	4.32	4.18
5	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	4.28	2.44
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.27	4.48
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	4.25	2.69
	422282	AF019225	Hs.114309	apolipoprotein L	4.25	3.75
	433867	AK000596	Hs.3618	hippocatin-like 1	4.23	5.13
10	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	4.20	2.15
	438619	AB032773		TU12B1-TY protein	4.19	3.32
	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.14
	420208	BE276055	Hs.95972	silver (mouse homolog) like	4.16	5.08
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	4.16	2.38
	430770	AA765694	Hs.123296	ESTs	4.15	3.67
15	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	4.15	3.98
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.14	3.51
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	4.14	4.42
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.13	5.07
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.12	6.43
20	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	4.11	8.73
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	4.11	4.48
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	4.10	4.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	4.07	2.76
25	442711	AF151073	Hs.8645	hypothetical protein	4.06	3.49
	423605	AF047826	Hs.129887	cadherin 19, type 2	4.06	2.42
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.05	3.26
	421712	AK000140	Hs.107139	hypothetical protein	4.02	7.60
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	4.00	3.87
30	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21026 fis, clone C	4.00	5.87
	412719	AW016610	Hs.816	ESTs	3.99	5.46
	437179	AA393508		serologically defined colon cancer antig	3.96	4.51
	420319	AW406289	Hs.96593	hypothetical protein	3.95	5.47
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.91	4.58
35	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.84	4.42
	420286	AI796395	Hs.111377	ESTs	3.83	4.56
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	3.80	5.70
	410326	AI368909	Hs.47650	ESTs	3.76	4.86
	424779	AL046851	Hs.153053	CD37 antigen	3.70	8.72
40	452194	AI694413		Ubiquitin-like protein FAT107?? - diubiq	3.69	6.38
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.65	5.40
	412140	AA219691	Hs.73625	RAB5 interacting, kinesin-like (rabkines	3.65	4.48
	424153	AA451737	Hs.141496	MAGE-like 2	3.64	5.82
	421666	AL035250	Hs.1408	endothelin 3	3.64	5.52
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60	5.56
	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	3.59	4.35
	421563	NM_006433	Hs.105806	granulysin	3.49	7.38
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	3.49	6.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.48	4.23
50	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	3.47	5.38
	408838	AI669535	Hs.40369	ESTs	3.45	4.59
	402829			C1002500.gij6754254[ref NP_034610.1 hea	3.42	5.01
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	3.42	8.14
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	3.40	4.35
55	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.36	4.84
	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	3.35	4.45
	421958	AA357185	Hs.109918	ras homolog gene family, member H	3.35	4.28
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.34	5.18
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31	8.00
60	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.29	4.50
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.28	5.42
	404854			Target Exon	3.28	4.28
	400860			Target Exon	3.26	4.41
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.24	5.65
65	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.24	4.35
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	3.24	4.90
	440065	W03476	Hs.266331	hypothetical protein MGC4595	3.20	6.21
	440704	M69241	Hs.162	insulin-like growth factor binding prote	3.20	4.72
	411088	BE247593	Hs.145053	ESTs	3.18	4.20
70	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.68
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	3.15	4.27
	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	3.15	4.28
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.12	4.09
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04	4.04
75	425706	AW406678	Hs.122559	hypothetical protein FLJ22570	3.04	4.28
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	3.03	4.30
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	3.01	4.82
	402994			NM_002463:Homo sapiens myxovirus (influ	2.99	5.74
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.97	5.07
80	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.96	4.15
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	2.96	5.81
	406621	X57809	Hs.8997	immunoglobulin lambda locus	2.93	7.88
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.91	13.22
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.90	8.37

	448275	BE514434	Hs.20830	kinesin-like 2		
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.87	4.15
	406782	AA430373		gb:zw20111.s1 Soares ovary tumor NbHOT H	2.86	5.53
5	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.81	4.60
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.80	5.89
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.78	4.90
	428380	NM_004271	Hs.184018	MD-1, RP105-associated	2.76	4.21
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.76	5.15
10	416511	NM_006762	Hs.79356	Lysosomal-associated multispinning membr	2.76	4.30
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.75	4.13
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.74	5.05
	453953	AW408337	Hs.36972	CD7 antigen (p41)	2.73	9.20
	407241	M34516		gb:Human omega light chain protein 14.1	2.72	4.38
15	437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.68	4.07
	453779	N35187	Hs.43388	28kD interferon responsive protein	2.66	4.71
	432874	W94322	Hs.279651	melanoma inhibitory activity	2.65	4.31
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	2.64	4.15
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.62	7.36
20	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.62	4.43
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.61	5.42
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	2.60	9.69
	411358	R47479	Hs.94761	KIAA1691 protein	2.60	5.17
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	2.59	4.01
25	426470	AA528794	Hs.128644	ESTs	2.58	13.24
	425535	AB007937	Hs.158287	KIAA0468 gene product	2.54	4.52
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.52	11.31
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.50	7.80
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, clone H	2.49	4.25
30	416426	AA180256	Hs.210473	Homo sapiens cDNA: FLJ14872 fis, clone PL	2.49	4.04
	441859	AW194364	Hs.94814	ESTs, Weakly similar to FIG1 MOUSE FIG-1	2.48	4.08
	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	2.48	5.25
	431186	NM_012249	Hs.250697	ras-like protein	2.48	4.88
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.46	6.04
35	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.45	5.34
	428437	AV656017	Hs.184325	CGI-76 protein	2.43	6.57
	427634	AI399745	Hs.18449	hypothetical protein MGC10820	2.42	4.96
	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.39	8.46
	428289	M26301	Hs.2253	complement component 2	2.38	5.90
40	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.38	5.32
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.37	6.99
	433671	AW138797	Hs.132906	19A24 protein	2.34	9.69
	432403	AA550815	Hs.124840	ESTs	2.34	4.81
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.34	4.99
45	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.32	4.56
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	2.30	4.22
	401591			Target Exon	2.30	6.18
	451708	AI306536	Hs.60975	ESTs	2.29	7.01
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.26	4.50
50	424618	L29472	Hs.1802	major histocompatibility complex, class	2.24	4.90
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	2.22	5.40
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.21	4.74
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.19	4.61
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.17	7.43
55	438555	AI222089	Hs.143878	Homo sapiens mRNA for FLJ000024 protein,	2.16	5.58
	407260	L09095		gb:Homo sapiens mRNA fragment	2.13	4.26
	448243	AW369771		integrin, beta 8	2.13	4.00
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.10	4.03
	425262	D87119	Hs.155418	GS3955 protein	2.07	4.45
60	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.06	4.36
	400261			Eos Control	2.05	4.66
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TTT3	2.04	4.22
	416967	BE616731	Hs.80645	interferon regulatory factor 1	2.02	4.23
65	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	1.99	4.45
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.98	4.42
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.98	4.55
	452244	N33530	Hs.176674	ESTs	1.96	4.54
	427239	BE270447		ubiquitin carrier protein	1.95	4.23
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.94	4.93
70	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.94	5.28
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.93	4.17
	404067			Target Exon	1.93	5.06
	426890	AA393167	Hs.41294	ESTs	1.92	6.16
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	1.91	4.23
75	401914			Target Exon	1.91	4.10
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	1.87	4.76
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.87	5.17
	425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.85	6.59
	416819	U77735	Hs.80205	pim-2 oncogene	1.85	4.03
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.84	4.57
80	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	1.84	6.40
	435968	AW161481	Hs.111577	integral membrane protein 3	1.78	4.02
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.76	5.26
	434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	1.75	4.30
					1.74	4.91

5	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.71	6.00			
	430148	BE387620	Hs.234489	lactate dehydrogenase B	1.70	4.34			
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.69	4.04			
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.66	5.95			
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.64	6.26			
	426666	AW500131	Hs.171763	CD22 antigen	1.63	4.33			
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.62	7.19			
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.61	4.33			
10	421859	AA356620	Hs.108947	KIAA0050 gene product	1.59	4.30			
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.56	4.12			
	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.55	4.29			
	413969	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidyl	1.53	4.63			
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.52	4.11			
15	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.52	4.36			
	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.50	8.67			
	406885	D28423		gb:Human mRNA for pre-mRNA splicing fact	1.49	5.07			
	443759	BE390832	Hs.134729	FXD domain-containing ion transport reg	1.48	4.50			
	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.48	4.91			
20	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.43	4.26			
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.43	4.74			
	417287	AI831678	Hs.285714	KIAA1599 protein	1.41	4.01			
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.38	4.07			
	403043			Target Exon	1.36	4.89			
25	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.32	4.57			
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.30	4.00			
	422934	BE244189	Hs.122492	hypothetical protein	1.30	4.37			
	442680	BE270707	Hs.8583	similar to APOBEC1	1.26	4.48			
30	TABLE 57B:								
	Pkey:	Unique Eos probeset identifier number							
	CAT number:	Gene cluster number							
	Accession:	Genbank accession numbers							
35	Pkey	CAT Number	Accession						
	438619	35124_1	NM_016575 AB032773 AI765521 BF593742 AI497757 AI761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 AI147248 AI086795 AA151317 T95298 AW083548 AA058371 N27951 AI769860 AI784548 AW205506 AI800679 AI041733 AI459902 BE327641 AI865829 AI254736 AI302433 AI744176 AI241825 AA027842 AL524933 AL524932 BF947764 BF340737 BF948700 BG996395 NS3455 N21027 AI127616 N35901 AA682443 AA678249 AA719371 AA132582 T15981 H99958 N40717 AW959402 AI267251 BF909329 AI142035 T95379 H29420 RS9632 H17318 H17331 H29327 R40829 R43395 R59573 AI749561 R56599 H16755 AI694500 AA027907						
40	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422						
45	410600	497855_1	BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 AI335824 AW408712 BM149172						
	452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339						
	406782	0_0	AA430373 AA968771						
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372						
50	448243	13061_2	AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946						
			BE006313 AA479726 BE622314 AL134913 BE006305 BE006312 BE006298 AA044582 AW994956 AA234175 AA043906 BE006303 BF327669						
	437938	66997_1	BE006317 BF326759 BF541959						
55			U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 AI653832 W87891 AI961530 T85904 H59397 R97278						
			W01059 AI820532 T82391 AI820501 T63226 R66056 R67840 AW961101 AA337499 W37181 AA180009 AW205862 AA988777 AA856975 BF172457						
			BG751124 AI741346 AI950344 AI689062 AI872193 AW102898 AW173586 AI763273 AI890387 AW150329 AI762688 AA488892 AI356394 AI539642						
			AA642789 AI950087 BF589902 N70208 AA283144 AA488954 H60052 R97040 BF886630 AW967677 AW971573 AW967671 AI308119 AA251875						
			AA908598 AI819225 AI564269 AA908741 AA293273 AA969759 AW276905 AA044209 H83488 T92487						
	400261	23110_1	BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472						
			AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606						
60	427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881						
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289						
			AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809						
			AJ252926 AJ252160 AJ251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764						
			AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057						
			AJ053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822						
65	406827	0_0	AA971409						
	432665	27095_3	BG165971 BE143233 AL577712 AI400326 AA769318 AA427866 AW088714 AI150755 AI924874 AI186243 AA804195 AA768972 AW574769						
			AW341643 AW204520 AA235326 AI005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639						
			AW514133 AI690331 AI673409 AA627727 AI923685 AA931499 AI249783 AI810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840						
			AA810885						
70	TABLE 57C:								
	Pkey:	Unique number corresponding to an Eos probeset							
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.							
75	Strand:	Indicates DNA strand from which exons were predicted.							
	NI_position:	Indicates nucleotide positions of predicted exons.							
80	Pkey	Ref	Strand	NI_position					
	400750	8119067	Plus	198991-199168, 199316-199548					
	402474	7547175	Minus	53526-53628, 55755-55920, 57530-57757					
	405506	6466489	Plus	80014-80401, 80593-81125					
	402829	8918414	Plus	101532-101852, 102006-102263					
	404854	7143420	Plus	14260-14537					

400860	9757499	Minus	151830-152104,152649-152744
402994	2996643	Minus	4727-4969
401591	9966977	Minus	55410-55835
404067	3282162	Plus	1415-2071
401914	9369520	Plus	62537-62945,63155-63308
403043	7768753	Minus	314423-316252

TABLE 58A: ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE

Table 58A lists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease
 R2: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccon	UnigenelD	Unigene Title	R1	R2
415668	AW957684	Hs.306814	hypothetical protein FLJ21889	12.74	12.92
447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.66	5.88
412659	AW753865	Hs.74376	octadecanoyl related ER localized protei	7.23	5.76
430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	6.91	14.26
414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	6.86	7.10
436485	X59135	Hs.156110	immunoglobulin kappa constant	6.85	6.81
426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.73	11.21
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.53	4.63
416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	5.48	7.08
423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp43480650 (f	5.27	5.94
433658	L03678	Hs.156110	immunoglobulin kappa constant	4.78	3.07
452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	4.68	3.27
413916	N49813	Hs.75615	apolipoprotein C-II	4.62	4.82
407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.55	3.12
406648	AA563730	Hs.277477	major histocompatibility complex, class	4.31	4.15
409060	AJ815867	Hs.50130	necdin (mouse) homolog	4.23	3.44
401941			Target Exon	3.89	3.19
447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.88	2.43
419628	H67546	Hs.49768	ESTs	3.66	4.16
414863	AW131473	Hs.106185	rat guanine nucleotide dissociation stim	3.63	2.81
423416	NM_004920	Hs.128316	apoptosis-associated tyrosine kinase	3.47	3.06
400275			NM_006513*:Homo sapiens seryl-tRNA synth	3.47	3.43
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	3.42	1.96
442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.41	2.89
411763	AW862589		gb:QV0-CT0387-180300-167-a07 CT0387 Homo	3.37	6.31
402007			C18000503*:gij8922165[ref]NP_060080.1 h	3.34	3.74
424775	AB014540	Hs.153026	SWAP-70 protein	3.30	2.00
424036	AA770688		H2A histone family, member L	3.30	3.16
453464	AJ884911	Hs.32989	receptor (calcitonin) activity modifying	3.30	5.58
401739			NM_005622*:Homo sapiens SA (rat hyperten	3.30	3.23
440274	R24595	Hs.7122	scrapie responsive protein 1	3.27	2.47
413398	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	3.26	2.61
417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	3.26	2.58
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.14	4.04
436965	Z11894	Hs.156110	gb:H.sapiens rearranged mRNA for immunog	3.13	2.38
453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.13	2.47
404405			Target Exon	3.11	4.69
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.11	2.10
443247	BE614387	Hs.333893	c-Myc target JPO1	3.10	2.26
400417	X72475		Target	3.08	2.32
401512			NM_014080:Homo sapiens dual oxidase-like	3.07	2.87
423242	AL039402	Hs.125783	DEME-6 protein	3.06	2.78
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	3.06	2.81
451952	AL120173	Hs.301663	ESTs	3.05	2.65
427419	NM_000200	Hs.177888	histatin 3	3.05	4.24
406663	U24683		immunoglobulin heavy constant mu	3.05	4.55
442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.03	1.90
451993	AA765776	Hs.122983	ESTs	3.02	1.71
421097	AJ280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.01	3.11
430129	BE301708	Hs.233955	hypothetical protein FLJ20401	3.00	3.47
427700	AA262294	Hs.180383	dual specificity phosphatase 6	3.00	2.22
400237			NM_001087*:Homo sapiens angio-associated	2.98	3.43
414063	H26904	Hs.75736	apolipoprotein D	2.97	5.76
426153	AF057169	Hs.182771	viteliform macular dystrophy (Best dise	2.94	2.38
414781	D50917	Hs.77293	KIAA0127 gene product	2.94	2.88
445823	AJ478563	Hs.145519	FKSG87 protein	2.92	1.98
404439			ENSP00000067222*:Mitochondrial 28S ribos	2.92	2.57
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	2.90	2.47
420350	AW406896	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	2.90	3.87
424855	AW204725	Hs.25560	ESTs	2.89	2.61
436700	AJ693690	Hs.301406	hypothetical protein PP3501	2.88	3.63

	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.87	2.92
	427157	U51166	Hs.173824	thymine-DNA glycosylase	2.87	2.11
	402273			Target Exon	2.87	2.48
5	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	2.83	3.09
	430643	AW970065	Hs.287425	MEGF10 protein	2.83	3.04
	451979	F06972	Hs.27372	endothelial tyrosine kinase (ETk) (BMX)	2.82	2.12
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.81	2.88
	407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobulin	2.81	3.43
	405441			Target Exon	2.80	3.15
10	450816	BE271927	Hs.87385	ESTs	2.80	2.48
	435675	AA694099	Hs.266820	ESTs	2.78	2.70
	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial)	2.78	2.53
	441623	AA315805		desmoglein 2	2.78	2.27
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.76	3.18
15	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.76	1.92
	437740	AA810265	Hs.122915	ESTs	2.76	1.88
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.75	8.06
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.74	3.30
	428422	AI557280	Hs.184270	capping protein (actin filament) muscle	2.73	2.31
20	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.72	2.19
	401454			NM_014226*:Homo sapiens renal tumor anti	2.72	1.99
	436825	AW341123	Hs.120275	ESTs	2.72	2.89
	407705	AB023139	Hs.37892	KIAA0922 protein	2.72	2.48
25	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.72	2.63
	449151	AI632331	Hs.196038	ESTs	2.72	2.99
	433464	N92481		gb:zb12g02.s1 Soares_fetal_lung_NbHL19W	2.69	3.17
	401009			Target Exon	2.69	3.28
	427227	AF103803	Hs.283690	hypothetical protein	2.68	2.02
30	405268			ENSP00000223174*:KIAA0783 PROTEIN.	2.67	2.18
	410295	AA741357		nidogen (enactin)	2.65	2.06
	435905	AW997484	Hs.5003	KIAA0456 protein	2.65	2.12
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	2.65	2.52
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.64	2.51
	448752	AA593867	Hs.300842	KIAA1608 protein	2.63	2.20
35	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.63	1.83
	441283	AA927670	Hs.131704	ESTs	2.62	1.92
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.60	2.21
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.60	3.06
40	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	2.54	3.06
	430278	AI673074	Hs.116567	ESTs, Weakly similar to T22914 hypotheti	2.49	3.44
	425970	AK001500	Hs.165186	hypothetical protein FLJ13852	2.47	3.46
	407363	AF035032	Hs.8997	gb:Homo sapiens clone MCA1L myosin-react	2.45	3.45
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	2.44	3.52
45	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, member	2.44	6.15
	418635	L11329	Hs.1183	dual specificity phosphatase 2	2.42	3.92
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.41	3.08
	430354	AA954810	Hs.239784	human homolog of Drosophila Scribble	2.36	3.99
	405701			ENSP00000004954*:Adseverin (Scinderin).	2.33	4.25
50	433427	AI816449	Hs.171889	cholinephosphotransferase 1	2.30	3.30
	401965			CGI-148 protein	2.29	3.45
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.23	4.07
	428142	NM_001308	Hs.2246	carboxypeptidase N, polypeptide 1, 50kD	2.19	3.17
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.18	4.18
55	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	2.12	3.48
	404835			NM_018943*:Homo sapiens tubulin, alpha-I	2.09	5.72
	401127			Target Exon	2.09	4.38
	406161			Target Exon	2.08	3.22
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.08	3.03
60	406632	AB006838		gb:Homo sapiens mRNA for HRV Fab N31-VH,	2.07	3.25
	447940	D86982	Hs.20060	KIAA0229 protein	2.05	4.80
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.05	5.33
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	2.02	4.74
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.01	3.76
65	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	1.96	5.27
	436420	AA443966	Hs.31595	ESTs	1.94	3.68
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.92	3.88
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	1.90	3.63
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.90	3.04
70	406652	AW150304	Hs.277477	major histocompatibility complex, class	1.88	3.00
	435624	AF218942	Hs.24889	formin 2	1.88	3.54
	435552	NM_014038	Hs.5216	HSPC028 protein	1.86	3.29
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	1.86	3.78
	402728			C1002541*:gi4758590[ref][NP_004249.1] im	1.86	3.14
75	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	1.84	4.72
	458559	AW028820	Hs.283614	ESTs	1.78	3.06
	400278			ENSP00000243264:Dolichyl-diphosphooligos	1.76	3.55
	425751	T19239	Hs.1940	crystallin, alpha B	1.76	5.31
	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	1.74	3.00
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	1.74	3.79
80	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.73	3.57
	426321	BE046490	Hs.180677	zinc finger protein 162	1.72	3.27
	402897			NM_023068*:Homo sapiens sialoadhesin (SN	1.69	3.81
	423639	AB037826	Hs.130411	KIAA1405 protein	1.67	3.31

5	448848	AF131851	Hs.22241	hypothetical protein	1.65	4.27
	414420	AA043424	Hs.76095	immediate early response 3	1.60	3.02
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H	1.56	3.28
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.55	3.73
	400252			NM_004651*:Homo sapiens ubiquitin specif	1.55	3.26
	411825	AK000334		hypothetical protein FLJ20327	1.55	3.18
	414328	Z21666	Hs.300463	aconitase 2, mitochondrial	1.52	4.03
	400263			Eos Control	1.51	3.42
10	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.50	3.19
	436673	AF201931	Hs.5258	hypothetical protein FLJ10479	1.49	3.33
	404739			Target Exon	1.49	3.10
	438344	BE387726	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.46	3.42
	421696	AF035306	Hs.106890	Homo sapiens clone Z3771 mRNA sequence	1.44	3.15
15	425240	AA306495	Hs.1869	phosphoglucosylase 1	1.44	3.04
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.43	3.71
	434642	W25739		chromobox homolog 5 (Drosophila HP1 atph	1.42	3.07
	404406			Target Exon	1.42	3.87
20	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.41	3.80
	447697	W52125		tubulin alpha 1	1.40	4.45
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.40	3.28
	447216	R75812	Hs.169248	p7NTR-associated cell death executor, o	1.39	3.77
	401772			NM_014520:Homo sapiens MYB binding prote	1.39	3.67
25	413031	BE515051	Hs.75160	phosphofructokinase, muscle	1.38	3.31
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	1.37	3.17
	428011	BE387514	Hs.181418	KIAA0152 gene product	1.37	3.05
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.35	3.11
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	1.34	3.05
	438277	AL022326	Hs.6139	synaptogyrin 1	1.34	3.09
30	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.32	3.23
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	1.31	3.01
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase	1.28	3.58
	452378	AA025855	Hs.19597	KIAA1694 protein	1.25	3.08
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 protein,	1.24	3.45
35	402212			KIAA0430 gene product	1.21	3.03
	428773	BE256238	Hs.193163	bridging integrator 1	1.20	3.20
	430067	U79458	Hs.231840	VW domain binding protein 2	1.18	3.03
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	1.17	3.32
40	405752			Target Exon	1.00	3.40
	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropporin	1.00	3.00

TABLE 58B:		
Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	

45	Pkey	CAT Number	Accession
	400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238
50			BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064
			BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975
			AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282
			AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AI659394 AI093582 AW965846
55			AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504
			AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BC402620 AA932098 W68695 AW182900
			W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI620320 T06029 BF447193 F29285 AL548949 BI333775
			BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518
			AL571118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE619606 C17428
	411763	1103041_1	AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85737 W37369
60	424036	6226_1	AW862589 AW860959
			NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377
			AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465
			AL531028 BG437151 BE868021 AA179427
	400237	9484_1	BC014122 M95627 NM_001087 BC020244 BC008809 AI542809 AL522027 AL517616 AL539615 AL555640 AL546094 AL528959 AL555071 BI858518
65			BI600907 AU120890 BE257146 AV707965 BI911155 BG575776 BE302876 BE277469 BE389232 AL533354 BE389814 BG829179 BE384687
			BE276341 BG746912 BG425149 AL047913 BE250277 BG116066 AW410799 BG478074 BG471558 BF813165 AA016192 BG334833 BE383857
			AA218784 AL517615 BI822297 BE677910 AW169102 AW410800 AU144298 AI215124 AW275306 AU147438 BE205773 AI343920 AI972200
			AA666173 AI568496 AA742466 AI075003 BE858669 BI789274 BI964722 AI310312 AI928567 F28593 BI962793 AA053407 AA603722 AI419246
			AA705597 BF445723 AA441804 AA774757 BG152609 AI301244 BF058147 AI879460 AI470194 D80510 AA923557 W69781 AI301243 AI880348
70			AL517973 AL542808 BE300552 AA143563 AL567123 AA553412 AA547999 AW262497 AW027349 AW469464 BE300553 AI687352 BG222276
			AU146833 AA847176 AA724639 AI868270 AL530431 AI583619 AI563298 BI857771 C00178 AW130086 AI312650 AI470187 AL577668 BF816236
			BF815492 BE221500 W48859 T54102 AI828100 AW190156 AI961278 AL565165 BF966475 BM013215 BG109077 BF793617 AA381776 AA381486
	406642	0_0	BF916382 BE745391 AA330239 BG117939 BF337403 BG770295 AL567952 AL571817 BE832508 BF032720
	441623	3362_1	AJ245210 AJ245212 AJ245211 AJ245213
75			BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853
			AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AJ742232 AI023964 AI458424 AA975373
			AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894
			AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AW672414 BE328145 AW600919 BF031306 AW172758
			BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822
80			AI227660 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702
			BC496559 BF248373 BG494800
	433464	1015899_1	N92481 AW674508 AA593748 AW974058 AI475594
	410295	2817_1	BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854
			BI497111 BF940043 AI29268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448
			W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268 AI336371

5				A1989381 A1131425 A1147483 A1311537 AW338638 A1141649 AA709414 A187177 AA780884 A1333805 AA045312 A1623918 A1349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 A1869152 N93462 N71889 A1537432 R71628 AA303089 A1498550 T60941 AV706417 AW067848 A1150677 AW338118 A1336313 AA826256 A139518 AA662948 AA902723 A1970175 W68682 A089380 A1148372 H99951 AW183001 A1270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914 A1862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 A1249109 U77534 U77537 AB006838 AB006837 AB006836 AB006834 AB006835
10	406678	0_0		Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 A1555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 A1371816 AA292474 AA375747 AA308414 BM454544 B1333370 BM049921 B1461428 B1465007 B1223401 BE856245 AW821164 BF914775 BF914761 A1125835 B1222678 B1091137 BF340536 BM462798 B1224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283 B1013120 BF818845 BF763468 AA305165 A1630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 B1869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 A1520674 BF435417 AW245648 A1952404 T29534 AU153459 AU152168 AW591591 AU146918 A1393187 AA478013 AU148143 A1224471 A1640728 A1871537 AW264752 N93787 A1189357 AV756134 A1471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 A1799771 F04407 A1285530 A1914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 A1923594 BF439180 B1770936 BF032438 AU154884 AA682793 AW072992 AU158815 A1884444 AL048031 AU158922 AU152546 A1695187 AL048033 A1245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE886727 A1890705 AU159092 A1982683 A1817553 AA236729 A1687858 BG163767 A1524675 A1678155 AA127100 A1762661 AU159718 A1469720 AA483627 AW131696 R26868 A1198885 AW875614 AW938694 AW578974 B1763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 A1018819 A1476552 B1492837 A1824440 BG996262 AA932887 A1380726 R79530 AA622108 A1262575 T56782 R27437 BE784153 AW129549 A1675567 A1866759 BG987935
15	400252	2656_2		U44839 NM_004651 BC000350 B1458316 AU117940 BG759024 BG749694 BE799505 BG831537 A1816335 AA325352 AL547005 AW157038 A1859331 A1816186 AU150786 AL043549 AW162880 AU159233 A143169 T03478 BE727648 AA764725 BE206603 A1369814 A1984369 AW157545 BE221486 H99016 AU159025 A1074496 A1494516 BE245950 AA704385 AA280862 A1479595 A1369776 BE671398 T05538 AA682249 B1677303 BE645335 A1359434 H92868 D52599 D53609 D54715 T06015 BE222174 A1954706 D53218 D53787 R69889 W68896 A1497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 B1044097 AL555239 BF220278 AA081991 A1819544 AW001573 AW131600 A1858764 D52367 W22034 BG818979 BG024561 BE702779 B1458863 B1910399 BG707755 BF348284 H10055 B1086315 BE620574 H14088 BG119517 W23267 W21941 AA328817
20	411825	7891_1		AK000695 AK000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW662636 A1281247 AA946921 AA424487 BE272330 A1830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 B1906631 AW083424 AA625199 NM_017767 AK000334 BF984048 AW815634 AL573992 AA430612 AA928390 AA644447 AW340827 AA424290 A1927759 BG951502 AW881353 B1765535 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG988348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084
25	434642	15461_1		AF147443 BM471094 AA948055 AA973157 AA284289 W25739 B1021926 BF898367 W02720 BF798341 BF378312 AA427766 BG955568 BF899591 BF884215
30	447697	MH497_6		BE742621 AL528391 AA328484 W52125 AA321596 AA022458 AW971024 A1052029 A1761638 AA628498 BE619513 AA412069 A1027538 AW514954 A1884599 A1097362 A1499259 A1419408 AW469200 A1992152 A1142045 A1066572 A1275439 AA581877 A1347308 A1016726 A127541 AW002064 A1141786 AW051842 A1355329 A1198198 A1347858 A1027870 A1039163 AA576695 A1183286 A1362001 A1361994 AA594668 AA459257 AA745778 A1139567 F20651 A1201510 AA832171 BM464599 BM464574 A1972621 A1183887 AW131911 AW771584 BE619828 AA492218 AA025767 AA977354 AA385481 N45137 W73596 A1864400 A1200026 A1270953 F18139 W46301 H55825 A1039867 A457570 A1928639 A1824685 A1083898 AW024570 AA285299 AW381097 AW582409 BE954181
35				
40				
45				
50				TABLE 58C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
55				
60				
65				
70				
75				
80				

TABLE 59A: ABOUT 201 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE

Table 59A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease
 10 R2: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.58	13.77
448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	7.43	5.91
440099	AL080058	Hs.6909	DKFZP564G202 protein	7.07	4.56
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.91	3.51
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.90	6.44
418067	AI127958	Hs.83393	cystatin E/M	6.62	10.34
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.47	13.26
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.25	3.41
401780			NM_005557:Homo sapiens keratin 16 (foca	6.10	4.24
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	5.97	6.60
422511	AU078442	Hs.117938	collagen, type XVII, alpha 1	5.89	3.57
412636	NM_004415		desmoplakin (DPI, DPII)	5.82	3.51
417124	BE122762	Hs.25338	ESTs	5.16	3.16
430686	NM_001942	Hs.2633	desmoglein 1	5.03	3.57
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	4.84	4.15
422192	AA305159	Hs.113019	fts485	4.79	4.59
407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.33	2.37
429493	AL134708	Hs.145998	ESTs	4.28	4.79
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23	4.82
409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	4.23	3.69
410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	4.11	2.33
409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	4.06	3.65
424670	W61215	Hs.116651	epithelial V-like antigen 1	4.02	4.07
417366	BE185289	Hs.1076	small proline-rich protein 18 (cornitin)	3.97	4.71
418663	AK001100	Hs.41690	desmocollin 3	3.95	5.08
402075			ENSP00000251056:Plasma membrane calcium	3.93	5.85
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.90	3.19
427809	M26380	Hs.180878	lipoprotein lipase	3.87	3.21
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.85	5.75
431048	RS0253	Hs.249129	cell death-inducing DFFA-like effector a	3.80	3.10
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (3.79	3.36
421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.67	3.35
429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.65	4.14
418686	Z36830	Hs.87268	annexin A8	3.65	3.62
448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	3.64	3.18
422963	M79141	Hs.13234	ESTs	3.60	4.10
428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	3.58	3.97
401785			NM_002275:Homo sapiens keratin 15 (KRT1	3.58	5.05
454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.56	1.92
419329	AY007220	Hs.288998	S100-type calcium binding protein A14	3.54	5.62
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.53	4.70
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.52	8.33
430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.51	2.32
454229	AW957744	Hs.278469	lacrimal proline rich protein	3.50	3.12
401781			Target Exon	3.45	3.57
408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	3.45	5.07
431567	N51357	Hs.260855	Homo sapiens cDNA: FLJ21410 fs, clone C	3.44	5.03
419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.42	7.72
414798	AI286323	Hs.97411	hypothetical protein MGC12335	3.41	2.65
442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	3.41	5.03
442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.32	2.86
410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	3.28	3.18
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	3.26	3.10
453309	AI791809	Hs.32949	defensin, beta 1	3.24	3.64
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.21	3.64
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.19	4.37
413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.16	5.48
452101	T60298	Hs.10844	Homo sapiens cDNA FLJ14476 fs, clone MA	3.15	3.60
412633	AF001891	Hs.74304	periplakin	3.15	3.98
407839	AA045144	Hs.161566	ESTs	3.15	4.11
427318	AF186081	Hs.175783	zinc transporter	3.11	3.58
427899	AA829286	Hs.332053	serum amyloid A1	3.10	3.53
421948	L42583	Hs.334309	keratin 6A	3.08	2.75
452744	AI267652	Hs.246107	Homo sapiens mRNA: cDNA DKFZp434E082 (fr	3.05	2.99
410001	AB041036	Hs.57771	kalikrein 11	3.04	3.02
413435	X51405	Hs.75360	carboxypeptidase E	3.00	2.40
428500	AI815395	Hs.184641	fatty acid desaturase 2	2.98	5.22
410099	AA081630		KIAA0036 gene product	2.97	2.05
437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.93	3.45
413835	AI272727	Hs.249163	fatty acid hydroxylase	2.93	4.78

5	446068	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	2.89	2.93
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.88	3.14
	426398	AJ249368	Hs.98558	ESTs	2.88	2.05
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.86	2.12
	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.84	2.98
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	2.83	2.82
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.83	2.37
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	2.73
10	428471	X57348	Hs.184510	stratiferin	2.79	3.31
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	2.79	3.72
	433147	AF091434	Hs.43080	platelet derived growth factor C	2.77	1.70
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.76	2.18
	425787	AA363867	Hs.155029	ESTs	2.75	2.42
15	450172	NM_005864	Hs.24587	signal transduction protein (SH3 contain	2.75	2.36
	421773	W69233	Hs.112457	ESTs	2.73	5.59
	408536	AW381532	Hs.135188	ESTs	2.73	5.17
	437143	AW204056	Hs.8917	ESTs	2.72	1.84
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	2.70	1.82
20	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	2.69	4.62
	410325	AB023154	Hs.62264	KIAA0937 protein	2.69	2.32
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.69	3.74
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.67	2.36
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	2.65	1.78
25	420876	AA918425	Hs.177744	ESTs	2.64	7.26
	426106	AJ678765	Hs.21812	ESTs	2.64	2.51
	419517	AF052107	Hs.90797	Homo sapiens clone Z3620 mRNA sequence	2.64	2.66
	409509	AL036923	Hs.322710	ESTs	2.62	2.09
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	2.62	2.68
30	432503	AA551196	Hs.188952	ESTs	2.62	4.64
	409341	AJ963376	Hs.12532	chromosome 1 open reading frame 21	2.62	1.74
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.62	2.90
	456247	R09746		gb:y127d10.r1 Soares fetal liver spleen	2.61	3.43
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.60	3.84
35	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI1_HUMAN DEATH	2.58	3.49
	440659	AF134160	Hs.7327	claudin 1	2.57	3.97
	459710	AJ701596	Hs.121592	ESTs	2.57	3.59
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.56	3.35
40	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-di	2.51	3.75
	427666	AJ791495	Hs.180142	catmodulin-like skin protein (CLSP)	2.51	3.02
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	2.47	3.53
	449550	AA353125	Hs.184721	ESTs	2.43	4.22
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.40	6.22
	442000	H38671	Hs.8071	KIAA0735 gene product, synaptic vesicle	2.38	3.14
45	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	2.36	3.59
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	2.36	2.91
	412477	AA150864		microsomal glutathione S-transferase 1	2.34	4.15
	450693	AW450461	Hs.203965	ESTs	2.32	3.93
	406433			Target Exon	2.29	3.20
50	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	2.24	4.40
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.23	4.87
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	2.23	4.22
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	2.22	5.71
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.21	4.86
55	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.19	3.90
	442572	AJ001922	Hs.135121	hypothetical protein FLJ22415	2.16	2.87
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.13	3.27
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	2.09	5.28
	428899	AA744610	Hs.194431	palladin	2.08	3.76
60	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.06	3.09
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.05	2.88
	450423	AA486735	Hs.31869	slitoadhesin	2.02	3.04
	444105	AW189097		ESTs	2.01	3.05
	430410	AF099144	Hs.347933	tryptase beta 1	2.01	3.71
65	409453	AJ885516	Hs.95612	ESTs	2.01	4.34
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	2.00	5.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.99	3.59
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.92	4.16
	451541	BE279383	Hs.26557	plakophilin 3	1.89	3.90
70	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.89	3.29
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.84	3.04
	401760			Target Exon	1.84	3.32
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	1.83	4.69
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.83	2.96
75	452208	AA024792	Hs.31895	hypothetical protein MGC4093	1.82	3.70
	420074	AA253425	Hs.190074	ESTs	1.81	2.90
	429299	AJ620463	Hs.347408	hypothetical protein MGC13102	1.79	3.65
	427540	R12014	Hs.20976	ESTs	1.77	2.92
	429259	AA420450	Hs.292911	Plakophilin	1.76	3.65
80	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.75	4.06
	453556	AA425414	Hs.33287	nuclear factor I/B	1.74	3.07
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.73	3.22
	406851	AA609784		major histocompatibility complex, class	1.73	3.96
	444726	NM_006147		interferon regulatory factor 6	1.71	3.65

444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.71	4.13
446051	BE048061	Hs.37054	ephrin-A3	1.68	3.61
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.67	3.00
450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.66	3.11
432004	BE018302	Hs.2894	placental growth factor, vascular endoth	1.66	3.23
431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	1.64	3.29
415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.57	3.94
423184	NM_004428	Hs.1624	ephrin-A1	1.56	2.88
414694	NM_015362	Hs.76907	HSPC002 protein	1.56	2.92
458746	AJ380797	Hs.158992	ESTs	1.56	2.92
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.55	3.75
438367	N79688	Hs.204354	ras homolog gene family, member B	1.54	4.56
403903			CS001632:gil10645308[gb]AAG21430.1[AC00	1.53	3.99
445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.52	3.16
443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.50	4.25
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.50	3.35
415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.49	3.21
418226	AA424202	Hs.83834	cytochrome b-5	1.49	3.90
454194	BE141599		gb:QV2-HT0083-071299-018-h01 HT0083 Homo	1.48	2.98
434879	M34572	Hs.159263	collagen, type VI, alpha 2	1.46	3.26
418400	BE243026	Hs.301989	KIAA0246 protein	1.46	4.00
409178	BE393948	Hs.50915	kallikrein 5	1.45	2.94
433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.44	3.18
429002	AW248439	Hs.2340	junction plakoglobin	1.43	3.07
422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.40	4.61
452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38	3.11
417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	1.37	4.32
427929	BE613835	Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.37	2.99
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	1.36	3.17
407143	C14076	Hs.332329	EST	1.36	2.99
416950	AL049798	Hs.80552	dermatopontin	1.35	3.39
406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	1.34	3.17
442599	AF078037	Hs.324051	RelA-associated inhibitor	1.33	3.30
413659	BE155647		gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.32	2.89
454478	AW805749		superoxide dismutase 2, mitochondrial	1.30	3.50
404467			Target Exon	1.29	3.57
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.28	3.00
412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.27	3.05
422354	U20982	Hs.1516	insulin-like growth factor-binding prote	1.24	2.86
406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.24	3.29
450796	NM_001988	Hs.25482	envoplakin	1.23	3.21
431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.23	3.65
452791	AA227581	Hs.30634	hypothetical protein FLJ20509	1.22	2.90
406742	AI468091	Hs.279860	tumor protein, translationally-controlled	1.19	3.47
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	2.91
443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.10	3.50
413048	M93221	Hs.75182	mannose receptor, C type 1	1.00	2.99
453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	1.00	2.91

TABLE 598:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

55	Pkey	CAT Number	Accession
412636	1438_1		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 RS8704 AA852212 AW366566 BI090358 BF087707 BE819045 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU158919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI17612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AJ571075 BE067786 AV721320 AJ022862 N29754 C03378 NB4767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AJ538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG945393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487

5	409010	10331_1	AL557207 AL551714 BM014781 BG542863 BG771232 AA429722 AJ377511 AJ770155 AA716665 BG003427 AA810811 AA442760 AA128610 AA059411 AJ796263 AJ494075 AJ572127 AA420992 BF436083 AJ648675 AA878813 BI488614 BG700886 AA128609 AV702879 AA731146 AJ580336 AJ373224 AA919169 AJ758175 AA976350 BG701414 BF057794 AW135598 AA062583 BI549631 AJ185077 AA933879 AW024454 AA193289 AA045194 BG928396 BE856883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499 N63065 BG548812 BF027898 BG779448
10	409760	865166_1	AA302840 T93016 T92950 AU184997 AA077551
10	410099	16732_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52882 AJ439658 BE551237 AA283724 BF109530 AJ457096 AJ805992 BE457736 AA693467 AI697593 AJ887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AJ18634 T31586 AA436630 AJ366472 AA706191 AJ422304 AJ204899 AJ041169 AA211402 AW827081 AA788593 T32736 AJ767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D62685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113
15	456247	2142387_1	R10170 R09746
15	412477	8669_2	AJ220117 AJ857837 AJ218371 BM091400 AJ304364 AJ198508 AJ400738 AW571549 AW950042 AJ089943 AA437280 AU150878 BF197070 AJ267984 BF594181 BF196688 AJ433152 AJ338921 AJ620364 AJ280197 AA652531 AJ674938 AJ342447 AJ620350 AJ281295 AJ148621 NS4787 AJ338121 AJ281153 N51899 AJ087072 AA954788 AW069054 AJ346309 BG529629 AJ340135 BF083036 AJ167365 AW819657 AA935468 AJ467868 AW148701 AJ383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AJ553922 AJ560688 AW950043 AJ961682 AV706506 R01853 AA126514 N62757 AJ536893 AJ926052 AJ18720 N99964 AJ568933 AJ915737 AJ080691 AJ185358 N48996 N68575 H82824 H60037 AJ247247 T95664 BF593863 AJ749637 AW088541 AA991294 AA887452 AJ073726 AA633132 AA629674 AA629649 AA629656 AA578595 AJ168758 AA804572 AJ085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AJ382639 AA194837 AA406284 AJ250750 R37035 AJ525586 W01244
20	444105	549788_1	AW189097 AJ123917 AJ123926
20	406851	0_0	AA609784 R97304
25	444726	3503_2	BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AJ745383 AU159045 AI693500 AW293668 AW371408 BE856107 AJ338042 AW188320 AI698246 BE673290 AW297653 AA156532 AJ017342 AJ916754 AI190644 AI184302 AA857671 BE857018 AJ307420 AJ318157 AW204327 AW664668 AW274339 AA582788 AJ345741 AW301433 AJ873468 AW137388 BF718731 BF718413 AA877495 BF001575 AJ824693 AW849604 AW849405 AW849396 AW849173 BE673179 AJ611327 AA705753 BE715478 AW849414 AW849399 AJ085759 AJ140849 T67412 AJ889885 AW104647 AJ912495 AJ889874 AJ744241 BE717113 BE717108 BE715564 AJ872527 AA029457 C00338 AJ469558 BE715577 AA045413 BF843813 BE141599 AW845895 AW178095 BE140914 BE140909 AW178107 AW178094 AW845883 BF349267 AW845898 AW845811 AW845814 BF767720 AA908548
30	454194	171445_1	BE155647 BE155627
30	406799	0_0	AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
30	413659	1526081_1	
30	454478	4273_16	

TABLE 59C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
402075	8117407	Plus	121907-122035,122604-122921,124019-12416
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
406433	9256507	Plus	58094-58565
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
403903	7710671	Minus	101165-102597
404457	8077630	Minus	24951-25853

TABLE 60A: ABOUT 53 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO NORMAL TISSUES

Table 60A lists about 53 genes upregulated in benign nevi relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	average of benign nevi AIs divided by the 90th percentile of normal tissue AIs
R2:	average of benign nevi AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	8.69	5.62
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	8.37	13.47
430686	NM_001942	Hs.2633	desmoglein 1	7.26	4.78
406964	M21305		FGFES predicted novel secreted protein	6.50	3.73
426555	NM_000372	Hs.2053	tyrosinase (oculocutaneous albinism 1A)	6.40	7.35
429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	6.23	8.85
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.49	4.32
420208	BE276055	Hs.95972	silver (mouse homolog) like	5.45	9.84
431360	NM_000427	Hs.251680	loricrin	3.88	3.00
421773	W69233	Hs.112457	ESTs	3.80	9.04
438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.74	4.23
431089	BE041395		ESTs, Weakly similar to unknown protein	3.21	2.34
420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	3.08	3.20
442503	AF147078	Hs.150853	p53-responsive gene 5	2.88	5.01
405451			dihydropyrimidinase-like 3	2.88	2.85
452240	AI591147	Hs.61232	ESTs	2.86	1.90
402525			NM_002699: Homo sapiens POU domain, clas	2.78	2.72
413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.65	5.58
439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.55	3.18
422656	AI870435	Hs.1569	LIM homeobox protein 2	2.45	2.38

5	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1		
	420783	A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	2.34	3.76
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.33	2.43
	427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.28	2.00
	459702	A1204995		gb:an03c03.x1 Stratagene schizo brain S1	2.28	2.50
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.25	1.85
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.23	2.42
	453511	AL031224	Hs.33102	AP-2 beta transcription factor	2.15	2.20
10	401780			NM_005557: Homo sapiens keratin 16 (foca	2.13	2.20
	416640	BE262478	Hs.79404	neuron-specific protein	2.13	2.02
	444105	AW189097		ESTs	2.11	2.02
	428748	AW593206	Hs.98785	Ksp37 protein	2.11	1.46
	418067	AI127958	Hs.83393	cystatin E/M	2.09	1.52
15	417017	AA976064	Hs.180842	ribosomal protein L13	2.09	2.32
	401781			Target Exon	2.08	2.52
	407178	AA195651		AP-2 beta transcription factor	2.02	2.03
	452308	AI167560	Hs.61297	ESTs	1.88	2.17
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.84	2.38
20	402880			Target Exon	1.83	3.26
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppressor	1.69	2.10
	401963			NM_006311: Homo sapiens nuclear receptor	1.69	2.20
	424010	AL080188	Hs.137556	Homo sapiens mRNA: cDNA DKFZp434A132 (fr	1.66	2.02
	432800	BE391046	Hs.278962	AIM-1 protein	1.65	2.05
25	400328	X87344		transporter 2, ATP-binding cassette, sub	1.61	2.83
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.57	2.27
	435292	N20514	Hs.172965	ESTs	1.55	2.42
	408561	AJ308037	Hs.84120	hypothetical protein MGC13016	1.53	2.21
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.52	2.01
30	447763	BE619911	Hs.115803	hypothetical protein	1.47	2.71
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.40	2.10
	427289	AI097346		phosphoserine aminotransferase	1.30	2.36
	430513	AJ012008	Hs.241586	G6C protein	1.24	2.02
	411388	X72925	Hs.69752	desmocollin 1	1.20	2.18
35					1.00	2.43
	TABLE 60B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
40	Pkey	CAT Number	Accession			
	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826			
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354			
	444105	649788_1	AW189097 AI123917 AI123926			
45	407178	683007_1	AW235123 AA195651			
	454478	4273_16	AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538			
	427289	1820_2	BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 AI889380 AA868504			
			AW612968 AA630644 AI751211 N26980 AI394506 AA747849 BF154926 BF477185 AA649647 R39135 AI750216 T35363 W36278 AW079375			
			AW612240 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715			
50			AV703420 H65047 AA485582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932653 BG502266 AW868934 AV683504			
			BI018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199			
	TABLE 60C:					
	Pkey:	Unique number corresponding to an Eos probeset				
55	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA				
	Strand:	sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	Nt_position:	Indicates DNA strand from which exons were predicted.				
		Indicates nucleotide positions of predicted exons.				
60	Pkey	Ref	Strand	Nt_position		
	405451	7622517	Minus	145949-146227		
	402525	9800048	Minus	19748-20683		
	401780	7249190	Minus	28397-28617, 28920-29045, 29135-29296, 2941		
	401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 8423		
65	402880	9926561	Minus	41555-41865		
	401963	3126783	Plus	51382-51521		
	TABLE 61A: ABOUT 72 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO PRIMARY MELANOMAS					
70	Table 61A lists about 72 genes upregulated in benign nevi relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.					
	Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.					
	Pkey:	Unique Eos probeset identifier number				
	ExAccon:	Exemplar Accession number, Genbank accession number				
	UnigenetID:	Unigene number				
75	Unigene Title:	Unigene gene title				
	R1	average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs				
	R2	average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs, where the 15th percentile of normal tissue AIs was subtracted from both the				
		numerator and denominator				
80	Pkey	ExAccon	UnigenetID	Unigene Title	R1	R2
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.80	2.50
	424897	D63216	Hs.153684	frizzled-related protein	3.40	2.69
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.90	3.25
	431089	BE041395		ESTs, Weakly similar to unknown protein	2.82	1.56

	456034	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_Su	2.73	3.00
	417017	AA976064	Hs.180842	ribosomal protein L13	2.71	3.73
	402880			Target Exon	2.56	3.55
5	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.45	3.38
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	2.41	1.91
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	2.32	2.24
	424797	AA622394	Hs.153177	ribosomal protein S28	2.29	2.53
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.25	2.19
10	406964	M21305		FGENES predicted novel secreted protein	2.24	1.65
	428748	AW593206	Hs.98785	Ksp37 protein	2.09	1.43
	402525			NM_002699: Homo sapiens POU domain, clas	2.06	2.03
	415823	R81864	Hs.205103	ESTs	2.05	1.87
	412432	AA126311	Hs.9879	ESTs	2.05	2.48
15	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	2.03	2.20
	414876	AW950925	Hs.924	crystallin, mu	2.02	2.30
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	2.02	2.39
	424010	AL080188	Hs.137556	Homo sapiens mRNA: cDNA DKFZp434A132 (lr	1.95	2.72
	453317	NM_002277	Hs.41896	keratin, hair, acidic, 1	1.95	2.66
20	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.88	2.85
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.85	3.07
	400496			ENSP00000224716: GTP-binding protein SAR	1.84	2.09
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.83	4.14
	406266			Target Exon	1.75	2.38
25	414309	AK000639	Hs.75884	DKFZP586A011 protein	1.73	2.80
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.72	2.27
	451849	AI199261	Hs.27191	hypothetical protein from clone 24796	1.70	2.09
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	1.68	2.37
	401963			NM_006311: Homo sapiens nuclear receptor	1.66	2.38
30	430947	U01212	Hs.248153	olfactory marker protein	1.65	2.00
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	1.63	2.18
	406387			Target Exon	1.57	2.14
	405776			cytochrome c-1	1.55	2.23
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	1.53	3.26
35	406807	AA057605	Hs.180920	ribosomal protein S9	1.53	2.67
	420438	AW403621	Hs.1311	CD1C antigen, c polypeptide	1.52	2.09
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.52	2.66
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.48	2.57
	402412			Target Exon	1.48	2.42
40	427795	BE268268	Hs.180842	ribosomal protein L13	1.48	3.48
	452547	AA335295	Hs.74120	adipose specific 2	1.47	3.89
	414323	NM_014759	Hs.334688	KIAA0273 gene product	1.46	3.14
	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	1.45	2.09
	457090	AL080243	Hs.180920	ribosomal protein S9	1.40	2.86
45	445431	AF137386	Hs.12701	plasmolipin	1.39	2.00
	445636	AW105401		ribosomal protein L29	1.38	2.08
	414582	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.37	3.32
	406845	AI567284	Hs.119598	ribosomal protein L3	1.37	2.04
	406808	AI690307	Hs.180920	ribosomal protein S9	1.36	3.32
50	403986			Target Exon	1.34	2.09
	402218			NM_022165: Homo sapiens Lin-7b protein (1.31	2.16
	400649			Target Exon	1.29	2.07
	432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.28	2.40
	403211			NM_005400: Homo sapiens protein kinase C	1.26	2.13
55	452678	AI243131	Hs.164661	ESTs, Weakly similar to TGLX_HUMAN PROTE	1.26	2.14
	406889	D50310	Hs.79933	cyclin I	1.26	2.37
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.25	2.39
	404406			Target Exon	1.24	2.09
	432894	AW167668	Hs.279772	brain specific protein	1.23	2.28
60	406757	T65957	Hs.77039	ATP synthase, H transporting, mitochondr	1.21	2.01
	425883	AL137708	Hs.161031	Homo sapiens mRNA: cDNA DKFZp434K0322 (l	1.20	2.07
	409726	AI479341	Hs.724	thyroid hormone receptor, alpha (avian e	1.17	2.62
	436398	H87136	Hs.5174	ribosomal protein S17	1.17	2.42
	444674	BE562200	Hs.244	amino-terminal enhancer of split	1.16	2.02
65	402450			Target Exon	1.16	2.08
	406758	AA552326	Hs.77039	ATP synthase, H transporting, mitochondr	1.16	2.03
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.13	2.23
	407032	U73799		gb:Human dynactin mRNA, partial cds.	1.10	2.01
	402921			ENSP00000244047: Cadherin-like protein V	1.00	2.00
70	TABLE 61B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
75	Pkey	CAT Number	Accession			
	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826			
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945			
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354			
	445636	8561_5	BF339388 AI345516 BC391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310			
80			AA090672			

Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NT_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	NT_position
402880	9926561	Minus	41555-41865
402525	9800048	Minus	19748-20683
400496	9743564	Plus	41515-41695
406266	7528342	Minus	2365-2518
401963	3126783	Plus	51382-51521
406387	9256180	Plus	116229-116371,117512-117651
405776	7159748	Minus	105911-107251
402412	7408036	Plus	75075-75679
403986	8576059	Plus	90692-91238
402218	7689783	Plus	127677-127886
400649	8117705	Plus	93097-93792
403211	7630841	Minus	159211-159369
404406	7329316	Minus	47543-47928
402450	9796674	Plus	137536-137682,137920-138045
402921	7981303	Minus	52242-52384,55599-55858,57124-57309,5963

TABLE 62A: ABOUT 121 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN

Table 62A lists about 121 genes upregulated in benign nevi relative to normal skin. These genes were selected from 59680 probesets on the Ecos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Ecos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of benign nevi AIs divided by the 90th percentile of normal skin AIs
 R2: average of benign nevi AIs divided by the 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	8.69	7.66
438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	6.71	8.11
406964	M21305		FGENES predicted novel secreted protein	6.50	3.35
426555	NM_000372	Hs.2053	tyrosinase (oculocutaneous albinism (A)	6.40	4.32
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.16	4.12
415752	BE314524	Hs.78776	putative transmembrane protein	4.77	3.59
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63	4.99
451668	Z43948	Hs.326444	cartilage acidic protein 1	4.62	6.04
449644	AW960707	Hs.148324	ESTs	3.97	3.41
435056	AW023337	Hs.5422	glycoprotein M6B	3.42	2.29
431089	BE041395		ESTs, Weakly similar to unknown protein	3.21	2.57
452973	H88409	Hs.40527	ESTs	3.16	3.12
408393	AW015318	Hs.23165	ESTs	3.12	2.00
417355	D13168	Hs.82002	endothelin receptor type B	3.11	2.45
415314	N88802	Hs.5422	glycoprotein M6B	2.86	2.39
417632	R20855	Hs.5422	glycoprotein M6B	2.78	2.16
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.75	3.71
456034	AW450979		gb:U1-H-BI3-ala-a-12-O-U1.s1 NCI_CGAP_Su	2.73	3.00
404356			Target Exon	2.63	2.69
414876	AW950925	Hs.924	crystallin, mu	2.57	3.15
420208	BE276055	Hs.95972	silver (mouse homolog) like	2.46	2.89
422656	AJ870435	Hs.1569	LIM homeobox protein 2	2.45	2.20
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.43	2.11
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.96
401116			Target Exon	2.29	2.24
410326	AI368909	Hs.47650	ESTs	2.27	2.77
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.25	3.49
435730	AB020635	Hs.4984	KIAA0828 protein	2.24	2.24
404977			Insulin-like growth factor 2 (somatomedi	2.24	1.99
414221	AW450979		gb:U1-H-BI3-ala-a-12-O-U1.s1 NCI_CGAP_Su	2.16	2.36
437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (I	2.13	2.09
402181			Target Exon	2.12	2.74
447907	AI439110	Hs.170796	ESTs	2.05	2.02
434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.04	3.14
459246	NM_006834	Hs.32217	RAB32, member RAS oncogene family	2.02	1.83
405451			dihydropyrimidinase-like 3	2.01	2.00
446727	AB011095	Hs.16032	KIAA0523 protein	2.01	2.36
417017	AA976064	Hs.180842	ribosomal protein L13	2.00	2.37
413171	AA318325	Hs.75219	tyrosinase-related protein 1	1.94	2.77
408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.94	2.76
455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.92	2.91
419200	AW966405		EST	1.85	2.91
419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.84	2.27
402217			C19001662:gil5753872reflNP_034345.1 i	1.83	2.33
406040			Target Exon	1.81	2.04
435292	N20514	Hs.172965	ESTs	1.81	3.41
430947	U01212	Hs.248153	olfactory marker protein	1.79	2.00
434574	AI424458	Hs.33470	ESTs	1.78	4.00

5	403532			NM_024638:Homo sapiens hypothetical prot	1.75	2.06
	402829			C1002500.gij6754254[ref]NP_034610.1] hea	1.72	2.20
	403828			C4000447*.gij7705570[ref]NP_038851.1] KJ	1.72	2.04
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	1.68	2.40
	407826	AA128423	Hs.40300	calpain 3, (p94)	1.67	2.13
10	441253	AI632744	Hs.129501	ESTs	1.67	2.13
	405776			cytochrome c-1	1.66	2.36
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fs, clone H	1.66	2.08
	445745	AB007924	Hs.13245	KIAA0455 gene product	1.66	2.34
	401963			NM_006311:Homo sapiens nuclear receptor	1.66	2.97
15	402994			NM_002463*:Homo sapiens myxovirus (influ	1.66	2.56
	406016			Target Exon	1.65	2.23
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	1.65	2.30
	402911			NM_021158*:Homo sapiens protein kinase d	1.63	2.46
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.61	2.28
20	440437	AI923201	Hs.192352	ESTs	1.59	2.07
	403960			ENSP00000174317*:KIAA0303 (FRAGMENT).	1.59	2.41
	406266			Target Exon	1.56	2.16
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	1.55	3.14
	403803			C4001432*.gij6009515[dbj]BAAB4941.1] (AB	1.54	2.04
25	407038	X00237		gb:Human F variable segment 5' to antiH	1.53	2.09
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	1.53	2.46
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.52	2.76
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.52	3.04
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	1.51	3.42
30	404790			C12001707*.gij7305215[ref]NP_038599.1] k	1.50	2.16
	434596	T59538		gb:ytb65g12.s1 Stratagene ovary (937217)	1.48	2.02
	425069	AA587465	Hs.298184	potassium voltage-gated channel, shaker-	1.47	4.05
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	1.46	2.48
	427289	AI097346		phosphoserine aminotransferase	1.44	4.46
35	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.43	2.32
	432800	BE391046	Hs.278962	AJM-1 protein	1.43	2.08
	447763	BE619911	Hs.115803	hypothetical protein	1.42	2.21
	443219	AI354669	Hs.187461	ESTs, Weakly similar to C29149 proline-r	1.41	2.31
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	1.41	2.35
40	459641	AW064121	Hs.279175	ESTs	1.41	2.01
	405318			C7002129*.gij3638957[gb]AAC36301.1] (ACO	1.40	2.31
	402343			Target Exon	1.40	2.35
	447108	AW449602	Hs.241493	natural killer-tumor recognition sequenc	1.40	2.11
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	1.39	2.06
45	400263			Eos Control	1.39	2.60
	403986			Target Exon	1.38	2.09
	437912	BE278594	Hs.5912	F-box only protein 7	1.36	2.27
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.36	2.77
	401914			Target Exon	1.33	2.43
50	450395	BE048545	Hs.161757	ESTs	1.29	2.01
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.29	2.94
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.28	2.84
	427560	AA405394	Hs.161851	ESTs	1.27	2.14
	402450			Target Exon	1.27	2.89
55	405885	D28423		gb:Human mRNA for pre-mRNA splicing fact	1.26	3.19
	404067			Target Exon	1.26	2.45
	406368			NM_022355:Homo sapiens putative dipeptid	1.25	2.06
	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.23	2.07
	414580	BE386918		gb:G01275386F1 NIH_MGC_20 Homo sapiens c	1.22	2.21
60	414060	BE246327	Hs.123164	gb:TCBAP1E1967 Pediatric pre-B cell acut	1.22	2.01
	400867			cofilin 1 (non-muscle)	1.21	2.19
	437026	AW976573		ESTs	1.21	2.31
	402605			Target Exon	1.20	2.09
	431008	H84058	Hs.25734	ESTs, Weakly similar to BING1 [H.sapiens	1.17	2.22
65	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.17	2.25
	416630	H69392	Hs.174051	small nuclear ribonucleoprotein 70kD pol	1.16	2.34
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.14	2.58
	419045	T85693		gb:yd60d06.r1 Soares fetal liver spleen	1.13	2.08
	443923	X60702	Hs.210	leukocyte tyrosine kinase	1.11	2.24
70	457585	AB040799	Hs.278283	G protein-coupled receptor 27	1.08	2.04
	452958	AA883929	Hs.40527	ESTs	1.03	2.28
	403969			ENSP00000034663:Zinc finger protein 131	1.00	2.04
	436878	BE465204	Hs.47448	ESTs	1.00	2.12
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	1.00	2.18
75	404632			NM_022490:Homo sapiens hypothetical prot	1.00	2.19
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	1.00	2.35
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	1.00	2.41

TABLE 62B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	456034	685585_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BID44354

459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
419200	9531_1	BF036043 AW190446 BG194731 AW662036 AJ445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345
5		AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608
		AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131
		AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028
10		BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D56274 BF085805 D31589 AW956405 AW994425 D81879
		BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856
		BE702099 BF035869 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836
		AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765964 T70171 BE938775 BE940057 D53502 AW373300 AL118798
15	430540 713_2	BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861585 AA251595
		AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AI164411 BI495332 BE858113
		AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
		BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
		BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
20		AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
		AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567
		BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
		BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420
		BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
25		AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953
		BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
		W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069
		F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114
		AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103
		AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809
		BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
30	434596 14701_1 427289 1820_2	AF147374 T59538 T59589 T59598 T59542
		BC007350 BG766159 BG769338 BG7644385 BG770572 AW370610 AW370581 AA978353 AW372973 AW404225 AI889380 AA868504
		AW612968 AA630644 AI751211 N26980 AI394506 AA747849 BF154926 BF477185 AA649647 R39135 AI750216 T35363 W36278 AW079375
		AW612240 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715
		AV703420 H65047 AA485582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AW683504
35	400263 18977_1	BI018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199
		Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935
		BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486
		BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719
		BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758
40		BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385
		BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479
		BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503
		BG674499 BG774174 BI015084
		BG333973 BE385437 BE408833 BE387650
45	414580 623093_1 437026 1240260_1 419045 348516_2	AW976573 AA742335 AA830000
		BF981324 BG723297 T85693 T81681 T81909

TABLE 62C:

Pkey:

Ref:

50

Strand:

Nt_position:

Unique number corresponding to an Eos probe set

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nt_position
	404356	7630858	Minus	126433-126623
	401116	9966559	Plus	123579-124447
	404977	3738341	Minus	43081-43229
	402181	8575912	Plus	449746-450040
	405451	7622517	Minus	145949-146227
60	402217	9795981	Minus	21521-21757
	406040	6758938	Minus	23063-23599
	403532	8076842	Minus	81750-81901
	402829	8918414	Plus	101532-101852,102006-102263
	403828	9838214	Plus	31755-32148
65	405776	7159748	Minus	105911-107251
	401963	3126783	Plus	51382-51521
	402994	2996643	Minus	4727-4969
	406016	8272661	Plus	41341-41940
	402911	7263904	Plus	142689-142979
70	403960	8224409	Minus	90999-94843
	406266	7528342	Minus	2365-2518
	403803	8112965	Plus	55513-55778
	404790	7230958	Plus	38611-38761
	405318	3638954	Plus	79689-79967
75	402343	8099256	Plus	4677-6084
	403986	8576059	Plus	90692-91238
	401914	9369520	Plus	62537-62945,63155-63308
	402450	9796674	Plus	137536-137682,137920-138045
	404067	3282162	Plus	1415-2071
80	406368	9256126	Minus	72447-72588,72673-72802,73119-73245
	400867	9838275	Plus	34136-34846
	402605	9909420	Minus	47680-47973
	403969	8569909	Plus	31237-31375,32405-32506

404632 9796668 Plus 45096-45229

TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES

Table 63A lists about 181 genes upregulated in benign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Altymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAcct: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of benign nevi AIs divided by the 90th percentile of melanoma metastasis AIs
 R2: average of benign nevi AIs divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAcct	UnigenelD	Unigene Title	R1	R2
401781			Target Exon	19.33	19.21
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	13.54	14.18
401780			NM_005557: Homo sapiens keratin 16 (foca	12.97	13.63
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	12.61	31.19
412636	NM_004415		desmoplakin (DPI, DPL)	11.73	6.91
420783	AF659838	Hs.99923	lectin, galactoside-binding, soluble, 7	10.18	14.08
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.48	6.79
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	8.28	9.62
430686	NM_001942	Hs.2633	desmoglein 1	7.26	5.64
429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	7.12	10.88
442577	AA292998	Hs.163900	ESTs	7.01	6.59
406964	M21305		FGENES predicted novel secreted protein	6.50	8.82
401785			NM_002275: Homo sapiens keratin 15 (KRT1	6.40	9.77
410001	AB041036	Hs.57771	kallikrein 11	6.18	6.16
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	5.73	16.57
418686	Z36830	Hs.87268	annexin A8	5.32	5.27
439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.89	9.81
452240	AI591147	Hs.61232	ESTs	4.89	6.67
402525			NM_002699: Homo sapiens POU domain, clas	4.74	4.80
431360	NM_000427	Hs.251680	loricrin	4.66	3.98
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63	5.69
418067	AI127958	Hs.83393	cystatin E/M	4.56	6.78
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	4.56	5.73
418663	AK001100	Hs.41690	desmocollin 3	4.44	5.23
419329	AY007220	Hs.288998	S100-type calcium binding protein A14	4.24	6.49
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	3.95	3.37
421773	W69233	Hs.112457	ESTs	3.88	9.60
408536	AW381532	Hs.135188	ESTs	3.82	10.18
418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.78	6.33
408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	3.77	4.92
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.70	5.30
424049	AB014524	Hs.138380	KIAA0624 protein	3.68	4.41
421948	L42583	Hs.334309	keratin 6A	3.62	3.13
427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.59	4.40
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.48	6.09
436895	AF037335	Hs.5338	carbonic anhydrase XII	3.42	3.28
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	3.28	3.89
401760			Target Exon	3.21	7.11
431089	BE041395		ESTs, Weakly similar to unknown protein	3.21	5.78
434293	NM_004445	Hs.3796	EphB6	3.14	3.11
412432	AA126311	Hs.9879	ESTs	3.14	4.85
442503	AF147078	Hs.150853	p53-responsive gene 5	3.11	5.92
414987	AA524394	Hs.294022	hypothetical protein FLJ14950	3.07	4.89
420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.99	3.09
433339	AF019226	Hs.8036	glioblastoma overexpressed	2.96	2.75
414876	AW950925	Hs.924	crystallin, mu	2.94	3.82
437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.87	3.42
424897	D63216	Hs.153684	frizzled-related protein	2.87	1.96
456034	AW450979		gb:U1-H-B13-ata-a-12-O-U1.s1 NCL_CGAP_Su	2.73	2.54
424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.72	2.92
427318	AF186081	Hs.175783	zinc transporter	2.71	2.21
452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	2.67	6.47
452308	AI167560	Hs.61297	ESTs	2.67	4.61
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.64	2.68
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.57	3.91
451541	BE279383	Hs.26557	plakophilin 3	2.49	5.47
453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.45	4.17
412633	AF001691	Hs.74304	periplakin	2.42	4.90
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.41	2.68
424797	AA622394	Hs.153177	ribosomal protein S28	2.39	2.67
424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	2.39	4.07
453241	H58995	Hs.37648	ESTs	2.39	2.34
426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	2.36	1.88
423467	AK000214	Hs.129014	hypothetical protein FLJ20207	2.32	2.24
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.99
430168	AW968343	Hs.145582	DKFZP434I1735 protein	2.30	2.60
457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	2.28	1.91

5	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.27	8.50
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.27	2.21
	429365	AA451798	Hs.95249	ESTs	2.25	2.54
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.25	2.35
	420511	AF052692	Hs.98485	gap junction protein, beta 3, 31kD (conn	2.23	2.17
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.23	3.23
	417017	AA976064	Hs.180842	ribosomal protein L13	2.21	2.74
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.21	1.68
10	430152	AB001325	Hs.234642	aquaporin 3	2.20	3.32
	444726	NM_006147		interferon regulatory factor 6	2.15	5.20
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.15	2.82
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	2.14	2.96
	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (2.14	2.25
15	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.12	2.99
	444105	AW189097		ESTs	2.11	2.98
	428748	AW593206	Hs.98785	Ksp37 protein	2.09	1.51
	456826	AB171742	Hs.302428	wingless-type MMTV integration site fami	2.09	3.25
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	2.09	4.97
20	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.06	5.68
	430285	AB17602	Hs.106440	ESTs	2.06	2.04
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.05	5.92
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.04	2.19
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	2.04	3.08
25	433428	T29975	Hs.33104	Huntingtin interacting protein C	2.04	1.63
	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	2.03	3.92
	446727	AB011095	Hs.16032	KIAA0523 protein	2.01	2.60
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.01	2.05
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.99	4.04
30	439625	AF086453	Hs.58611	ESTs	1.99	2.31
	402880			Target Exon	1.99	2.75
	428471	X57348	Hs.184510	stratifin	1.98	2.10
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.97	3.16
	452547	AA335295	Hs.74120	adipose specific 2	1.95	3.89
35	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	1.94	2.06
	429259	AA420450	Hs.292911	Plakophilin	1.93	2.96
	406387			Target Exon	1.92	2.97
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.91	3.46
	437202	AA326110		nuclear transcription factor Y, gamma	1.89	2.00
40	426150	NM_003658	Hs.167218	BarH-like homeobox 2	1.86	2.60
	434574	AJ424458	Hs.33470	ESTs	1.85	4.61
	446051	BE048061	Hs.37054	ephrin-A3	1.85	3.48
	424471	AA341329	Hs.311524	ESTs	1.84	2.62
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.83	4.69
45	451721	NM_005946	Hs.26915	spectrin, beta, non-erythrocytic 2	1.82	2.00
	451849	AI199261	Hs.27191	hypothetical protein from clone 24796	1.81	2.31
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.79	3.07
	423523	AW299828	Hs.193580	ESTs	1.77	3.37
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.76	2.46
50	403828			C40004477:gi7705570ref NP_038851.1 KJ	1.73	2.06
	412445	AI768015		ESTs	1.68	3.16
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	1.67	2.22
	411274	NM_002776	Hs.69423	kalikrein 10	1.66	2.26
	401963			NM_006311:Homo sapiens nuclear receptor	1.66	2.52
55	435016	AI284219	Hs.130749	ESTs, Weakly similar to I38022 hypothei	1.65	2.20
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	1.64	3.21
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	1.63	2.94
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.62	2.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62	3.92
60	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.60	3.43
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.60	2.18
	416305	AU076628	Hs.79187	coxsaackie virus and adenovirus receptor	1.60	2.47
	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.59	2.99
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.59	2.82
65	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.57	2.64
	432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.56	2.74
	429002	AW248439	Hs.2340	junction plakoglobin	1.56	2.97
	430171	AF086289	Hs.234766	skin-specific protein	1.54	2.18
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	1.51	2.19
70	414323	NM_014759	Hs.334688	KIAA0273 gene product	1.51	3.73
	423184	NM_004428	Hs.1624	ephrin-A1	1.50	2.18
	433101	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFp566L203 (fr	1.50	2.00
	424362	AL137646		Homo sapiens mRNA: cDNA DKFp586F0824 (f	1.48	2.04
75	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.46	2.83
	445431	AF137386	Hs.12701	plasmofipin	1.46	2.00
	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	1.44	2.04
	442599	AF078037	Hs.324051	RelA-associated inhibitor	1.42	3.50
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.42	2.53
	444672	Z95636	Hs.11669	taminin, alpha 5	1.40	2.36
80	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.40	2.29
	418462	BE001596	Hs.85266	integrin, beta 4	1.39	2.86
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	1.38	2.28
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	1.38	2.24
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.38	2.14

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.36	2.34
	432894	AW167668	Hs.279772	brain specific protein	1.36	5.09
	439733	AL365412	Hs.107203	hypothetical protein from EUROMAGE 1759	1.36	2.00
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.35	2.85
	423515	AA327017	Hs.176594	ESTs	1.35	2.45
	436663	AW410458	Hs.5258	chromosome 11 open reading frame2	1.35	2.07
	404246			Target Exon	1.34	2.96
	411939	AI365585	Hs.146246	ESTs	1.33	2.31
	409178	BE393948	Hs.50915	kallikrein 5	1.33	2.03
10	427795	BE268268	Hs.180842	ribosomal protein L13	1.33	2.29
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.32	2.78
	447330	BE279949	Hs.18141	ladinin 1	1.32	3.37
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer	1.31	2.71
	403986			Target Exon	1.31	2.09
15	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	1.30	2.28
	450796	NM_001988	Hs.25482	envoplakin	1.30	3.45
	415550	L13720	Hs.78501	growth arrest-specific 6	1.29	2.76
	415512	Y16270	Hs.78482	paralemmin	1.26	2.49
	430513	AJ012008	Hs.241586	G6C protein	1.26	3.07
20	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor	1.23	2.04
	420048	AW206824	Hs.25766	ESTs	1.23	2.01
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (I	1.23	2.22
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.23	2.42
25	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.23	2.20
	402218			NM_022165*:Homo sapiens Lin-7b protein (1.23	2.01
	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	1.18	2.24
	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	1.16	2.16
	426068	AF029778	Hs.166154	jagged 2	1.15	2.07
30	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.14	2.33
	411388	X72925	Hs.69752	desmocollin 1	1.00	2.61
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.00	2.63

TABLE 63B:

Pkey:	Unique Eos probe identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

35	Pkey	CAT Number	Accession
	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680518 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA853716 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW868475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 RS8704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW507238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI17612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI345078 W95070 AA149191 AA026864 AI830049 AW780435 AW078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE896209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 AW188320 AI698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327 AW664668 AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF18731 BF18413 AA877495 BF001575 AI824693 AW849604 AW849405 AW849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 AI140849 T67412 AI889885 AW104647 AI912495 AI889874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813 AW189097 AI123917 AI123926 BE091833 BE091874 BE091871 AL110199 AI598719 AA152097 W84430 AI304351 BE670780 BF003019 AI271659 AW338914 AI127763 AI191873 AI922951 AI568416 AI077680 AA358674 AI138802 AI589070 AI088745 AW418696 BF475830 AI144150 AA724257 AA622339 AI375884 AI880453 AW874251 BF941345 AI619746 AI225114 AI801268 AI554474 BM023333 AI093946 AI699306 AI803839 AA496797 AI361531 AI123010 AW169313 BM023082 AI081626 AA513457 AA227820 AW518810 AA361091 AI499891 AI686346 BF436872 AI681496 AL572961 AI334148 AW138291 AI419063 AA278226 AA370719 AA152023 AI401749 AA127464 AL573761 BG913208 T07824 AI346417 H44939 AV721378 N48299 W72005 AA302424 AI611143 AW514684 BE041749

5	412446	63467_1	AW370992 R42918 H10757 R10703 C01061 R27637 A1827230 AW151953 AA651675 AA228006 AA233950 BE858910 R30801 W32704 H39784 BE090279 BG697660 AW877265 B1818938 BF528291 AW953624 R57461 BF969694 BC021735 A1669212 AL120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 AF284421 AL137646 BG542551 A1278088 A1423919 A1274095 BE638965 BE839174 BE839102 BF924520 B1913343 AW238809 AL134380 AW793289 AL534638 T97116 AW855182 C02210 A1783480 AW024874 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
	424362	2318_7	
10	454478	4273_16	

TABLE 63C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
402525	9800048	Minus	19748-20683
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402880	9926561	Minus	41555-41865
406387	9256180	Plus	116229-116371,117512-117651
403828	9838214	Plus	31755-32148
401963	3126783	Plus	51382-51521
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,8314
403986	8576059	Plus	90692-91238
402218	7689783	Plus	127677-127886

TABLE 64A: ABOUT 929 GENES DOWNREGULATED IN PRIMARY MELANOMAS AND/OR MELANOMA METASTASES RELATIVE TO NORMAL SKIN

Table 64A lists about 929 genes downregulated in primary melanomas and/or melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of normal skin AIs divided by the 90th percentile of primary melanoma and melanoma metastasis AIs
 R2: 90th percentile of normal skin AIs divided by the 90th percentile of primary melanoma and melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
420813	X51501	Hs.99949	prolactin-induced protein	27.72	20.12
408591	AF015224	Hs.46452	mammaglobin 1	26.40	24.26
431360	NM_000427	Hs.251680	loricrin	26.16	20.45
401781			Target Exon	19.68	19.56
412636	NM_004415		desmoplakin (DPI, DP11)	18.12	10.36
429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	16.61	18.06
418067	A1127958	Hs.83393	cystatin E/M	16.00	25.32
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	15.64	11.81
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	15.03	37.51
401780			NM_005557: Homo sapiens keratin 16 (foca)	14.20	14.86
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)	13.95	28.08
420783	A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	13.52	18.85
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	13.14	13.81
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	12.78	6.35
421733	AL119571	Hs.1420	fibroblast growth factor receptor 3 (ach	12.78	15.22
428824	W23624	Hs.173059	ESTs	12.67	13.24
453309	A1791809	Hs.32949	defensin, beta 1	12.02	12.42
446227	A1281459	Hs.270114	ESTs	11.79	12.32
421948	L42583	Hs.334309	keratin 6A	11.58	9.02
432877	AW974111	Hs.292477	ESTs	11.18	11.30
412047	AA934589	Hs.49696	ESTs	11.04	11.07
407230	AA157857	Hs.182265	keratin 19	10.79	11.40
421296	NM_002666	Hs.103253	perilipin	10.73	7.94
410001	AB041036	Hs.57771	kallikrein 11	10.72	10.70
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	10.33	7.16
447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	10.09	9.67
401203			Target Exon	9.95	7.37
452308	A1167560	Hs.61297	ESTs	9.71	20.05
425580	L11144	Hs.1907	galanin	9.66	8.41
433124	U51712	Hs.13775	hypothetical protein SMAP31	9.50	4.96
420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	6.34
443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58
427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	9.19	11.73
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (8.85	17.76
408536	AW381532	Hs.135188	ESTs	8.82	26.43
430686	NM_001942	Hs.2633	desmoglein 1	8.73	6.58
436895	AF037335	Hs.5338	carbonic anhydrase XII	8.69	6.81
418663	AK001100	Hs.41690	desmocollin 3	8.61	9.15

	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	8.51	13.13
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.44	9.61
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (8.39	5.13
	442577	AA292998	Hs.163900	ESTs	8.34	7.92
5	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	8.16	10.08
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	8.04	7.55
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	7.68	7.81
	452240	AI591147	Hs.61232	ESTs	7.63	9.39
	442757	AI739528	Hs.28345	ESTs	7.62	7.31
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	6.17
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	7.12
	407328	AA508857	Hs.8364	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	7.16	8.39
	417240	NS7568	Hs.48028	EST	7.13	15.05
15	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fs, clone MA	7.13	7.28
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.85
	439394	AA149250	Hs.56105	ESTs	7.00	4.53
	422963	M79141	Hs.13234	ESTs	6.99	5.30
20	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.97	20.68
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.96	6.68
	427890	AA435761		ESTs	6.94	6.68
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fs, clone PL	6.84	8.44
25	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	6.83	6.37
	451029	AA852097	Hs.25829	ras-related protein	6.81	8.96
	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	6.80	7.68
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	6.77	14.06
	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.11
30	451253	H48299	Hs.26126	claudin 10	6.71	7.17
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.67	11.68
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	7.90
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	6.60	7.29
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	6.58	6.78
35	421773	W69233	Hs.112457	ESTs	6.55	17.59
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	6.55	6.79
	411388	X72925	Hs.69752	desmocollin 1	6.55	8.97
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	6.51	9.94
	406867	AA157857	Hs.182265	keratin 19	6.50	6.23
40	429504	X99133	Hs.204238	lipocatin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	426106	AI678765	Hs.21812	ESTs	6.41	7.69
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	6.39	7.71
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.36	9.23
45	437176	AW176909	Hs.42346	calcineurin-binding protein calcarsin-1	6.30	5.45
	440383	AA884208	Hs.30484	ESTs	6.26	6.25
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	6.22	10.13
	418686	Z36830	Hs.87268	annexin A8	6.19	6.14
	440116	AI798851		hemoglobin, gamma G	6.18	4.28
50	424049	AB014524	Hs.138380	KIAA0624 protein	6.18	6.91
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	6.17	7.42
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fs, clone C	6.16	6.85
	414449	AA557660	Hs.76152	decorin	6.15	3.93
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
55	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	6.12	5.33
	431319	AA873350	Hs.302232	ESTs	6.11	6.84
	444105	AW189097		ESTs	5.97	6.20
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	5.15
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.71	5.83
60	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	5.69	4.49
	428566	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	410541	AA065003	Hs.64179	syntenin-2 protein	5.62	5.84
	431926	AW972724		gb:EST384816 IMAGE resequences, MAGL Homo	5.61	5.75
	430332	RS1790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
65	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	5.53	9.25
	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fs, clone TH	5.48	5.38
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.46	3.19
	414407	AA147026	Hs.76704	ESTs	5.43	5.29
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
70	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN 2	5.40	3.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	5.39	9.12
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	5.39	6.06
	436090	AI640635	Hs.332879	EST	5.37	5.33
	411274	NM_002776	Hs.69423	kallikrein 10	5.37	5.97
75	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	5.36	9.35
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34	4.08
	430171	AF086289	Hs.234766	skin-specific protein	5.32	10.40
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.31	6.01
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.31	3.81
80	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	5.92
	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	5.25	16.94
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	5.20	5.01
	431416	AA532718	Hs.178604	ESTs	5.18	5.38

	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,		
	446082	AI274139	Hs.156452	ESTs	5.17	5.72
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	5.16	5.14
5	434625	W01370	Hs.45824	ESTs	5.14	4.97
	426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.12	6.18
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	5.11	3.79
	438962	BE046594		gb:hn41c11.1 NCI_CGAP_RDF2 Homo sapiens	5.08	13.64
	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (5.08	4.09
10	420583	H77859	Hs.65450	reticulon 4	5.08	4.77
	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	5.06	5.56
	445263	H57646	Hs.42586	KIAA1560 protein	5.05	6.32
	407839	AA045144	Hs.161566	ESTs	5.03	5.22
	434293	NM_004445	Hs.3796	EphB6	5.03	5.27
15	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	5.03	4.91
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	4.99	16.04
	445493	AI915771		metallothionein 1E (functional)	4.94	8.14
	429365	AA451798	Hs.99249	ESTs	4.93	4.33
	412633	AF001691	Hs.74304	periplakin	4.90	5.19
20	448490	AI523897	Hs.271692	ESTs, Weakly similar to I38022 hypotheti	4.90	11.71
	408491	AI088063	Hs.7882	ESTs	4.85	4.88
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.80	4.39
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	4.80	6.05
	421998	R74441		poly(A)-binding protein, nuclear 1	4.78	7.23
25	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	4.77	4.78
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.72	6.24
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	4.71	3.72
	450626	AW190989	Hs.1508	insulin-degrading enzyme	4.70	3.60
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	4.68	5.14
30	408239	AA053401		ESTs, Moderately similar to ALU7_HUMAN A	4.68	15.83
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	4.67	6.17
	443827	AI087867	Hs.134667	ESTs	4.64	4.48
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	4.63	5.06
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	4.63	8.48
35	427318	AF186081	Hs.175783	zinc transporter	4.63	3.19
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.62	3.57
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.62	5.14
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	4.61	6.80
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	4.60	6.19
40	402294			Target Exon	4.59	2.45
	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57	5.47
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	4.57	5.12
	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.57	4.76
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	4.54	4.49
45	414798	AI286323	Hs.97411	hypothetical protein MGC12335	4.54	4.32
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	4.53	3.04
	400109			Eos Control	4.53	2.91
	407242	M18728		gb:Human nonspecific crossreacting antig	4.52	3.94
	431901	AW295050	Hs.272023	transforming, acidic coiled-coil contain	4.51	4.07
50	435992	AI033259	Hs.118317	Homo sapiens cDNA FLJ12088 fis, clone HE	4.50	4.16
	447365	BE383676	Hs.334	Rho guanine nucleotide exchange factor (4.50	4.77
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	4.50	3.99
	424620	AA101043	Hs.151254	kalikrein 7 (chymotryptic, stratum com	4.49	4.02
	432559	AW452948	Hs.257631	ESTs	4.47	5.43
55	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.47	3.10
	422313	AF045941	Hs.115166	scielin	4.45	3.17
	416305	AI076628	Hs.79187	coxsackievirus and adenovirus receptor	4.45	5.07
	432314	AA533447	Hs.312989	ESTs	4.44	5.25
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	4.44	3.52
60	424670	W61215	Hs.116651	epithelial V-like antigen 1	4.43	2.64
	414489	AI620677	Hs.73105	ESTs	4.42	4.27
	413040	AA193338	Hs.12321	sodium calcium exchanger	4.41	3.77
	426974	AB002298	Hs.173035	KIAA0300 protein	4.36	4.58
	448249	AW855331	Hs.337124	ESTs	4.35	4.97
65	451743	AW074266	Hs.23071	ESTs	4.35	4.49
	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	4.34	4.52
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.33	3.94
	408104	AW972927	Hs.293968	ESTs	4.32	7.20
	447945	AI922838	Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.31	3.53
70	439349	AI660898	Hs.6834	ESTs	4.30	3.72
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.29	4.16
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen gene 52	4.29	3.94
	453574	AI767947	Hs.50841	ESTs	4.28	4.97
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	4.25	3.66
75	424833	NM_003894	Hs.153405	period (Drosophila) homolog 2	4.25	17.64
	426248	T18988	Hs.293668	ESTs	4.22	3.13
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	4.21	4.09
	406805	AI686003	Hs.296031	ESTs	4.19	2.76
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	4.19	3.87
80	451831	NM_001674	Hs.460	activating transcription factor 3	4.18	5.93
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.18	4.74
	434936	AI285970	Hs.183817	ESTs	4.17	2.83
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	4.17	4.39
	448429	D17408	Hs.21223	catponin 1, basic, smooth muscle	4.17	2.38
					4.16	5.15

5	421978	AJ243662	Hs.110196	NICE-1 protein	4.15	8.07
	437135	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.14	4.92
	442554	AW467376	Hs.129640	ESTs	4.12	4.00
	451814	AA847992	Hs.137003	ESTs	4.11	4.58
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	4.10	3.92
10	457121	AJ743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09	3.19
	426539	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	4.09	3.69
	430191	AI149880	Hs.188809	ESTs	4.07	4.49
	430433	AA478883	Hs.273766	ESTs	4.07	3.74
	425992	AA367069	Hs.100636	ESTs	4.06	4.37
15	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	4.05	4.15
	452392	L20815	Hs.507	comeodesmosin	4.04	11.00
	402845			ENSP00000246267-KIAA0444 PROTEIN (FRAGME	4.03	4.18
	439873	BE159253	Hs.300638	ESTs	4.03	3.86
	432305	M62402	Hs.274313	insulin-like growth factor binding prote	4.02	8.79
20	420789	AJ670057	Hs.199882	ESTs	4.02	4.34
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	4.02	5.13
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	4.01	4.29
	429556	AW139399	Hs.98988	ESTs	4.01	4.59
	448585	AB020676	Hs.21543	KIAA0869 protein	4.01	4.52
25	403710			C4000160.gi12735793.ref XP_011926.1 pr	4.00	3.31
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.98	6.61
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.98	3.79
	437611	AA897108		gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s	3.97	4.24
	426500	NM_014638	Hs.170156	KIAA0450 gene product	3.96	4.93
30	448710	T62926	Hs.304184	ESTs	3.96	4.54
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	3.95	5.57
	428340	AF261088	Hs.154721	aconitase 1, soluble	3.94	3.24
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.94	9.16
	456972	AJ054347	Hs.2017	ribosomal protein L38	3.93	4.37
35	418381	AA682393	Hs.119237	ESTs	3.93	3.45
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.92	15.00
	456332	AA228357		gb:nc39d05.r1 NCL_CGAP_Pr2 Homo sapiens	3.91	4.88
	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	3.91	3.19
	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	3.90	4.50
40	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	3.90	3.89
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.89	5.11
	452894	AI598065	Hs.61558	ESTs	3.88	3.73
	430570	AJ417881	Hs.292464	ESTs	3.87	4.47
	439625	AF086453	Hs.58611	ESTs	3.86	4.81
45	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.85	3.01
	431247	AL021578	Hs.278489	matrilin 4	3.85	3.35
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.85	5.15
	441319	AI354869	Hs.133081	ESTs, Weakly similar to T08700 hypothei	3.84	5.03
	452877	AI250789	Hs.32478	ESTs	3.84	3.26
50	444252	R21135	Hs.54985	ESTs	3.83	5.58
	416265	AA177088	Hs.190065	ESTs	3.82	3.87
	418875	W19971	Hs.233459	ESTs	3.80	2.92
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypothei	3.80	4.36
	442503	AF147078	Hs.150853	p53-responsive gene 5	3.80	7.53
55	427081	AJ474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !	3.77	4.81
	458222	AW139592		hypothetical protein DKFZp434K1421	3.77	3.56
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypothei	3.77	3.20
	436283	AI480319	Hs.120058	ESTs	3.76	3.76
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	3.76	2.65
60	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	3.75	7.59
	434206	AW136973		ESTs, Weakly similar to S69890 mitogen i	3.72	3.96
	424824	AI217440	Hs.143873	ESTs	3.72	3.52
	457411	AW085961	Hs.130093	iroquis-class homeobox protein IRX2	3.71	3.05
	452241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	3.70	4.84
65	421845	AW021631	Hs.16515	ESTs	3.69	3.59
	413922	AI535895	Hs.221024	ESTs	3.68	4.22
	422746	NM_004484	Hs.119651	glypican 3	3.68	4.29
	433934	AW273261	Hs.216292	ESTs	3.68	4.39
	452547	AA335295	Hs.74120	adipose specific 2	3.66	12.23
70	400295	W72838		AI905687:IL-BT095-190199-019 BT095 Homo	3.66	9.25
	419098	AA234041	Hs.87271	ESTs	3.66	4.94
	417054	AF017060		aldehyde oxidase 1	3.65	4.51
	423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	3.65	4.32
	431362	AI874223	Hs.293560	ESTs	3.65	3.73
75	420506	AW977779	Hs.194613	ESTs	3.65	3.25
	448065	AI459177	Hs.172759	ESTs, Moderately similar to ALU7_HUMAN A	3.64	4.62
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	3.64	4.54
	451951	AW082870	Hs.210954	ESTs	3.64	3.69
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	3.64	3.39
80	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.62	3.62
	412668	AA456195		hypothetical protein FLJ14621	3.62	4.22
	413899	AF083892	Hs.75608	tight junction protein 2 (zona occludens	3.62	3.06
	444726	NM_006147		interleukin regulatory factor 6	3.59	10.65
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.59	3.31
	429973	AI423317	Hs.164680	ESTs	3.59	3.71
	452413	AW082633	Hs.215030	ESTs	3.58	4.66
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	3.58	4.44

	430397	AI924533	Hs.105607	bicarbonate transporter related protein	3.57	3.74
	411939	AI365585	Hs.146246	ESTs	3.57	12.42
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	3.57	4.11
5	432406	AI340571	Hs.343666	KIAA0969 protein	3.57	2.84
	439609	AW971945	Hs.293236	ESTs	3.56	3.14
	435381	AW136397	Hs.175382	ESTs	3.56	3.48
	410173	AA706017	Hs.119944	ESTs	3.56	3.37
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	3.56	9.93
10	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.55	4.24
	434360	AW015415	Hs.127780	ESTs	3.55	4.77
	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.53	5.65
	425681	AB018297	Hs.159183	KIAA0754 protein	3.52	4.79
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.46
15	451184	T87943		transcription factor 7-like 2 (T-cell sp	3.51	3.63
	448496	BE379077	Hs.130849	ESTs, Weakly similar to 138022 hypothei	3.51	3.30
	425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	3.48	8.66
	428232	BE272452	Hs.183109	monoamine oxidase A	3.48	9.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	3.48	6.05
20	401760			Target Exon	3.48	7.86
	427899	AA829286	Hs.332053	serum amyloid A1	3.47	3.67
	451767	AI625014	Hs.187328	ESTs	3.46	3.85
	452849	AF044924	Hs.30792	hook2 protein	3.45	5.66
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	3.45	5.02
25	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.45	3.61
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.45	7.71
	420876	AA918425	Hs.177744	ESTs	3.44	8.46
	421114	AW975051	Hs.293156	ESTs, Weakly similar to 178885 serineth	3.44	4.47
	426233	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC0	3.44	3.96
30	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	3.42	4.32
	403593			Target Exon	3.42	6.35
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	3.42	3.34
	447731	AA373527	Hs.19385	CGI-58 protein	3.41	2.44
	456327	H68741	Hs.38774	ESTs	3.40	3.46
35	413880	AI660842	Hs.110915	interleukin 22 receptor	3.37	3.61
	429501	AI700588	Hs.293388	ESTs, Weakly similar to A34612 zinc fing	3.37	3.44
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	3.36	4.87
	420231	R06866	Hs.19813	ESTs	3.36	8.60
	424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	3.36	6.20
40	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.34	3.40
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.34	3.35
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	3.34	4.06
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.33	4.36
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.32	9.47
45	428496	AA769986	Hs.185802	ESTs	3.32	3.88
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.31	4.01
	409095	AW337272	Hs.293656	ESTs, Moderately similar to S72481 proba	3.31	3.31
	443072	AI937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	3.31	4.40
	437596	AA761490		ESTs, Moderately similar to S65657 alpha	3.30	5.31
50	444094	AI695764	Hs.202394	ESTs	3.29	3.47
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.29	3.76
	407334	AA494411	Hs.296031	ESTs	3.28	4.30
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	3.28	3.78
	447875	R22029	Hs.13905	ESTs	3.28	3.44
55	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.27	3.71
	411962	AA099050		gb:zkb85d12.r1 Soares_pregnant_uterus_Nbh	3.27	4.28
	424395	AA165082	Hs.146388	microtubule-associated protein 7	3.27	3.82
	400494			ENSP00000238970*:CIG30 (Fragment),	3.27	2.60
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	3.26	6.19
60	409231	AA446644	Hs.692	GAT33-2 antigen; epithelial glycoprotein	3.26	4.24
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	3.26	5.17
	445234	AW137636	Hs.146059	ESTs	3.25	5.59
	426150	NM_003658	Hs.167218	BarH-like homeobox 2	3.25	5.21
	400076			Eos Control	3.25	3.60
65	421462	AF016495	Hs.104624	aquaporin 9	3.25	3.93
	420677	AW086215	Hs.246096	ESTs	3.25	3.53
	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	3.24	3.88
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.24	5.64
	420682	AI380552	Hs.88602	ESTs	3.24	4.13
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.23	4.90
	431157	AI823969	Hs.132678	ESTs	3.23	3.97
	440469	AA886068		gb:ny40e07.s1 NCI_CGAP_Pr12 Homo sapiens	3.23	3.39
	449961	AW265634	Hs.133100	ESTs	3.21	5.36
	407948	AW085161	Hs.56279	ICEBERG caspase-1 inhibitor	3.21	4.61
75	400835			chromosome 2 open reading frame 2	3.21	3.62
	413329	AI056885	Hs.133539	ESTs	3.21	3.43
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.21	3.72
	450860	AA021007		integrin, beta 8	3.20	5.89
	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.19	6.84
80	453855	AA039576	Hs.37858	ESTs, Weakly similar to ALUB_HUMAN !!!	3.19	3.59
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.19	3.51
	420074	AA253425	Hs.190074	ESTs	3.18	5.50
	418481	M81945		CD34 antigen	3.18	3.65
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	3.18	7.43

	435337	AI078307	Hs.134317	ESTs, Weakly similar to PC4259 ferritin	3.17	3.51
	445502	AW379160	Hs.12813	DKFZP434J214 protein	3.17	3.62
	412477	AA150864		microsomal glutathione S-transferase 1	3.17	5.39
5	421757	Z20897	Hs.296259	paraoxonase 3	3.16	3.60
	413835	AI272727	Hs.249163	fatty acid hydroxylase	3.16	5.56
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.15	1.99
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	3.15	4.45
	414869	AA157291	Hs.21479	ubiquitin 1	3.13	4.40
	412947	AA122277		gb:zk97e09.s1 Soares_pregnant_uterus_NbH	3.13	3.30
10	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.12	4.62
	421335	X99977	Hs.103505	ARS component B	3.11	11.54
	401905			ENSP00000252232::Sterol regulatory eleme	3.10	2.85
	443514	BE464288	Hs.141937	ESTs	3.09	3.66
	418817	AA913229	Hs.19339	ESTs	3.08	3.88
15	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	3.08	4.18
	435858	AF254260	Hs.283009	tufetin 1	3.08	3.96
	430285	AI917602	Hs.106440	ESTs	3.07	3.30
	448106	AI800470	Hs.171941	ESTs	3.07	5.19
	432908	AI861896		ESTs	3.07	3.85
20	450086	AW016343	Hs.233301	ESTs	3.07	3.38
	451529	AI917901	Hs.208641	ESTs	3.07	3.29
	418443	NM_005239	Hs.85146	v-els avian erythroblastosis virus E26 o	3.06	4.12
	426848	H72531	Hs.36190	ESTs	3.05	4.34
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05	3.97
25	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	3.05	3.29
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.05	3.89
	434230	AA551569		hypothetical protein PRO2822	3.04	3.63
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.04	8.09
	415696	AI821552	Hs.188682	ESTs	3.03	3.43
30	449618	AI076459	Hs.15978	KIAA1272 protein	3.01	3.29
	414665	AA160873		serum amyloid A1	3.01	9.22
	446682	AW205632	Hs.211198	ESTs	3.00	3.30
	443801	AW206942	Hs.253594	intron of trichorhinophalangeal syndro	2.99	3.74
	412446	AI768015		ESTs	2.99	4.47
35	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	2.99	4.35
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.98	3.49
	403180			Target Exon	2.98	3.92
	434442	AA737415		ESTs	2.98	3.61
	439593	BE073597	Hs.124863	ESTs	2.98	3.86
40	410453	AW749036		gb:RC2-BT0318-241199-011-410 BT0318 Homo	2.98	3.49
	414766	AW293452	Hs.16228	ESTs	2.97	3.63
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	2.97	3.99
	451541	BE279383	Hs.26557	plakophilin 3	2.97	6.90
	452195	AA994712	Hs.116878	ESTs	2.97	3.30
45	401747			Homo sapiens keratin 17 (KRT17)	2.97	4.10
	431316	AA502663	Hs.145037	ESTs	2.96	3.05
	445437	AI224165	Hs.148725	ESTs	2.95	7.12
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	2.95	5.68
	456371	S76825	Hs.89695	insulin receptor	2.94	4.59
50	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	2.94	4.12
	436664	AW197887	Hs.253353	ESTs	2.93	3.57
	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	2.66
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.92	7.48
55	428769	AW207175	Hs.106771	ESTs	2.92	3.28
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.92	3.48
	444204	AI129194	Hs.143040	ESTs	2.92	3.92
	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	2.91	6.55
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.90	3.92
	429538	BE182592	Hs.139322	small proline-rich protein 2A	2.88	4.75
60	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.88	6.74
	417184	N52510	Hs.268597	Homo sapiens cDNA: FLJ21498 fis, clone C	2.87	3.97
	412093	BE242691	Hs.14947	ESTs	2.86	3.48
	424135	AW994455	Hs.140978	Homo sapiens mRNA; cDNA DKFZp762H106 (fr	2.86	3.32
	437167	AL050184	Hs.21610	DKFZP434B203 protein	2.86	3.87
65	454065	BE394588		gb:G01311808F1 NIH_MGC_44 Homo sapiens c	2.86	3.43
	420230	AL034344	Hs.284186	forkhead box C1	2.85	3.67
	403108			ENSP00000241415::Hypothetical 67.7 kDa p	2.85	2.62
	434433	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
70	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	2.66
	429429	AA829725	Hs.334437	hypothetical protein MGCA248	2.83	3.59
	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocytic 2	2.83	3.36
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	2.83	4.50
	429259	AA420450	Hs.292911	Plakophilin	2.81	4.81
	423523	AW299828	Hs.193580	ESTs	2.80	7.08
75	433637	AW024214	Hs.102307	ESTs	2.80	3.39
	452089	T97294	Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	2.80	3.62
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	2.80	3.52
	421965	AA301100	Hs.346482	gb:EST14128 Testis tumor Homo sapiens cD	2.79	3.49
	432098	AF252297	Hs.91546	cytochrome P450 resinoid metabolizing pr	2.79	2.31
80	429128	AA444689	Hs.119316	ESTs	2.78	4.17
	438913	AI380429	Hs.172445	ESTs	2.77	3.65
	445029	AF196481		midline 2	2.76	3.79
	419923	AW081455	Hs.120219	ESTs	2.76	3.00

	416508	R39769	Hs.56406	ESTs, Moderately similar to ALU8_HUMAN A	2.76	3.59
	412507	L36645	Hs.73964	EphA4	2.76	3.90
	446339	ALD46962	Hs.14845	forkhead box O3A	2.75	3.50
5	433710	AI341867	Hs.188920	ESTs	2.75	3.33
	432375	BE536089	Hs.2962	PTK6 protein tyrosine kinase 6	2.74	5.77
	409213	U61412	Hs.51133	S100 calcium-binding protein P	2.74	3.76
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.74	8.19
	408839	AW277084		gb:xp61h09.x1 NCL_CGAP_Ov39 Homo sapiens	2.73	3.93
10	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.73	11.46
	444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.73	6.17
	433713	AW976511	Hs.112592	ESTs	2.72	3.42
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.72	4.76
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.72	3.74
15	432947	AA570710	Hs.270998	ESTs, Weakly similar to I38022 hypothe	2.72	3.44
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	2.72	4.95
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.72	4.29
	435016	AI284219	Hs.130749	ESTs, Weakly similar to I38022 hypothe	2.71	4.45
	449667	AB023227	Hs.23860	KIAA1010 protein	2.71	3.72
20	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.70	3.82
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.70	2.76
	430152	AB001325	Hs.234642	aquaporin 3	2.69	4.26
	456063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	2.69	6.72
	424471	AA341329	Hs.311524	ESTs	2.68	4.57
25	453201	AI432195	Hs.135098	ESTs	2.68	3.69
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	2.68	4.25
	404996			Target Exon	2.67	4.28
	409453	AI885516	Hs.95612	ESTs	2.65	6.51
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.65	3.78
30	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	2.64	6.38
	444169	AV648170	Hs.58756	ESTs	2.64	3.40
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.64	3.47
	408395	BE072425	Hs.44579	hypothetical protein FLJ20199	2.64	4.01
	432093	H28383		gb:y152c03.r1 Soares breast 3NbHBst Homo	2.63	4.08
35	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	2.62	2.51
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	2.61	3.62
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.61	3.68
	431166	AW971186	Hs.293839	ESTs	2.61	3.33
	440659	AF134160	Hs.7327	claudin 1	2.61	3.53
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	2.61	4.48
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.60	3.51
	407299	AA460205	Hs.289770	ESTs, Weakly similar to I38022 hypothe	2.59	3.82
	449539	W80363	Hs.58446	ESTs	2.58	4.05
	413884	AI668892	Hs.239758	hypothetical protein FLJ12389 similar to	2.58	4.19
45	445620	AI245225	Hs.17441	ESTs	2.57	3.44
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	2.56	3.57
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.56	3.47
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	3.61
	406790	AA293303		ribosomal protein L27a	2.54	4.36
50	450472	AI190071	Hs.55278	ESTs	2.54	4.30
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.54	3.82
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.54	3.44
	430821	AA487264	Hs.154974	Homo sapiens mRNA: cDNA DKFZp667N064 (fr	2.54	4.55
	402575			Rho GTPase activating protein 1	2.53	5.47
55	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	2.40
	431631	AA548906	Hs.122244	ESTs	2.52	3.79
	408806	AW847814	Hs.75608	Homo sapiens cDNA: FLJ21532 fis, clone C	2.52	4.51
	420235	AA256756	Hs.31178	ESTs	2.51	4.21
	436314	AI983409		ESTs	2.51	3.11
60	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog	2.50	5.62
	429547	AW009166	Hs.99376	FGFENSH predicted novel secreted protein	2.49	2.60
	410532	T53088	Hs.155376	hemoglobin, beta	2.49	4.73
	413475	AW021488	Hs.26981	ESTs	2.49	3.90
	429325	AW088739	Hs.243770	ESTs	2.48	3.71
65	424604	AW865388	Hs.151076	KIAA1243 protein	2.48	4.16
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.48	3.80
	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.47
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.47	2.09
	444935	AA262449	Hs.223569	ESTs	2.47	5.96
70	445389	NM_016831	Hs.12582	period (Drosophila) homolog 3	2.47	3.41
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.47	6.80
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.46	7.37
	409178	BE393948	Hs.50915	kallikrein 5	2.46	5.59
	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	2.46	6.03
75	447179	AW015633	Hs.157299	ESTs	2.46	3.23
	414459	Y11525	Hs.76171	CCAAT/enhancer binding protein (C/EBP),	2.46	3.95
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	2.45	3.94
	428593	AW207440	Hs.185973	degenerative spermatocytia (homolog Dros	2.44	2.17
	436009	H57130	Hs.120925	ESTs	2.44	2.94
80	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.43	3.61
	416749	AW068550.comp	Hs.79732	fibulin 1	2.43	4.46
	444672	Z95636	Hs.11669	laminin, alpha 5	2.42	6.39
	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.42	3.45
	406997	U07807		metallothionein IV	2.42	3.92

5	423184	NM_004428	Hs.1624	ephrin-A1	2.41	4.34
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	2.41	5.08
	456826	AJ871742	Hs.302428	wingless-type MMTV integration site fami	2.41	3.92
	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	2.41	5.18
	400232			NM_001895*:Homo sapiens casein kinase 2,	2.41	3.82
10	421481	AW391972	Hs.104696	KIAA1324 protein	2.40	4.03
	442083	R50192	Hs.165062	ESTs	2.39	4.21
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.39	8.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.39	2.57
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown (H.sapie	2.39	3.85
15	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, atp	2.38	3.84
	431179	AJ338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.37	7.89
	432563	NM_013261	Hs.198468	peroxisome proliferative activated recep	2.37	3.77
	402338			Target Exon	2.37	3.46
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.37	4.57
20	436723	AW975895	Hs.307486	ESTs	2.37	6.39
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	2.37	3.92
	409212	AJ082423	Hs.141892	ESTs	2.36	3.79
	451323	AJ903313	Hs.34579	ESTs, Moderately similar to ALU5_HUMAN A	2.35	3.29
	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.35	9.96
25	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	2.35	5.16
	451092	AJ207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	2.34	5.24
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	2.34	3.77
	424425	AB031480	Hs.146824	SPR1 protein	2.34	4.43
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	2.34	5.64
30	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.33	3.51
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	2.33	6.95
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.33	5.57
	453999	BE328153	Hs.240087	ESTs	2.32	3.40
	419358	T78763	Hs.90063	neurocalcin delta	2.32	6.72
35	430468	NM_004673	Hs.241519	angiotensin-like 1	2.32	3.90
	456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypothesi	2.32	3.27
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	2.32	4.43
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	2.31	7.22
	438282	BE268288	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.31	3.34
40	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.31	8.47
	419245	AJ732742	Hs.87440	ESTs	2.31	3.39
	444920	AW450967	Hs.235240	ESTs	2.30	3.30
	417314	N68168		gb:za11c01.s1 Soares fetal liver spleen	2.30	3.12
	409586	AL050214	Hs.55044	DKFZP586H2123 protein	2.30	3.52
45	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	2.29	6.11
	451176	AA046457	Hs.60677	ESTs	2.29	6.59
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29	3.29
	425982	R05327	Hs.189726	ESTs	2.29	3.37
	435684	NM_001290	Hs.4980	LIM domain binding 2	2.29	4.54
50	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	2.28	3.70
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.28	10.57
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	2.28	4.06
	401205			Target Exon	2.27	2.71
55	443102	AJ247472	Hs.132965	ESTs	2.27	5.66
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.26	3.94
	434987	AW975114		ESTs	2.26	3.72
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	2.26	3.42
	423515	AA327017	Hs.176594	ESTs	2.25	6.21
60	434903	AF161369	Hs.187763	Homo sapiens HSPC106 mRNA, partial cds	2.25	3.62
	443049	AJ028613	Hs.132343	ESTs	2.25	3.13
	444637	T19101	Hs.11494	fibulin 5	2.24	6.43
	410026	AJ912061	Hs.55016	hypothetical protein FLJ21935	2.23	3.31
	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7	2.23	4.17
65	429587	AA283969	Hs.334706	Homo sapiens cDNA FLJ11801 fis, clone HE	2.23	3.79
	431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	2.22	3.54
	409571	AA504249	Hs.187585	ESTs	2.22	3.87
	446051	BE048061	Hs.37054	ephrin-A3	2.22	4.57
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	2.21	4.25
70	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.21	5.07
	435748	AA699756	Hs.117335	ESTs	2.20	3.35
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.19	6.55
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	2.19	3.51
	433052	AW971983	Hs.293003	ESTs, Weakly similar to PC4259 femiun	2.19	3.32
75	430310	U60115	Hs.239069	four and a half LIM domains 1	2.19	3.83
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	2.19	15.65
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.18	3.54
	452689	F33868	Hs.284176	transferrin	2.18	3.30
	417061	AJ675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.18	3.77
80	432647	AJ807481	Hs.278581	fibroblast growth factor receptor 2 (bac	2.18	5.64
	401192			Target Exon	2.17	3.33
	421752	AK001521	Hs.107882	hypothetical protein FLJ10659	2.16	3.44
	456646	AJ243662	Hs.110196	NICE-1 protein	2.16	2.39
	421263	AB020638	Hs.103000	KIAA0831 protein	2.16	3.37
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	2.16	5.17
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	2.15	3.87
	429350	AJ754634	Hs.131987	ESTs	2.15	3.90

	448144	AW169230		ESTs, Moderately similar to PC4259 ferri	2.14	3.28
	429002	AW248439	Hs.2340	junction plakoglobin	2.14	3.28
	429297	X82494	Hs.198862	fibulin 2	2.14	5.05
5	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586A0723 (f	2.14	4.32
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	2.14	3.99
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	2.14	3.39
	453155	AF052126	Hs.552	steroid-5-alpha-reductase, alpha polypep	2.14	3.38
	453283	AA694386	Hs.290914	ESTs	2.14	2.51
10	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	2.13	3.28
	414815	AW292140	Hs.130286	ESTs	2.13	3.76
	417155	T75125	Hs.299148	hypothetical protein FLJ21801	2.13	4.16
	416673	T77052	Hs.14039	ESTs	2.13	3.57
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	2.13	3.43
15	413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	2.12	5.67
	430967	H16791	Hs.100895	ESTs	2.12	4.76
	429015	BE168484	Hs.194737	KIAA0453 protein	2.12	2.64
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.12	3.30
	426468	AA379306	Hs.117558	ESTs	2.11	2.59
20	407555	Z48511		gb:H.sapiens XG mRNA (clone PEP11).	2.10	3.56
	418226	AA424202	Hs.83834	cytochrome b-5	2.10	3.66
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.10	5.14
	436961	AW375974	Hs.156704	ESTs	2.10	3.64
	432633	A1796390	Hs.210667	ESTs	2.10	3.21
25	426102	AF200496	Hs.166371	interleukin 1, zeta	2.10	2.58
	445467	AJ239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.09	3.77
	437124	AA554458		KIAA0666 protein	2.09	3.85
	407757	BE048414	Hs.165215	hypothetical protein MGC5395	2.09	3.35
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	2.08	4.41
30	443906	AA348031	Hs.7913	ESTs	2.08	5.01
	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.40
	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	2.08	3.92
	437704	AA766142	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A	2.07	4.19
	412533	AA679863	Hs.69606	ESTs	2.07	3.30
35	426310	NM_000909	Hs.169266	neuropeptide Y receptor Y1	2.07	3.39
	411821	BE299339	Hs.72249	three-PDZ containing protein similar to	2.06	3.55
	442599	AF078037	Hs.324051	RelA-associated inhibitor	2.06	4.98
	432212	AW137742		ESTs	2.06	7.23
	453469	AB014533	Hs.33010	KIAA0633 protein	2.04	3.52
40	443652	AJ080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	2.04	4.01
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.04	3.36
	424464	R68537	Hs.17962	ESTs	2.03	3.64
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	2.03	4.36
	439908	A1168031	Hs.155507	ESTs	2.03	3.31
45	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	2.03	3.83
	406784	A1144297	Hs.169401	apolipoprotein E	2.02	5.56
	427309	NM_005714	Hs.175218	potassium channel, subfamily K, member 7	2.02	3.40
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	2.02	4.58
	404246			Target Exon	2.02	3.57
50	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	2.01	7.30
	410669	AW805749		superoxide dismutase 2, mitochondrial	2.01	5.81
	446193	AJ279390	Hs.144658	ESTs, Weakly similar to T17257 hypothi	2.01	3.05
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.01	2.32
55	434346	AA630445		ESTs	2.00	5.10
	456098	AW747800	Hs.55016	hypothetical protein FLJ21935	2.00	3.51
	452467	AW500815		ESTs	2.00	4.96
	442866	AJ743317	Hs.283622	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.00	4.66
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.72
60	417553	L09190		trichohyalin	1.98	3.11
	449142	R15913	Hs.194987	ESTs	1.98	2.09
	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	1.98	3.50
	429299	AJ620463	Hs.347408	hypothetical protein MGC13102	1.98	6.25
	423031	AJ278995		ESTs	1.97	3.77
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.97	3.62
65	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	1.96	4.57
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	1.96	6.09
	418462	BE001596	Hs.85266	integrin, beta 4	1.95	5.77
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.95	6.09
70	437220	AL117542	Hs.334305	GS1999full	1.95	3.33
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.94	3.45
	443595	AF169312	Hs.9613	PPAR(gamma) angiotensin related protein	1.94	5.46
	409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (f	1.94	4.67
	408717	AF045458	Hs.47061	unc-51 (C. elegans)-like kinase 1	1.94	3.59
	420055	NM_001487	Hs.94672	GCN5 (general control of amino-acid synt	1.94	4.29
75	430392	NM_000627	Hs.241257	latent transforming growth factor beta b	1.93	3.38
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	1.93	3.75
	423527	AJ206965	Hs.105861	hypothetical protein FLJ13824	1.93	4.06
	447151	AJ022813	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.93	4.70
80	422101	AW404176	Hs.111611	ribosomal protein L27	1.91	3.77
	456653	AJ807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.18
	443444	AW952619	Hs.17235	Homo sapiens clone TCCIA00176 mRNA sequ	1.91	3.41
	420924	R01026	Hs.245321	ESTs	1.91	3.52
	426048	AJ768853	Hs.134478	ESTs	1.91	3.22
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	1.90	3.56
					1.90	4.15

5	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.90	5.88
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	2.28
	418418	R61527	Hs.237517	ESTs	1.90	3.56
	449372	AA001266	Hs.133521	ESTs	1.89	3.90
	438752	AW238673	Hs.146038	ESTs	1.89	5.24
10	428193	NM_004235		Kruppel-like factor 4 (gaf)	1.89	5.21
	433251	AB040955	Hs.322735	KIAA1522 protein	1.89	5.00
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.89	7.09
	427795	BE268268	Hs.180842	ribosomal protein L13	1.89	4.51
	410209	AI583661	Hs.60548	hypothetical protein PRO1635	1.89	3.35
15	449243	AW295031	Hs.198671	ESTs	1.89	4.26
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	1.88	6.20
	443932	AW888222	Hs.9973	tensin	1.88	9.28
	427929	BE613835	Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.87	4.25
	400078			Eos Control	1.87	6.73
20	422639	AI929377	Hs.173724	creatine kinase, brain	1.87	5.51
	447374	AF263462	Hs.18376	KIAA1319 protein	1.87	3.42
	430346	AK000331	Hs.297641	KIAA0462 protein	1.87	4.15
	428223	AA424313	Hs.98402	ESTs	1.87	3.70
	408792	L29433	Hs.47913	coagulation factor X	1.87	4.08
25	433855	AA834082	Hs.307559	ESTs	1.87	4.16
	451583	AI653797	Hs.24133	ESTs	1.87	3.81
	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.86	5.55
	431647	AL138578	Hs.266738	hypothetical protein dJ796117.1	1.86	3.74
	422055	NM_014320	Hs.111029	putative heme-binding protein	1.86	4.68
30	425750	AL050276	Hs.42400	zinc finger protein 288	1.86	4.04
	422491	AA338548	Hs.117546	neuronatin	1.86	4.37
	438942	AW875398	Hs.6451	PRO0659 protein	1.85	5.06
	400198			Eos Control	1.85	5.22
	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	1.85	3.41
35	427605	NM_000997	Hs.337445	ribosomal protein L37	1.85	4.73
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.84	5.94
	441912	AA971484	Hs.159938	ESTs	1.84	3.73
	421632	AA825426	Hs.334689	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.83	3.62
	440602	AI743491	Hs.292692	ESTs	1.83	2.39
40	431882	NM_001426	Hs.271977	engrailed homolog 1	1.83	3.30
	420772	AW752656	Hs.222707	KIAA1718 protein	1.83	3.73
	429197	H24471	Hs.26930	ESTs, Weakly similar to T20272 hypotheti	1.82	3.41
	450796	NM_001988	Hs.25482	envoplakin	1.82	7.73
	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-c	1.82	3.38
45	415409	AW993701		NS1-associated protein 1	1.82	3.60
	401131			NM_001651*:Homo sapiens aquaporin 5 (AQP	1.82	5.53
	421324	BE257515	Hs.103503	deoxyribonuclease I-like 2	1.81	5.53
	400079			Eos Control	1.81	6.79
	430513	AJ012008	Hs.241586	G6C protein	1.81	7.49
50	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.81	3.55
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.80	5.43
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.79	5.90
	432417	AL040360	Hs.162203	ESTs, Weakly similar to alternatively sp	1.79	3.63
	406467			Target Exon	1.79	4.16
55	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	1.79	3.32
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.78	3.51
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.78	3.72
	425880	X01630	Hs.160786	argininosuccinate synthetase	1.78	3.29
	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	1.78	3.44
60	451304	M92642	Hs.26208	collagen, type XVI, alpha 1	1.78	3.57
	400082			Eos Control	1.78	3.82
	446603	NM_014835	Hs.15519	oxysterol-binding protein-related protei	1.77	3.48
	425415	M13903	Hs.157091	involucrin	1.77	4.64
	400083			Eos Control	1.77	6.31
65	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	1.76	3.47
	446971	AI652143	Hs.288382	hypothetical protein FLJ13111	1.76	4.21
	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	1.76	2.63
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.76	3.82
	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.76	4.31
70	439927	AA854650	Hs.124597	ESTs	1.75	3.63
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	1.75	3.79
	414500	W24087	Hs.76285	DKFZP564B167 protein	1.75	3.55
	448182	AF244137	Hs.20597	host cell factor homolog	1.75	3.40
	439651	AF086480	Hs.56255	ESTs	1.75	2.55
75	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	1.75	3.54
	424389	AA339786		lymphocyte-specific protein 1	1.75	4.48
	450837	D58463	Hs.85969	hypothetical protein FLJ12270	1.74	3.40
	425920	AL049977	Hs.162209	claudin 8	1.74	3.33
	435680	HS0946	Hs.284183	Homo sapiens galectin-related inhibitor	1.74	3.47
80	439639	AA370045	Hs.6607	AXIN1 up-regulated	1.73	5.22
	416950	AL049798	Hs.80552	dermatopontin	1.73	4.99
	400199			Eos Control	1.73	6.25
	409737	AB011539	Hs.56186	EGF-like-domain, multiple 3	1.73	4.28
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.72	3.42
	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	1.72	2.12
	414323	NM_014759	Hs.334688	KIAA0273 gene product	1.71	4.82
	407228	M25079	Hs.155376	hemoglobin, beta	1.70	7.02

5	406643	N77976	Hs.347939	hemoglobin, alpha 2	1.70	3.60
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.70	5.10
	439733	AL365412	Hs.107203	hypothetical protein from EUROMAGE 1759	1.69	2.92
	415512	Y16270	Hs.78482	paralemmin	1.69	4.92
	407100	R29657		gb:F1-1179D 22 week old human fetal live	1.69	3.96
	425503	W92517	Hs.158203	actin binding LIM protein 1	1.68	5.97
	433738	A1684802		ESTs	1.68	2.88
	406791	A1220684	Hs.347939	hemoglobin, alpha 2	1.68	3.44
10	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase	1.68	2.74
	435661	AF220263	Hs.193920	MOST2 protein	1.67	3.56
	459317	BRCA1b		Eos Control	1.67	3.34
	426923	AF112977	Hs.172887	phytanoyl-CoA hydroxylase (Refsum disease)	1.67	4.53
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polypeptide	1.67	3.36
15	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G protein)	1.67	5.22
	437201	F29279	Hs.171625	hypothetical protein MGC14697	1.67	5.75
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.67	4.55
	406710	A1708347	Hs.184014	ribosomal protein L31	1.66	3.80
	431593	NM_002108	Hs.276590	ESTs	1.66	2.45
20	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	1.66	2.44
	441899	A1372588	Hs.8022	TU3A protein	1.66	4.06
	414186	U33446	Hs.75799	protease, serine, 8 (protease)	1.65	6.52
	418116	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.65	3.44
	403105			Target Exon	1.64	4.12
25	450014	N41322	Hs.18441	ESTs	1.64	2.90
	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp434M245 (tr	1.64	4.49
	401429			C14001067:gi4126465 dbj BAA36581.1 (AB	1.64	3.82
	420983	W95228	Hs.100764	cathepsin G	1.64	3.64
	433126	AB021262	Hs.99816	beta-catenin-interacting protein ICAT	1.63	3.29
30	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polypeptide	1.63	7.05
	412295	AW088826		poly(A)-binding protein, nuclear 1	1.63	4.01
	430831	AA703239	Hs.269804	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	3.60
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.62	2.64
	407082	Z47055		gb:Human partial cDNA sequence, farnesyl	1.62	2.13
35	452556	H78517	Hs.33905	ESTs	1.62	4.64
	415688	AA166963		gb:zo86d01.s1 Striatogene ovarian cancer	1.62	3.33
	446515	AL048875		hypothetical protein DKFZp566i133	1.62	3.66
	445919	TS3519	Hs.334692	hypothetical protein MGC14141	1.62	5.65
	447330	BE279949	Hs.18141	laminin 1	1.61	5.61
40	412374	X01388	Hs.73849	apolipoprotein C-III	1.61	5.18
	400229			NM_021724: Homo sapiens nuclear receptor	1.61	3.57
	414814	D14697	Hs.77393	farnesyl diphosphate synthase (farnesyl	1.61	2.08
	424397	A1950320		gb:wp08d10.x1 NCL CGAP_Kd12 Homo sapien	1.60	3.59
45	451335	AB023192	Hs.26285	imidazole receptor candidate	1.60	5.54
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	1.60	4.79
	456267	A1127958	Hs.83393	cystatin E/M	1.60	2.50
	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	1.60	3.98
	421397	S67368	Hs.103998	gamma-aminobutyric acid (GABA) A recepto	1.60	3.28
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.60	3.69
50	440160	BE560269	Hs.7010	NPD002 protein	1.59	2.49
	417481	AA203281	Hs.6191	ESTs	1.59	3.60
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (tr	1.58	3.98
	402991			Target Exon	1.58	3.36
55	425169	AW292500	Hs.128514	ESTs	1.58	4.00
	446429	A1681807	Hs.201391	ESTs	1.58	3.20
	426445	AA378739	Hs.187711	ESTs	1.57	3.63
	425196	AL037915	Hs.155097	carbonic anhydrase II	1.57	3.44
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor	1.57	3.55
60	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.56	3.39
	415988	BE407713	Hs.78943	bleomycin hydrolase	1.56	2.43
	441860	AW451330	Hs.348198	hypothetical protein FLJ20262	1.55	3.38
	428462	A1571486	Hs.30258	ESTs	1.55	3.65
	449518	BE395253	Hs.30861	ESTs	1.55	3.80
	420075	AF142482	Hs.203846	TEA domain family member 3	1.55	3.81
65	406799	AA908548		gb:og83g12.s1 NCL CGAP_Ov8 Homo sapiens	1.54	3.87
	450787	AB006190	Hs.25475	aquaporin 7	1.54	4.06
	419659	AB023206	Hs.92186	Leman coiled-coil protein	1.54	3.82
	408543	N78098	Hs.44289	ESTs	1.54	3.10
	410169	A1373741	Hs.59384	hypothetical protein MGC3047	1.54	4.73
70	426068	AF029778	Hs.166154	jagged 2	1.54	4.82
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon11a	1.54	5.83
	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.54	4.58
	410048	W76467	Hs.343874	proline oxidase homolog	1.54	4.66
	430502	A1123657	Hs.127264	ESTs, Weakly similar to JC5314 CDC28/cdc	1.53	3.41
75	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fs, clone L	1.53	4.57
	413353	AW293542	Hs.75309	eukaryotic translation elongation factor	1.53	3.99
	431021	A1869664		thiosulfate sulfurtransferase (rhodanese)	1.53	3.73
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.52	6.09
	433019	A1208513	Hs.279915	translocase of inner mitochondrial membr	1.52	4.49
80	406801	AW242054	Hs.190813	ribosomal protein L9	1.51	5.56
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.51	3.77
	432894	AW167668	Hs.279772	brain specific protein	1.51	6.72
	415550	L13720	Hs.78501	growth arrest-specific 6	1.50	4.02
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fs, clone MA	1.49	4.21

5	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-I	1.48	3.61
	445071	AI280246	Hs.149504	ESTs	1.48	3.39
	40763	A8028988	Hs.7407	KIAA1065 protein	1.48	4.03
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	1.47	3.58
	427841	AW883367		hypothetical protein MGC5306	1.47	3.61
	426335	AI054347	Hs.2017	ribosomal protein L38	1.47	3.76
	454098	W27953	Hs.292911	Plakophilin	1.46	2.95
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	1.46	3.40
10	440526	AI832243		ESTs	1.46	3.38
	452586	AW958479	Hs.289043	spindlin	1.45	3.48
	433399	N46406	Hs.84700	similar to phosphatidylcholine transfer	1.45	3.44
	430238	N72519	Hs.236545	hydroxyacid oxidase 2 (long chain)	1.45	4.00
	425456	T70445	Hs.157850	ribosomal protein L9	1.45	4.79
15	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	1.45	4.43
	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIc	1.44	3.89
	445156	N89367	Hs.12373	adenylate cyclase 6	1.44	3.60
	446576	AI659477		dystroglycan 1 (dystrophin-associated gl	1.44	3.07
	440433	AA252452	Hs.7187	hypothetical protein FLJ10707	1.43	3.67
20	434536	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho	1.42	3.35
	423513	AF035960	Hs.129719	transglutaminase 5	1.42	3.18
	418681	AA287786	Hs.23449	insulin receptor tyrosine kinase substra	1.42	3.38
	421935	AA131632	Hs.109672	CMP-NeuAC(beta)-N-acetylglactosaminide	1.41	4.04
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.41	4.27
25	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	1.41	3.80
	435879	AW084463	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	1.41	3.55
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.40	4.07
	412669	AW880841	Hs.96908	p53-induced protein	1.40	3.59
	415523	AL042003	Hs.296847	cell matrix adhesion regulator	1.40	4.38
30	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.39	4.03
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.39	3.65
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.37	3.99
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheli	1.36	3.30
	408198	AA131111		gbzo16b06.r1 Stratagene colon (937204)	1.36	3.33
35	419600	AA448958	Hs.91481	NEU1 protein	1.35	3.49
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	1.34	3.47
	408250	R92918	Hs.19597	KIAA1694 protein	1.34	3.89
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.32	4.24
	425183	W76098	Hs.19223	HCCA2 protein	1.32	3.52
40	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.32	3.50
	438303	A8028998	Hs.6147	KIAA1075 protein	1.32	3.71
	406800	AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	1.32	3.65
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD)	1.32	4.14
	428475	AF172940	Hs.184542	CGI-127 protein	1.31	3.43
45	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	1.30	3.34
	432295	BE091049	Hs.343665	ribosomal protein S15a	1.30	3.29
	422959	AV647015		paired immunoglobulin-like receptor beta	1.28	3.53
	402956			ENSP00000244002: KIAA1335 protein (Fragm	1.24	3.38
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	1.24	3.70
50	437142	AI791617	Hs.145068	ESTs, Moderately similar to A46010 X-lin	1.23	3.48
	424372	AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fis, clone HE	1.18	2.44
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	1.18	3.43
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.49
	406587			C15000544: gij5454148refjNP_006368.1 U	1.06	2.25
55	409574	AW419080	Hs.250645	ESTs	1.00	3.60
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	1.00	3.44
	402075			ENSP00000251056: Plasma membrane calcium	1.00	3.37
	422330	D30783	Hs.115263	epiregulin	1.00	3.35
	418986	AI123555	Hs.81796	ESTs	1.00	3.28
	404175			Target Exon	1.00	3.08
60	452640	AA027115	Hs.100206	ESTs, Weakly similar to A53856 aryl-acyl	1.00	2.82
	443564	AI921685	Hs.199713	ESTs	1.00	2.51

TABLE 64B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 B1467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 B1791553 AI700963

		BE061934 H01096 R69613 AI383162 AU133723 AA311526 R67942 H01097 H72113 R72430 R39494 AV744074 AA535925 B1759288 B1052385 BF854687 AW608286 AA043438 R72478 AL513811 R69214 AA188435 AA054965 AI220117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984 BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701 AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AI553922 AI560688 AW950043 AI961682 AV706506 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 N48996 N68575 H82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA633132 AA629674 AA629649 AA629656 AA578595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AI382839 AA194837 AA406284 AI250750 R37035 AI525586 W01244 AI122277 BE183957 BE183956 AF150424 AI861896 AA570057 AV738855 AF119900 NM_018539 AA702388 N53043 BF351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252 BG567713 AW665841 AI814924 AW978339 AW264036 AI373950 AW183157 AW082249 AI201658 AI364196 AA150743 AA160873 AA453757 BF871646 BF871640 AA565311 AA989511 R10152 AA807154 T77900 AV751591 BC021735 AI669212 L120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960559 AA987907 Z14149 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW898037 AW898604 BF957405 BF963433 BG704815 AA662701 AA633929 AA737415 BE065904 AW749036 BE175748 BE175746 BE175747 BE175745 T64217 BE394588 AW024754 BE183167 BE183166 BE378353 AA633408 AW749955 AW629759 AI651005 AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W06091 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012 BG566720 AA010276 W92098 BE837833 BF541660 AW889587 AI651246 AI339033 AI078183 AI686504 AA813616 BF056955 R43664 BF509917 W563717 W95054 AI382907 AI399929 F10511 AA427819 AW269408 BE825398 BG654856 AA037082 AI203007 AW593522 H65211 AA010218 AI355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662 AW972670 AA525808 H28359 H28383 AA293303 AA492458 AA948195 AI341912 AI436673 AA708982 AI095911 AI983409 NA AL581381 BE220341 AI695121 BG149299 AI205526 AI968389 B1752979 AI291204 AI954763 AA344460 AA344581 BF082319 AU125758 BE825566 AA954549 AI286069 AA948280 BG149854 BI862122 AI024440 AI090013 NM_001895 M55265 BC002615 BC011668 BM452475 AL560958 AU125134 BE408670 AL134963 AI589577 AI952244 AW972197 AW403214 AW069872 AI804464 AU123365 AI342226 H50982 AV738572 R94284 BG536938 AI970166 AI58205 J02853 AU131772 BE841258 AW867858 AA19595 AL597675 BF361319 AW877122 AW877060 AW876962 AU126276 AA279620 AA805295 AU132198 AU130091 AI375524 AW183031 AU129003 AI373257 H92896 BE244655 AW028253 AW571546 BI258630 AI807134 AW672915 AW893438 BF035080 AW054815 AW963200 AI797895 AA604241 AI014611 BE092080 BE092076 AA639870 AA714906 N39594 AA173857 AW951102 AW951101 BG823603 AI478558 R32009 AW149282 BG818283 R69507 T29481 BE766560 AI693579 H06201 AF005081 BG193848 AW846590 AW846515 AW846584 AW846592 AW846621 AW846610 N68168 N69188 N90450 H88044 BE156092 AW752953 AF005081 BG193848 AW975114 AI096634 AI767001 AA658364 AW517542 BC015871 AI521618 AI471709 AW169230 BG539605 BI058963 BI058949 BG548398 BG952412 AW842037 AW842040 AW890573 AF086341 W76326 W72300 AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 AI49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422 AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 AK056896 AI924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AI274929 AI281211 AI821178 BC020841 BF352476 BF843140 BF917041 W80832 AA630445 BF350167 BE162052 BE931808 AI572329 BG536379 AA026381 AW500815 AI806691 AW502933 AW303573 BE328059 AI201422 BE673566 AW182125 H13705 AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243 AI278995 AW964552 AI885189 AI571775 AI660803 AI293327 AI719401 Z39652 H25636 BF091855 AI218354 AI928704 AI817774 AI885495 AI695453 BF340929 AV749610 AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661 AK056188 BM455117 BG527027 AA480032 AW993701 AA164703 AL537682 AA836491 AA515961 AL537681 BF437856 AA683484 AW152367 AV691022 AA025156 AI624297 AW071132 BG951486 AI907206 BF348688 AI904222 BG954414 AI590133 AW080151 AA480116 BF360696 AI689419 N75837 AW373844 BF991704 BG222449 BI030443 BE698057 BG954850 AI905836 BF984111 AU123871 BF634727 AI904283 AI909847 BF757857 BF923905 BG283493 AA299475 R80150 BG987145 BF837559 BG469759 AA496412 BF758339 BG957192 AW373869 BG952345 BF229957 BE697472 BE697475 AA011005 BG005000 T56558 AA908196 AA716585
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424389	1059_4	BG190758 AW961118 W77994 AA339877 AW845121 AW845129 BG181820 BE716719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786
433738	593682_1	BE838286 BE838282 BE716635 AA777158 W94063 BE716628 BE716625 BE838371 BF371044 BE716631 BE716402
454478	4273_16	AL037666 AW607643 AI280025 AL037665 AW291619 AI280142 AA765506 AI684802 AW085941 AI688062
412295	133592_1	AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
		BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728
		AA101632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161 R79192 W85852
		AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388 AI241532 BF448184 AI209012
		AA865528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI933266 AI991774 AI807726 AI218667 AA301750
		R44328
415688	1235745_1	AW971218 AA493942 AA166963
446515	11382_1	BE178766 AI909166 W79619 AA346208 N54022 R98542 AA005419 AA890703 AW510832 BM126988 BF526760 AA858017 BM126698 AI423291
		AW173383 AA742205 AI693060 AA746651 AA490661 AW217170 AI635076 AI073737 AA875841 AA907556 N50889 AW438573 AW273496 AA633604
		AW303990 AI685291 AI076127 AW470084 AI022394 AI298624 AA253418 W79538 AA719820 AA253398 AI400823 AW294450 AI022396 AA907775
		BF445607 AA699324 AA025643 AW573103 AI167444 AA580002 AW103144 AI640654 AA857115 AA923021 AI066439 AI358865 AA843287 AI824604
		AA732370 AW002202 AI219540 AA621697 AI950639 AA904277 AI867527 BF437695 AA808593 AI784144 AI648539 AV752557 AV752603 AA025642
		AA767444 AW149075 N30700 H92303 W79523 AI762795 AA282784 H78923 AA252879 H98107 R23754 AA005152 N99239 N74632 H80133 H24710
		R38907 R66368 R42466 R52648 H11010 R98493
		NM_021724 M24898 X72631 BE550221 BF436030 F18898 AL567477 BG033127 BG747927 BF823716 AA371902 AL137978 AL577786 BI490529
		AA021622 AA151679 AA745053 AA454168 R85506 AA016015
		AI950320 AA340023
		AA908548
		NM_003312 BC010148 AK000862 D87292 BG709214 BF927266 BG740474 BI771592 BI159859 BI820468 BI523933 AI896664 AA314620 BF724353
		BC194276 BG195282 B1524679 BF435589 AI300546 AA481682 AW780207 AI800832 AI380540 BE222877 AW300707 AA481445 AW015893 AI381541
		AA768558 AI138798 AA432063 AA948713 AI869485 AI307419 AI336589 AI301672 BF055581 AI312785 AI521208 AI927918 AI989759 M78015
		BF178621 AI927654 AI795909 AI335381 BF334524 AW007444 AW067797 AA975178 AA884739 AA443837 AA933897 AI826464 AI271737 AA053419
		H79704 AI984483 BG952614 BF345358 AW083336 AA643660 AI478232 AA603071 BE714413 AW078660 AW070418 R02364 BG925951 AL568823
		AA053459 AA446748 BG954446 BF760569
		W74622 BF055071 AW135949 AI184884 AI393557 AI830476 AA416697 AI400728 AW183266 T83655 AW883367 AI963037 BF964042
		AI832243 AI742643 AW839701 AA888497
		BI517686 T89902 BI518252 AI659477 T89628 H22349
		AA132869 AA131111 AA053057
		AA505535
		AJ400845 AI954159 AL041618 AI028269 AA769325 AW780241 AW129462 AI271476 BF798303 AA836991 AW273346 AI436321 AI375545 AL040967
		AA889495 AI922524 AA598667 AA423804 AL040910 N80292 AI954063 AI923968 AI400578 AA748499 BE677845 AW020788 AA860230 AW519209
		AA767391 AI860419 AA476935 AW452389 AI017695 AA806940 BI497005 AI051533 AI650706 AI811516 AA609569 AI439198 BF430946 AA749268
		AI624860 AI784422 BI491753 AI206880 BE671796 AI431957 AI187038 AI678429 AI273421 AA897667 AA586499 BE241923 AF161081 NM_013440
		BE073169 AI700673 AV689908 AV684786 AV688081 AV689220 AV689216 AA132636 BF086186 BF917106 AV762653 BI064033 BE168145 AA778650
		AJ984255 W69468 AA132452 N53166 AI949278 AW158519 F26886 AA908333 F37181 BI002729

40	TABLE 64C:	
	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
45	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401203	9743387	Minus	172961-173056,173868-173928
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
402294	2282012	Minus	2575-3000
402845	9369286	Plus	160451-160617,160788-161009
403710	6437516	Plus	27413-28978
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
403593	6862650	Minus	62554-62712,69449-69602
400494	9714719	Plus	169845-170272
400835	8954121	Plus	89366-89622
401905	8671966	Plus	153965-154441,156599-156819
403180	7523976	Minus	63603-63759
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
403108	8980955	Plus	93253-93667
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402575	9884830	Minus	109742-109883
402338	6957691	Minus	36915-37250
401205	9743388	Plus	167373-167433,167936-168031
401192	9719502	Minus	69559-70101
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,8314
401131	8699812	Minus	94802-94987,95804-95887,96323-96487,9759
406467	9795551	Plus	182212-182958
403105	8980016	Minus	145287-145744
401429	8217890	Minus	86946-87579
402991	7631064	Minus	161294-161579
402956	9408727	Minus	135901-136035
406587	8189273	Minus	120577-120718
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
404175	9931117	Minus	107420-107547,109625-109796

TABLE 65A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN

Table 65A lists about 838 genes downregulated in benign nevi relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of normal skin AIs divided by the average of benign nevi AIs
 R2: 90th percentile of normal skin AIs divided by the average of benign nevi AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	
10	420813	X51501	Hs.99949	prolactin-induced protein	27.72	28.59
	408591	AF015224	Hs.46452	mammaglobin 1	26.40	28.34
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	21.33	21.57
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	18.06	18.96
15	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	16.61	18.06
	428087	AA100573	Hs.182421	troponin C2, fast	14.70	14.60
	407245	X90568	Hs.172004	titin	13.08	13.84
	428824	W23624	Hs.173059	ESTs	12.89	13.36
	428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin,	12.78	13.98
	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.26	9.86
20	453309	AI791809	Hs.32949	defensin, beta 1	12.02	10.62
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	11.90	10.86
	446227	AI281459	Hs.270114	ESTs	11.79	12.32
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	11.19	10.82
	432877	AW974111	Hs.292477	ESTs	11.18	11.30
25	426752	X69490	Hs.172004	titin	10.97	12.63
	427899	AA829286	Hs.332053	serum amyloid A1	10.85	13.85
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	451029	AA852097	Hs.25829	ras-related protein	10.78	10.35
	421296	NM_002666	Hs.103253	perilipin	10.73	11.25
30	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.66	7.24
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	10.57	9.92
	405121			mitogen-activated protein kinase 8 inter	10.41	10.54
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10.26	23.20
35	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	10.25	9.45
	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	10.15	9.88
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	10.13	11.58
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	10.09	5.51
	401203			Target Exon	9.95	10.74
40	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	9.94	11.47
	425580	L11144	Hs.1907	galanin	9.66	6.60
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	9.45	6.44
	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	10.49
	443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58
45	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.91	10.27
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	8.90	7.26
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	8.86	8.94
	417240	N57568	Hs.48028	EST	8.81	18.90
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	8.72	6.86
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (8.39	10.26
	408491	AI088063	Hs.7882	ESTs	8.00	8.20
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	7.99	8.14
	409738	BE222975	Hs.56205	insulin induced gene 1	7.95	7.75
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.89	8.86
55	451831	NM_001674	Hs.460	activating transcription factor 3	7.79	7.51
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	7.76	7.55
	444984	H15474	Hs.132898	fatty acid desaturase 1	7.75	5.64
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	7.68	5.65
	410532	T53088	Hs.155376	hemoglobin, beta	7.64	4.73
	442757	AI739528	Hs.28345	ESTs	7.62	7.66
60	412047	AA934589	Hs.49696	ESTs	7.61	7.48
	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.52	7.28
	439394	AA149250	Hs.56105	ESTs	7.52	6.72
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	7.51	6.27
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	4.10
65	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	8.08
	407334	AA494411	Hs.296031	ESTs	7.48	6.78
	414449	AA557660	Hs.76152	decorin	7.39	8.30
	432305	M62402	Hs.274313	insulin-like growth factor binding prote	7.38	8.79
70	407328	AA508857		ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.85
	445502	AW379160	Hs.12813	DKFZP434J214 protein	7.01	6.63
	419285	D31887	Hs.89868	KIAA0062 protein	7.01	5.82
	409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.99	4.58
75	422963	M79141	Hs.13234	ESTs	6.99	4.08
	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	6.98	6.49
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothei	6.95	8.08
	417993	AW963705	Hs.301183	molecule possessing ankyrin repeats indu	6.94	7.12
80	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	6.94	6.79
	427890	AA435761		ESTs	6.94	6.68
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.93	4.66
	442083	RS0192	Hs.165062	ESTs	6.92	6.92

5	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.87	5.07
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.87	4.99
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	6.84	5.33
	414841	H55601	Hs.77490	glutathione S-transferase theta 1	6.84	3.47
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	6.79	7.14
	427704	AW971063	Hs.292882	ESTs	6.72	7.30
	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.10
	451253	H48299	Hs.26126	claudin 10	6.71	7.20
10	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	6.68	3.02
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	6.08
	434625	W01370	Hs.46824	ESTs	6.61	6.92
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	6.55	6.79
15	411388	X72925	Hs.69752	desmocollin 1	6.55	3.44
	413731	BE243845	Hs.75511	connective tissue growth factor	6.52	4.86
	455863	AA907305	Hs.36475	ESTs	6.50	4.24
	412247	AF022375	Hs.73793	vascular endothelial growth factor	6.49	4.56
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	6.47	7.23
20	421407	T82331	Hs.182278	ESTs, Weakly similar to CGH06C collagen	6.47	8.55
	406867	AA157857	Hs.182265	keratin 19	6.44	6.23
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	446945	AI193115	Hs.16611	tumor protein D52-like 1	6.43	5.66
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
25	407395	AF005082		gb:Homo sapiens skin-specific protein (x	6.39	4.76
	450626	AW190989	Hs.1508	insulin-degrading enzyme	6.37	6.22
	450713	AL133611	Hs.25362	Homo sapiens mRNA; cDNA DKFZp43401317 (f	6.37	4.91
	437596	AA761490		ESTs, Moderately similar to S65657 alpha	6.35	5.31
	430191	AI149880	Hs.188809	ESTs	6.34	6.15
30	433713	AW976511	Hs.112592	ESTs	6.34	5.67
	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	6.33	6.39
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	6.33	5.77
	437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.30	5.45
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	6.29	6.68
35	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	6.28	10.35
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.21	5.98
	440116	AI798851		hemoglobin, gamma G	6.18	6.86
	454229	AW957744	Hs.278469	lactin-like protein rich protein	6.17	6.54
40	441188	AW292830	Hs.255609	ESTs	6.12	6.68
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	6.12	5.79
	431319	AA873350	Hs.302232	ESTs	6.11	7.91
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	6.10	5.63
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	6.08	6.96
	418321	D63477	Hs.84087	KIAA0143 protein	6.08	4.71
45	443072	AI937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	6.07	5.48
	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.04	5.81
	442679	R53718		hypothetical protein FLJ10659	6.03	5.67
	424824	AI217440	Hs.143873	ESTs	6.02	5.46
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.01	7.05
50	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	7.17
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	5.92	5.79
	424670	W61215	Hs.116651	epithelial V-like antigen 1	5.92	5.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypothe	5.91	6.81
	418205	L21715	Hs.83760	troponin I, skeletal, fast	5.91	6.95
55	400440	X83957	Hs.83870	nebulin	5.89	7.01
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	5.89	5.49
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	5.86	5.88
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	5.85	5.58
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	5.81	5.09
60	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	5.79	6.33
	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	5.78	5.91
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	5.78	3.74
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fs, clone C	5.76	4.21
65	408819	AW163483	Hs.48320	double ring-finger protein, Dorfin	5.71	4.59
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	5.70	4.71
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	5.68	6.12
	408515	AI289507	Hs.299883	hypothetical protein FLJ23399	5.67	4.81
	443827	AI087867	Hs.134667	ESTs	5.67	5.54
70	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	5.67	4.12
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	5.66	4.27
	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	5.65	4.52
	427081	AA474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !	5.65	4.81
	419731	S47242	Hs.92909	SON DNA binding protein	5.64	3.77
75	420787	AA564248		ESTs, Weakly similar to I38022 hypothe	5.64	3.27
	420682	AI380552	Hs.88602	ESTs	5.63	4.13
	410541	AA065003	Hs.64179	syntenin-2 protein	5.62	5.84
	431360	NM_009427	Hs.251680	loricrin	5.61	5.14
	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	5.61	4.28
80	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	5.51	16.04
	429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro	5.49	5.28
	422082	AA016188	Hs.111244	hypothetical protein	5.49	5.23
	419461	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	5.49	4.40

	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH	5.48	5.38
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	5.46	5.11
	400494			ENSP00000238970:ClG30 (Fragment),	5.45	3.63
5	415062	H45100	Hs.49753	uveal autoantigen with coiled coil domain	5.43	4.25
	449291	BE176893	Hs.23440	KIAA1105 protein	5.41	3.82
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.41	2.62
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
	434535	AI611729	Hs.167619	ESTs, Moderately similar to ALUC_HUMAN I	5.40	5.20
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	5.39	4.59
10	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	5.37	14.96
	436090	AI640635	Hs.332879	EST	5.37	5.33
	406805	AI686003	Hs.296031	ESTs	5.35	5.49
	426510	AW861225	Hs.251928	BANP homolog, SMAR1 homolog	5.35	6.83
15	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34	7.50
	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	5.34	4.88
	421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	5.34	4.75
	418479	AA829976		mannosidase, alpha, class 1A, member 2	5.34	3.59
	417059	AL037672	Hs.81071	extracellular matrix protein 1	5.34	4.71
20	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.34	4.75
	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	5.34	8.69
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.31	5.81
	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	5.30	4.35
	437135	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.29	4.92
25	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	5.29	5.02
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	5.28	5.33
	453999	BE328153	Hs.240087	ESTs	5.28	3.40
	408958	T99607	Hs.49346	signal recognition particle 54kD	5.28	2.84
	452496	AA114926	Hs.169531	ESTs	5.28	5.48
30	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	5.27	3.72
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	5.26	4.62
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	5.26	6.21
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	5.26	4.21
	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	5.26	4.43
35	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheri	5.25	5.61
	446267	AW450103	Hs.151124	ESTs	5.24	4.44
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.23	3.14
	448585	AB020676	Hs.21543	KIAA0869 protein	5.23	6.21
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	5.22	6.84
40	414407	AA147026	Hs.76704	ESTs	5.22	5.29
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	5.22	5.85
	415997	NM_003590	Hs.78946	culin 3	5.21	3.66
	411531	AB014511	Hs.70604	ATPase, Class II, type 9A	5.21	3.95
	441619	NM_014056	Hs.7917	DKFZP564K247 protein	5.20	4.38
45	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	5.19	4.52
	415167	AA160784	Hs.26410	ESTs	5.19	3.13
	431416	AA532718	Hs.178604	ESTs	5.18	5.38
	439995	AL137480	Hs.6834	KIAA1014 protein	5.17	3.14
	416784	AA334592	Hs.79914	lumican	5.17	6.18
50	446082	AI274139	Hs.156452	ESTs	5.16	5.14
	400196			Eos Control	5.16	5.05
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	5.16	4.31
	414242	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	5.15	4.89
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	5.14	5.22
55	440383	AA884208	Hs.30484	ESTs	5.13	5.09
	431628	AF146277		CD2-associated protein	5.13	5.03
	407047	X65965		gb:Hsapiens SOD-2 gene for manganese su	5.13	4.31
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.12	3.57
	437704	AA766142	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A	5.12	3.30
60	426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (tr	5.11	6.08
	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	5.10	4.31
	416382	D86985	Hs.79276	KIAA0232 gene product	5.10	3.79
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.10	6.58
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	5.09	4.82
65	434647	W74158	Hs.103189	lipopolysaccharide specific response-68	5.09	4.90
	418730	AA091027	Hs.325625	Homo sapiens clone 23938 mRNA sequence	5.09	3.46
	449338	H73444	Hs.394	adrenomedullin	5.09	6.26
	438962	BE046594		gb:hm41c11.x1 NCI_CGAP_RDF2 Homo sapiens	5.08	5.60
	431693	AI459519		serine (or cysteine) proteinase inhibito	5.07	2.83
70	420583	H77859	Hs.65450	reticulon 4	5.06	6.71
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	5.06	6.06
	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	5.05	6.32
	447945	AI922838	Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	3.72
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	2.86
75	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	5.03	4.43
	445263	H57646	Hs.42586	KIAA1560 protein	5.03	6.67
	448490	AI523897	Hs.271692	ESTs, Weakly similar to I38022 hypotheri	5.03	4.88
	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	5.03	4.36
	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	5.01	5.48
80	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	5.01	5.61
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	5.01	5.32
	413475	AW021488	Hs.26981	ESTs	5.01	3.90
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	5.00	4.54
	424074	AI902456	Hs.210761	ESTs, Weakly similar to I38022 hypotheri	5.00	3.19

5	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	4.99	6.25
	439039	AI656707	Hs.48713	ESTs	4.99	6.60
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.98	9.59
	410579	AK001628	Hs.64691	KIAA0483 protein	4.98	4.52
	449710	AA002207	Hs.17385	Homo sapiens clone IMAGE:119716, mRNA se	4.98	3.84
10	434230	AA551569		hypothetical protein PRO2822	4.98	3.63
	426468	AA379306	Hs.117558	ESTs	4.98	3.56
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	4.96	6.41
	448144	AW169230		ESTs, Moderately similar to PC4259 ferri	4.96	3.28
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.96	5.75
15	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ111174 fis, clone PL	4.96	3.21
	433934	AW273261	Hs.216292	ESTs	4.95	4.39
	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	4.95	4.01
	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	4.94	4.54
	453225	BE258769		acetyl-Coenzyme A acyltransferase 2 (mit	4.94	4.49
20	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	4.94	4.19
	445493	AI915771		metallothionein 1E (functional)	4.93	5.68
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	4.93	5.47
	417054	AF017060		aldehyde oxidase 1	4.93	4.51
	425917	W28517	Hs.117167	Homo sapiens cDNA: FLJ23067 fis, clone L	4.93	3.34
25	408681	AW953853	Hs.281462	ESTs, Weakly similar to I38022 hypothe	4.93	5.61
	451267	AI033894	Hs.117865	solute carrier family 17 (anion/sugar tr	4.92	3.27
	447137	AW970192	Hs.171942	ras responsive element binding protein 1	4.91	4.26
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	4.90	6.00
	432314	AA533447	Hs.312989	ESTs	4.90	3.79
30	440692	AL031591	Hs.73770	phosphatidylinositol transfer protein, b	4.89	3.71
	428594	BE387236	Hs.75415	beta-2-microglobulin	4.89	3.27
	437802	AI475995	Hs.122910	ESTs	4.87	4.06
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.86	6.54
	427156	BE621719	Hs.173802	KIAA0603 gene product	4.86	5.15
35	433179	AW362945	Hs.162459	ESTs	4.86	5.50
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	4.85	5.29
	453855	AA039576	Hs.37858	ESTs, Weakly similar to ALUB_HUMAN !!!	4.85	3.59
	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.85	3.45
	429279	AB018271	Hs.198689	KIAA0728 protein	4.83	3.80
40	445773	H73456	Hs.13299	Homo sapiens mRNA: cDNA DKF7p761M0111 (f	4.82	4.20
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.82	4.01
	408138	AA535740		tumor protein p53-binding protein, 1	4.81	4.19
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	4.80	3.99
	444677	AL110212	Hs.301005	purine-rich element binding protein B	4.80	3.50
45	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	4.80	10.20
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	4.79	4.39
	407839	AA045144	Hs.161566	ESTs	4.79	2.98
	421998	R74441		poly(A)-binding protein, nuclear 1	4.77	4.78
	416987	D86957	Hs.80712	KIAA0202 protein	4.76	3.99
50	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	4.76	7.59
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	4.75	4.38
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.75	3.92
	413276	Z24725	Hs.75260	mitogen inducible 2	4.75	5.68
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	4.74	5.57
55	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	4.74	11.58
	429587	AA283969	Hs.334706	Homo sapiens cDNA FLJ11801 fis, clone HE	4.74	3.79
	407242	M18728		gb:Human nonspecific crossreacting antig	4.73	4.88
	445229	BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	4.73	4.79
	447429	AB007920	Hs.18586	KIAA0451 gene product	4.72	2.38
60	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	5.10
	414848	AI803447	Hs.77496	small nuclear ribonucleoprotein polypept	4.71	2.51
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	4.70	6.13
	453145	R63438	Hs.183454	Homo sapiens cDNA FLJ14883 fis, clone PL	4.70	3.06
	421302	T34462	Hs.103291	neurtin	4.69	4.96
65	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.68	5.01
	448079	R76981		thyroid hormone receptor-associated prot	4.68	3.97
	434558	AW264102	Hs.39168	ESTs	4.67	3.42
	408239	AA053401		ESTs, Moderately similar to ALU7_HUMAN A	4.67	6.17
	454416	AI912097	Hs.163208	ESTs	4.66	3.97
70	427215	AW246148	Hs.268371	hypothetical protein FLJ20274	4.66	3.37
	451583	AI653797	Hs.24133	ESTs	4.65	3.81
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	4.65	6.14
	436176	AL121422	Hs.54900	serologically defined colon cancer antig	4.65	3.65
	450528	NM_014072	Hs.25063	PRO0461 protein	4.64	2.99
75	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	4.64	4.72
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	4.63	5.55
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	4.63	5.04
	436280	AI690734		Homo sapiens cDNA: FLJ22562 fis, clone H	4.63	3.55
	428744	BE267033	Hs.192853	ubiquitin-conjugating enzyme E2G 2 (homo	4.63	2.85
80	427007	NM_006283	Hs.173159	transforming, acidic coiled-coil contain	4.63	3.00
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.62	5.14
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	4.62	4.49
	409598	NM_014018	Hs.55097	mitochondrial ribosomal protein S28	4.62	3.56
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	4.62	4.24
	412577	Z22968	Hs.74076	CD163 antigen	4.61	8.03
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.61	6.86
	452289	BE568205	Hs.28827	mitogen-activated protein kinase kinase	4.61	4.33

5	458971	AL119206	Hs.101874	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.61	4.16
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypothe	4.61	3.58
	440595	H13032	Hs.103378	hypothetical protein MGC11034	4.61	3.22
	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (I	4.60	4.74
	424651	AI93206	Hs.32425	ESTs	4.60	4.11
10	436701	AW959032		ESTs, Moderately similar to I78885 serin	4.60	2.34
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	4.59	4.36
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.59	4.00
	436283	AI480319	Hs.120058	ESTs	4.59	3.76
	451710	AW867467	Hs.278712	eukaryotic translation initiation factor	4.59	3.51
15	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	4.59	3.64
	434697	AL133033	Hs.4084	KIAA1025 protein	4.58	5.10
	402294			Target Exon	4.57	5.47
	424098	AF077374	Hs.139322	small proline-rich protein 3	4.57	5.12
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.57	4.66
20	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	4.57	4.15
	441566	AA604110	Hs.151725	ESTs	4.57	3.21
	400109			Eos Control	4.56	4.76
	419740	AB037835	Hs.92991	KIAA1414 protein	4.56	3.63
	421481	AW391972	Hs.104696	KIAA1324 protein	4.55	7.16
25	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.55	4.44
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	4.55	4.36
	408702	AW958893	Hs.27099	hypothetical protein FLJ23293 similar to	4.54	5.78
	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.54	4.61
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	4.54	4.32
30	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	4.54	2.59
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	4.53	6.18
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	4.53	5.87
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	4.53	4.87
	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	4.53	10.61
35	452924	AW580939	Hs.97199	complement component C1q receptor	4.51	6.07
	454000	AA040620	Hs.5672	hypothetical protein AF140225	4.51	4.59
	404730			Target Exon	4.51	4.30
	449943	AF104266	Hs.24212	latrophilin	4.51	3.40
	414217	AI309258	Hs.275898	Homo sapiens cDNA: FLJ23165 fis, clone L	4.50	2.97
40	435992	AI033259	Hs.118317	Homo sapiens cDNA FLJ12088 fis, clone HE	4.50	4.77
	421311	N71848	Hs.283609	hypothetical protein PRO2032	4.50	3.30
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	4.49	5.06
	437611	AA897108		gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s	4.49	4.24
	419612	AI498267	Hs.110613	KIAA0421 protein	4.49	4.16
45	414496	W73853		ESTs	4.49	3.15
	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.48	3.38
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	4.47	4.45
	432559	AW452948	Hs.257631	ESTs	4.47	5.39
	442554	AW467376	Hs.129840	ESTs	4.47	4.00
50	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-li	4.46	4.47
	422313	AF045941	Hs.115166	scellin	4.45	5.07
	435748	AA699756	Hs.117335	ESTs	4.45	3.35
	453283	AA694386	Hs.290914	ESTs	4.45	3.28
	441925	R83113		protein kinase C substrate 80K-H	4.45	3.28
55	440030	AA932693		EST	4.45	3.20
	446515	AL048875		hypothetical protein DKFZp5661133	4.44	3.66
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	4.44	5.90
	432341	AL137662	Hs.274401	Homo sapiens mRNA; cDNA DKFZp434P086 (fr	4.44	3.99
	410453	AW749036		gb:RC2-BT0318-241199-011-f10 BT0318 Homo	4.44	3.49
60	450196	AW956868	Hs.24608	DKFZP564D177 protein	4.43	4.13
	444147	AB002306	Hs.10351	KIAA0308 protein	4.43	3.95
	427809	M26380	Hs.180878	lipoprotein lipase	4.42	3.88
	428157	AI738719	Hs.198427	hexokinase 2	4.42	5.46
	413299	AA857487	Hs.75275	ubiquitination factor E4A (homologous to	4.42	3.77
65	440245	AK001913	Hs.7100	hypothetical protein	4.42	3.51
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	4.42	1.79
	408569	BE066047	Hs.86412	chromosome 9 open reading frame 5	4.42	3.35
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	4.41	5.78
	414489	AI620677	Hs.73105	ESTs	4.41	5.43
70	447731	AA373527	Hs.19385	CGI-58 protein	4.41	5.28
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	4.41	4.41
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	4.41	3.68
	432546	BE618778	Hs.180638	hypothetical protein FLJ13081	4.41	3.55
	445620	AI245225	Hs.17441	ESTs	4.41	3.44
75	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sapiens c	4.41	3.43
	418802	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	4.40	2.04
	431816	T87431	Hs.190738	ESTs	4.39	4.26
	429138	AB020657	Hs.197298	NS1-binding protein	4.39	4.47
	426643	AA857131	Hs.171595	HIV TAT specific factor 1	4.39	3.09
80	448943	AI608810	Hs.193288	ESTs	4.39	2.63
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.37	19.16
	403593			Target Exon	4.37	6.35
	408104	AW972927	Hs.293968	ESTs	4.31	5.82
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.31	4.14
	429538	BE182592	Hs.139322	small proline-rich protein 2A	4.25	6.61
	414505	R45389	Hs.23558	ESTs, Weakly similar to A48042 lysosomal	4.18	5.28
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	4.18	5.81

5	426143	BE379836		proteasome (prosome, macropain) subunit,		
	414527	BE241739	Hs.76359	catalase	4.15	5.12
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	4.14	5.13
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	4.13	8.60
	412477	AA150864		microsomal glutathione S-transferase 1	4.12	5.94
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.10	10.00
	444252	R21135	Hs.54985	ESTs	4.09	5.39
	400295	W72838		ESTs	4.07	6.01
10	438746	AI885815	Hs.184727	AI905687:IL-BT095-190199-019 BT095 Homo	4.06	13.32
	429856	AA971576	Hs.225951	Human melanoma-associated antigen p97 (m	4.06	7.57
	422168	AA586894	Hs.112408	topoisomerase-related function protein 4	4.05	6.24
	403710			S100 calcium-binding protein A7 (psorias	4.01	4.61
	406643	N77976	Hs.347939	C4000160:gil12735793[refXP_011928.1] pr	4.00	4.06
15	436372	AW972301	Hs.310286	hemoglobin, alpha 2	3.97	7.22
	426340	AF261088	Hs.154721	ESTs	3.96	5.41
	424604	AW865388	Hs.151076	aconitase 1, soluble	3.94	5.33
	426653	AA530892	Hs.171695	KIAA1243 protein	3.91	7.59
	410204	AJ243425	Hs.326035	dual specificity phosphatase 1	3.91	14.81
20	448520	AB002367	Hs.21355	early growth response 1	3.87	9.96
	443021	AA368546	Hs.8904	doublecortin and CaM kinase-like 1	3.87	5.09
	430418	R98852	Hs.36029	Ig superfamily protein	3.86	7.65
	447796	AW953622	Hs.223025	heart and neural crest derivatives expre	3.81	6.19
	419407	AW410377	Hs.41502	RAB31, member RAS oncogene family	3.76	5.10
25	443725	AW245680	Hs.3701	hypothetical protein FLJ21276	3.76	5.12
	426281	AK000987	Hs.169111	growth arrest and DNA-damage-inducible,	3.75	5.46
	423973	AF038461	Hs.136574	oxidation resistance 1	3.74	5.14
	445234	AW137636	Hs.146059	arachidonate 12-lipoxygenase, 12R type	3.74	6.30
	457411	AW085961	Hs.130093	ESTs	3.72	5.59
30	456063	NM_006744	Hs.76461	iroquois-class homeobox protein IRX2	3.71	4.85
	413880	AI660842	Hs.110915	retinol-binding protein 4, interstitial	3.71	6.72
	422640	M37984	Hs.118845	interleukin 22 receptor	3.71	4.01
	452241	AL050204	Hs.28540	troponin C, slow,	3.71	9.10
	453560	AA348626	Hs.5890	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	3.70	3.21
35	410197	NM_005518	Hs.59889	hypothetical protein FLJ23306	3.69	5.13
	413922	AI535895	Hs.221024	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.69	7.69
	426698	AA852773	Hs.334838	ESTs	3.68	4.80
	451951	AW082870	Hs.210954	KIAA1866 protein	3.64	5.22
	452308	AI167560	Hs.61297	ESTs	3.64	3.69
40	441128	AA570256		ESTs	3.64	4.35
	421978	AJ243652	Hs.110196	ESTs, Weakly similar to T23273 hypotheti	3.63	2.91
	418533	NM_004533	Hs.85937	NICE-1 protein	3.61	6.05
	452413	AW082633	Hs.215030	myosin-binding protein C, fast-type	3.61	6.22
	453003	AA808466	Hs.103395	ESTs	3.58	3.03
45	408522	AI541214	Hs.46320	hypothetical protein FLJ14146	3.55	6.39
	423503	M92843	Hs.343586	Small proline-rich protein SPRK (human,	3.54	10.68
	419879	Z17805	Hs.93564	zinc finger protein homologous to Zfp-36	3.53	15.11
	428382	AF007132	Hs.184019	Homer, neuronal immediate early gene, 2	3.53	5.29
	447165	AL042400	Hs.75668	Homo sapiens clone Z3551 mRNA sequence	3.51	4.46
50	418067	AI127958	Hs.83393	Homo sapiens, Similar to RIKEN cDNA 1700	3.51	3.67
	420202	AL036557	Hs.95910	cystatin E/M	3.51	3.74
	432543	AA552690	Hs.152423	putative lymphocyte G0/G1 switch gene	3.50	14.64
	442321	AF207664	Hs.8230	Homo sapiens cDNA: FLJ21274 fis, clone C	3.50	2.79
	450860	AA021007		a disintegrin-like and metalloprotease (3.48	7.91
55	414665	AA160873		integrin, beta 8	3.47	5.89
	413663	BE247585	Hs.75462	serum amyloid A1	3.46	9.22
	427408	AA583206	Hs.2156	BTG family, member 2	3.46	5.63
	430171	AF086289	Hs.234766	RAR-related orphan receptor A	3.45	3.08
	453655	AW960427	Hs.342874	skin-specific protein	3.45	4.77
60	450607	AL050373	Hs.25213	transforming growth factor, beta recepto	3.42	8.09
	412596	AA161219	Hs.799	hypothetical protein	3.41	6.43
	427681	AB018263	Hs.180338	diphtheria toxin receptor (heparin-bindi	3.41	6.10
	440590	AI863446	Hs.266308	tumor necrosis factor receptor superfam	3.39	6.59
	452669	AA216363	Hs.262958	mosaic serine protease	3.34	3.09
65	422101	AW404176	Hs.111611	hypothetical protein DKFZp434B044	3.31	10.06
	431986	AA536130	Hs.149018	ribosomal protein L27	3.30	3.93
	412649	NM_002206	Hs.74369	Novel human gene mapping to chromosome 20	3.30	3.54
	423017	AW178761	Hs.227948	integrin, alpha 7	3.28	6.89
	425163	D10040	Hs.154890	serine (or cysteine) proteinase inhibito	3.28	5.44
70	412061	AA833763	Hs.330211	fatty-acid-Coenzyme A ligase, long-chain	3.28	5.93
	437592	NM_003851	Hs.5710	ESTs	3.27	5.75
	452849	AF044924	Hs.30792	cellular repressor of E1A-stimulated gen	3.27	5.83
	421462	AF016495	Hs.104624	hook2 protein	3.26	5.66
	422083	NM_001141	Hs.111256	aquaporin 9	3.25	4.98
75	444935	AA262449	Hs.223569	arachidonate 15-lipoxygenase, second typ	3.24	6.56
	422057	AI205785	Hs.30348	ESTs	3.24	5.96
	410017	AW952426	Hs.109438	ESTs	3.22	5.72
	407948	AW085161	Hs.56279	Homo sapiens clone 24775 mRNA sequence	3.21	5.26
	452089	T97294	Hs.271492	ICEBERG caspase-1 inhibitor	3.21	4.61
	448249	AW855331	Hs.337124	ESTs, Weakly similar to PC4211 hepatocel	3.19	4.42
80	430869	D10511	Hs.37	ESTs	3.18	2.97
	443623	AA345519	Hs.9641	acetyl-Coenzyme A acetyltransferase 1 (a	3.17	5.66
	452865	AI924046	Hs.119567	complement component 1, q subcomponent,	3.16	12.00
	452392	L20815	Hs.507	ESTs, Weakly similar to A47582 B-cell gr	3.16	6.03
				comedodermosin	3.15	5.70

5	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	3.15	5.87
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.15	4.98
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	3.13	17.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.12	4.63
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.12	3.02
10	432375	BE536069	Hs.2962	S100 calcium-binding protein P	3.12	8.51
	417713	D42047	Hs.87432	KIAA0089 protein	3.12	5.82
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	3.11	6.51
	444195	AB002351	Hs.10587	KIAA0353 protein	3.11	5.44
	415704	NM_001677	Hs.78629	ATPase, Na ⁺ transporting, beta 1 polypep	3.11	6.61
15	401905			ENSP0000025232: Slerol regulatory eleme	3.10	3.52
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.10	5.10
	427095	AA316080	Hs.173554	ubiquinol-cytochrome c reductase core pr	3.10	5.39
	413835	AI272727	Hs.249163	fatty acid hydroxylase	3.08	5.56
	448106	AI800470	Hs.171941	ESTs	3.07	5.19
20	432908	AI861896		ESTs	3.07	3.47
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.07	7.48
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05	3.97
	449498	U58515	Hs.154138	chitinase 3-like 2	3.02	6.75
	419358	T78763	Hs.90063	neurocalcin delta	3.00	7.68
25	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.99	5.44
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	2.99	6.84
	450472	AI190071	Hs.55278	ESTs	2.98	5.06
	421335	X99977	Hs.103505	ARS component B	2.97	9.31
	431316	AA502663	Hs.145037	ESTs	2.96	4.30
30	420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.96	2.97
	451176	AA046457	Hs.60677	ESTs	2.95	6.59
	444204	AI129194	Hs.143040	ESTs	2.93	3.92
	435723	AW975895	Hs.307486	ESTs	2.93	6.64
	436664	AW197887	Hs.253353	ESTs	2.93	3.82
35	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	3.10
	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed in	2.93	5.35
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	2.91	9.84
	430310	U60115	Hs.239069	four and a half LIM domains 1	2.91	7.02
	420876	AA918425	Hs.177744	ESTs	2.91	5.41
40	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	2.91	5.64
	428232	BE272452	Hs.183109	monoamine oxidase A	2.90	9.54
	413796	AW408094	Hs.75545	interleukin 4 receptor	2.89	5.37
	413884	AI668892	Hs.239758	hypothetical protein FLJ12389 similar to	2.88	5.34
	411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	2.86	6.31
45	428500	AI815395	Hs.184541	fatty acid desaturase 2	2.86	3.93
	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	2.86	6.05
	452689	F33868	Hs.284176	transferrin	2.85	6.11
	403108			ENSP00000241415: Hypothetical 67.7 kDa p	2.85	3.17
	434433	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
50	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.83	4.05
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	3.57
	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase [human, adipo	2.82	3.80
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.82	6.40
	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	2.82	2.97
55	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.81	5.15
	415409	AW993701		NS1-associated protein 1	2.80	6.16
	433848	AF095719	Hs.93764	carboxypeptidase A4	2.80	2.88
	425750	AL050276	Hs.42400	zinc finger protein 288	2.79	5.99
	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIc	2.78	5.25
60	429128	AA446869	Hs.119316	ESTs	2.78	4.17
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.77	7.37
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.76	6.09
	419923	AW081455	Hs.120219	ESTs	2.76	4.31
	407555	Z48511		gb:H.sapiens XG mRNA (clone PEP11).	2.76	4.12
65	425240	AA306495	Hs.1869	phosphoglucomutase 1	2.74	5.92
	459317	BRCA1b		Eos Control	2.74	19.85
	425819	N92165	Hs.93231	ESTs	2.74	5.72
	408839	AW277084		gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.73	3.93
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	2.72	5.94
70	409453	AI885516	Hs.95612	ESTs	2.72	6.51
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	2.72	3.80
	420074	AA253425	Hs.190074	ESTs	2.71	4.04
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.71	2.84
	444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.71	6.17
75	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.70	5.23
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	2.69	5.33
	419098	AA234041	Hs.87271	ESTs	2.69	3.22
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	2.69	6.64
	443102	AI247472	Hs.132965	ESTs	2.68	5.85
80	411939	AI365585	Hs.146246	ESTs	2.68	5.38
	453201	AI432195	Hs.135098	ESTs	2.68	3.69
	420231	R06866	Hs.19813	ESTs	2.67	4.70
	404996			Target Exon	2.67	4.97
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.66	6.36
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	2.65	15.65
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	2.65	7.74
	444169	AV648170	Hs.58756	ESTs	2.64	3.40

	431247	AL021578	Hs.278489	matrilin 4		
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	2.64	3.35
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbhBst Homo	2.63	5.12
5	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.63	4.08
	440924	AF151872	Hs.7527	small fragment nuclease	2.61	6.44
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.59	6.37
	425320	U29344	Hs.83190	fatty acid synthase	2.59	6.46
	402315			NM_003430:Homo sapiens zinc finger prote	2.59	3.93
10	449539	W80363	Hs.58446	ESTs	2.58	6.09
	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	2.58	4.05
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.58	5.61
	438752	AW238673	Hs.146038	ESTs	2.58	3.54
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.57	5.24
15	438763	AI583207	Hs.99029	CCAA1/enhancer binding protein (C/EBP),	2.57	5.16
	413630	AL036883	Hs.75450	delta sleep inducing peptide, immunoreac	2.57	6.45
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT	2.56	6.38
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.56	2.90
	426403	NM_000361	Hs.2030	thrombomodulin	2.56	2.67
20	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog	2.56	5.19
	420924	R01026	Hs.245321	ESTs	2.55	5.62
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	2.55	3.22
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	5.45
	445437	AI224165	Hs.148725	ESTs	2.55	4.50
25	425097	NM_014247		PDZ domain containing guanine nucleotide	2.54	4.72
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.54	5.28
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	6.55
	408896	AI610447	Hs.48778	niban protein	2.53	2.84
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	2.53	7.08
30	420235	AA256756	Hs.31178	ESTs	2.52	8.68
	436314	AI983409		ESTs	2.51	4.21
	440602	AI743491	Hs.292692	ESTs	2.51	3.11
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.50	2.71
35	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	2.48	2.86
	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	5.37
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	2.48	3.21
	421811	AA022550	Hs.108548	PABP-interacting protein 2	2.48	7.88
	414420	AA043424	Hs.76095	immediate early response 3	2.48	5.28
40	420693	NM_001972	Hs.99863	elastase 2, neutrophil	2.47	8.33
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	2.47	2.78
	447179	AW015633	Hs.157299	ESTs	2.46	10.12
	451687	AL041260	Hs.25837	Homo sapiens mRNA: cDNA DKF2p586K1123 (f	2.46	3.45
	420322	AB014555	Hs.96731	huntingtin interacting protein-1-related	2.46	5.47
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.45	6.18
45	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	2.45	5.75
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.45	6.73
	439639	AA370045	Hs.6607	AXIN1 up-regulated	2.44	10.55
	436009	H57130	Hs.120925	ESTs	2.44	5.22
	414814	D14697	Hs.77393	farnesyl diphosphate synthase (farnesyl	2.44	2.94
50	434060	AA744902	Hs.197922	hypothetical protein PRO1489	2.43	5.17
	425335	BE394327	Hs.296267	folistatin-like 1	2.43	5.56
	406997	U07807		metallothionein IV	2.43	10.52
	431545	AF095703	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase	2.42	4.35
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	2.42	6.72
55	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fs, clone PL	2.41	5.22
	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.41	5.56
	448954	AB014564	Hs.22616	KIAA0664 protein	2.41	5.24
	447218	BE617762	Hs.10748	hypothetical protein DKF2p434B195	2.40	5.31
60	423810	AL132665	Hs.132955	BCL2/adenovirus E1B 19kD-interacting pro	2.40	5.24
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.39	5.55
	430356	N87990	Hs.239870	Homo sapiens mRNA: cDNA DKF2p564H0764 (f	2.39	7.63
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	2.38	5.99
	416273	AW575691	Hs.79123	KIAA0084 protein	2.38	3.84
	427272	NM_001096	Hs.174140	ATP citrate lyase	2.38	5.22
65	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	2.38	5.41
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	2.35	5.13
	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.33	5.81
	418400	BE243026	Hs.301989	KIAA0246 protein	2.33	7.89
	456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.33	5.36
70	407082	Z47055		gb:Human partial cDNA sequence, farnesyl	2.32	3.27
	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	2.31	4.65
	408536	AW381532	Hs.135188	ESTs	2.31	9.37
	410552	XG6945	Hs.748	fibroblast growth factor receptor 1 (fms	2.31	2.60
	437201	F29279	Hs.171625	hypothetical protein MGC14697	2.30	5.94
75	417314	N68168		gb:za11c01.s1 Soares fetal liver spleen	2.30	5.75
	433738	AI684802		ESTs	2.30	3.12
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.30	3.91
	422491	AA338548	Hs.117546	neurotatin	2.29	3.61
	434411	AA632649	Hs.201372	ESTs	2.29	5.66
80	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.28	4.40
	401131			NM_001651:Homo sapiens aquaporin 5 (AQP	2.28	5.14
	401205			Target Exon	2.27	5.62
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.27	2.98
	456646	AJ243662	Hs.110196	NICE-1 protein	2.26	3.94
					2.26	2.52

	443049	AI028613	Hs.132343	ESTs	2.25	3.13
	440160	BE560269	Hs.7010	NP0002 protein	2.25	4.93
	436367	N79688	Hs.204354	ras homolog gene family, member B	2.25	9.58
5	442987	AA075975		Homo sapiens clone TCCIA00427 mRNA sequ	2.24	6.19
	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	2.24	2.58
	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	2.23	9.03
	450014	N41322	Hs.18441	ESTs	2.23	4.50
	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	2.22	5.64
10	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske	2.22	5.57
	427569	BE299197	Hs.179665	cyclin-dependent kinase inhibitor 1A (p2	2.22	5.10
	444637	T19101	Hs.11494	fibulin 5	2.22	6.43
	406710	AI708347	Hs.184014	ribosomal protein L31	2.21	9.10
	424909	S78187	Hs.153752	cell division cycle 25B	2.20	6.13
15	407228	M25079	Hs.155376	hemoglobin, beta	2.20	11.34
	450612	AL359946	Hs.14779	acetyl-CoA synthetase	2.20	7.03
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothei	2.20	5.68
	407370	AA682384	Hs.182084	ESTs	2.20	7.00
	438942	AW875398	Hs.6451	PRO0659 protein	2.19	6.09
20	400228			NM_021724: Homo sapiens nuclear receptor	2.19	6.95
	410185	BE294068	Hs.737	immediate early protein	2.18	11.72
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polype	2.17	7.05
	400307	AF005081		Homo sapiens skin-specific protein (xp32	2.17	6.41
	424425	AB031480	Hs.146824	SPR1 protein	2.17	3.68
25	414459	Y11525	Hs.76171	CCAA1/enhancer binding protein (C/EBP),	2.17	3.11
	400082			Eos Control	2.16	8.40
	434702	AL039734	Hs.4099	nardilysin (N-arginine diabolic convertas	2.16	6.83
	439651	AF086480	Hs.56255	ESTs	2.16	3.72
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.15	3.34
30	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	2.14	6.20
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	2.14	3.42
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	2.14	9.81
	434454	AF217798	Hs.3850	US1-interacting protein NUDEL; endocyt	2.14	6.75
	452467	AW500815		ESTs	2.13	4.66
35	418226	AA424202	Hs.83834	cytochrome b-5	2.13	5.41
	414815	AW292140	Hs.130286	ESTs	2.12	4.14
	430967	H16791	Hs.100895	ESTs	2.12	4.14
	426102	AF200496	Hs.166371	interleukin 1, zeta	2.12	3.77
	410223	S73775	Hs.60708	cathepsin 1 (fast-twitch, skeletal m	2.11	5.30
40	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.11	4.01
	427228	AA115770	Hs.174051	small nuclear ribonucleoprotein 70kD pol	2.10	5.13
	436961	AW375974	Hs.156704	ESTs	2.10	3.33
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.10	8.13
	445831	NM_006055	Hs.13351	LanC (bacterial antibiotic synthetase c	2.08	5.42
45	431593	NM_002108	Hs.276590	ESTs	2.08	4.43
	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.92
	424389	AA339786		lymphocyte-specific protein 1	2.07	5.52
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.06	5.93
	400198			Eos Control	2.05	10.48
50	426335	AI054347	Hs.2017	ribosomal protein L38	2.04	5.57
	443652	AI080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	2.04	3.36
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.02	3.32
	443932	AW888222	Hs.9973	tensin	2.02	9.28
	421324	BE257515	Hs.103503	deoxyribonuclease I-like 2	2.02	5.71
55	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.01	5.49
	410669	AW805749		superoxide dismutase 2, mitochondrial	2.01	3.05
	446193	AI279390	Hs.144658	ESTs, Weakly similar to T17257 hypothei	2.01	2.77
	400078			Eos Control	2.00	11.41
	456267	AI127958	Hs.83393	cystatin E/M	1.99	3.59
60	413125	BE244589	Hs.75207	glyoxalase I	1.98	6.70
	415433	W70067	Hs.58066	ESTs	1.98	5.59
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.52
	417553	L09190		trichothyalin	1.98	3.39
	403105			Target Exon	1.98	5.05
65	414081	AW969976		matrix Gla protein	1.97	8.74
	422639	AI929377	Hs.173724	creatine kinase, brain	1.97	5.51
	452208	AA024792	Hs.31895	hypothetical protein MGC4093	1.97	5.67
	436106	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	1.97	5.75
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	1.96	5.09
70	430037	BE409649	Hs.227789	mitogen-activated protein kinase-activat	1.96	5.49
	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.95	5.95
	417088	M54915	Hs.81170	pim-1 oncogene	1.95	8.19
	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	1.95	5.19
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.95	6.78
75	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.94	5.98
	414860	BE255593	Hs.77502	methionine adenosyltransferase II, alpha	1.94	5.13
	437220	AL117542	Hs.334305	GS1999tuf	1.94	3.42
	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	1.94	5.66
	424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.93	5.28
80	413945	NM_000591	Hs.75627	CD14 antigen	1.93	5.38
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93	5.75
	415988	BE407713	Hs.78943	bleomycin hydrolase	1.92	4.65
	425783	AI026740	Hs.1948	ribosomal protein S21	1.92	9.79
	431476	BE612705	Hs.256697	histidine triad nucleotide-binding prote	1.91	7.00

	456653	AJ807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.41
	401846			NM_000988*:Homo sapiens ribosomal protein	1.91	5.62
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	4.00
5	400199			Eos Control	1.89	15.74
	429367	AB007867	Hs.278311	plexin B1	1.88	5.58
	400083			Eos Control	1.88	9.07
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	1.88	5.16
	400079			Eos Control	1.87	8.57
10	411807	AK000290	Hs.44033	dipeptidyl peptidase 8	1.86	5.19
	409178	BE393948	Hs.50915	kallikrein 5	1.85	2.75
	422624	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.85	5.33
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membrane protei	1.85	6.01
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.84	2.82
15	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	1.83	5.10
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.83	6.48
	439927	AA854650	Hs.124597	ESTs	1.82	3.63
	415089	N25117	Hs.299465	ribosomal protein S26	1.82	6.69
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	1.82	2.95
20	406467			Target Exon	1.79	2.65
	426672	AW270555	Hs.171774	hypothetical protein	1.79	5.24
	414088	AW797956	Hs.75748	proteasome (prosome, macropain) subunit,	1.78	6.02
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	1.78	5.92
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.77	5.44
25	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.77	5.79
	425603	W92517	Hs.158203	actin binding LIM protein 1	1.77	9.27
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.77	5.44
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	1.77	6.97
	431021	AI869664		thiosulfate sulfurtransferase (rhodanese	1.77	5.23
30	432891	AF161483	Hs.279761	HSPC134 protein	1.75	5.73
	432872	AI908984	Hs.279623	selenoprotein X, 1	1.75	5.72
	451335	AB023192	Hs.26285	imidazoline receptor candidate	1.75	6.87
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase	1.74	3.01
	417824	AA084798	Hs.82646	DnaJ (Hsp40) homolog, subfamily B, membe	1.74	5.75
35	439908	AI168031	Hs.155507	ESTs	1.74	2.63
	427349	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	1.74	6.80
	446919	T53519	Hs.334692	hypothetical protein MGC14141	1.74	5.65
	427391	W60675		hypothetical protein FLJ10350	1.73	6.13
	425299	AW505214	Hs.155560	cathexin	1.73	5.88
40	430449	AA352723	Hs.241471	RNB6	1.72	5.14
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	1.71	4.35
	407694	U77594	Hs.37682	retinoic acid receptor responder (lazar	1.71	6.16
	412374	X01388	Hs.73849	apolipoprotein C-III	1.70	5.18
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	1.70	7.46
45	410584	AB011112	Hs.64742	KIAA0540 protein	1.69	6.19
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.68	2.63
	441379	AW175787	Hs.334841	selenium binding protein 1	1.67	7.42
	422115	AI878953	Hs.111811	microsomal glutathione S-transferase 3	1.67	6.93
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	1.66	6.26
50	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon/Ita	1.65	5.83
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.65	7.54
	446623	AF279865	Hs.15711	kinesin family member 13B	1.65	5.36
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.65	12.30
	402022			NM_002795*:Homo sapiens proteasome (pros	1.64	5.70
55	401429			C14001067:gi4126465[dbj]BAA36581.1[AB	1.64	3.82
	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.62	5.95
	410169	AJ373741	Hs.59384	hypothetical protein MGC3047	1.61	6.60
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.60	11.13
	453027	AJ879341	Hs.539	ribosomal protein S29	1.60	10.97
60	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.60	5.90
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.57	5.60
	400201			NM_006156*:Homo sapiens neural precursor	1.57	5.32
	407049	X72632		NM_021724*:Homo sapiens nuclear receptor	1.57	5.42
65	430775	AI879186	Hs.250895	ribosomal protein L34	1.57	7.09
	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	1.56	5.37
	407143	C14076	Hs.332329	EST	1.56	6.54
	436127	W94824	Hs.11565	RIKEN cDNA 2010100O12 gene	1.56	6.35
	413659	BE155647		gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.55	5.96
70	445624	AW140103	Hs.78880	livB (bacterial acetolactate synthase)-I	1.55	4.09
	435044	NM_002802	Hs.4745	proteasome (prosome, macropain) 26S subu	1.55	5.71
	410397	AF217517	Hs.63042	DKFZp564J157 protein	1.54	5.14
	429071	AW794126	Hs.195453	ribosomal protein S27 (metalloproteinstimuli	1.54	8.70
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	1.54	6.57
	446429	AI681807	Hs.201391	ESTs	1.53	2.87
75	414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, short chain,	1.53	6.07
	406801	AW242054	Hs.190813	ribosomal protein L9	1.52	5.63
	437895	AB014568	Hs.5898	KIAA0668 protein	1.51	5.74
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.51	6.40
	425456	T70445	Hs.157850	ribosomal protein L9	1.51	7.08
80	409635	Z37166	Hs.55296	HLA-B associated transcript-1	1.50	5.26
	404467			Target Exon	1.50	5.82
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	1.50	5.25
	454098	W27953	Hs.292911	Plakophilin	1.48	3.14
	429205	AI492393	Hs.198248	UDP-Gal:betaGalNAc beta 1,4- galactosylt	1.48	6.24

5	413825	BE299181	Hs.75564	CD151 antigen	1.47	5.64
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing le	1.45	6.19
	440254	AI879332	Hs.7101	anaphase-promoting complex subunit 5	1.45	5.50
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.42	11.24
	423513	AF035960	Hs.129719	transglutaminase 5	1.42	3.18
	406896	D00159		gb:Homo sapiens gene for pancreatic elas	1.41	6.92
	433453	BE548307	Hs.3297	ribosomal protein S27a	1.40	5.38
	406800	AA505535		gb:nh84h10.s1 NC1_CGAP_Br1.1 Homo sapien	1.37	5.51
10	421748	NM_014718	Hs.107809	KIAA0726 gene product	1.37	5.46
	424372	AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fls, clone HE	1.36	4.06
	408250	R92918	Hs.19597	KIAA1694 protein	1.27	2.74
	41931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.65
	406587			C15000544:gi5454148[ref]NP_006368.1 U	1.06	3.11
15	409574	AW419080	Hs.250645	ESTs	1.00	3.60
	404175			Target Exon	1.00	3.08
	452640	AA027115	Hs.100206	ESTs, Weakly similar to A53856 aryl-acyl	1.00	2.82
	443564	AI921685	Hs.199713	ESTs	1.00	2.51

TABLE 65B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

20	Pkey	CAT Number	Accession
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			AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430
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			AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096
			R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970
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45	443072	449629_1	AV734838 AI937532 AI032318 AW749500 AA091720
	442679	31783_3	BG621493 BI056706 BG496376 R53718 W65356 R79357 BG434247 AA357769 AW978686 BG573200 BF132113 BF086709 AA366938 D79234
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35 BG567713 AW665841 AI814924 AW978339 AW264036 AI373950 AW183157 AW082249 AI201658 AI364196 AA150743 AA160873 AA453757
BF871646 BF871640 AA565311 AA589511 R10152 AA807154 T77900 AV751591
AF150424 AI861896 AA570057 AV738855
40 AA633408 AW749955 AW629759 AI651005
AK056188 BM455117 BG527027 AA480032 AW993701 AA164703 AI537682 AA836491 AA515961 AL537681 BF437856 AA683484 AW152367
AI769509 AA907521 AW105404 AI521557 AA870165 AI564471 N22106 AA479060 AI472006 AA164704 N30335 AI224391 AA969890 BE856571
AI284716 AA918763 AA773661 BG942266 AA507486 AI934383 AA502847 AA516351 AA653124 AI360432 R75834 AA636111 AI972795 BI870444
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AW972670 AA525808 H28359 H28383
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W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103
AA400024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634
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NA
N68168 N69188 N90450
AL037666 AW607643 AI280025 AL037665 AW291619 AI280142 AA765506 AI684802 AW085941 AI688062
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BG113250 N99606 AA312166 BF696463 D61610 AV757976 AA092342 BE972583 BG776159
NM_021724 M24898 X72631 BE550221 BF436030 F18898 AL567477 BG033127 BG747927 BF823716 AA371902 AL137978 AL577786 BI490529
60 AA021622 AA151679 AA745053 AA454168 R85506 AA016015
AF005081 BG193848
AA026381 AW500815 AI806691 AW502933 AW303573 BE328059 AI201422 BE673566 AW182125 H13705
AF086341 W76326 W72300
65 BG190758 AW961118 W77994 AA339877 AW845121 AW845129 BG181820 BE716719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786
BE838286 BE838282 BE716636 AA777158 W94063 BE716628 BE716625 BE838371 BF371044 BE716631 BE716402
AF005081 BG193848
AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
70 AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878
AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749
AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041
AA987847 AA983329 AA737219 AA916443 AW128994 AI92560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530
BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631
AI423041 AW071181 AI898936 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI080799 BE083097 BG896220 AW997681 BF668788
BE083124 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AI415584 AA836749 AA836844
AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151
AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459
BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI56165 AA484893 AA643953 AW591063 BG203275 BG211093
AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785 BG219510 BG201686 BG195572 AW019904
AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 AW023542 AA827300 AA582214 AI701289 AA228293 AI906950
75 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097
AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798
80 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215

428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI258661 NM_003312 BC010148 AK000862 D87292 BG709214 BF972766 BG740474 BI771592 BI159859 BI820468 BI523933 AI869664 AA314620 BF724353 BG194276 BG195282 BI524679 BF435589 AI300546 AA481682 AW780207 AI800832 AI380540 BE222877 AW300707 AA481445 AW015893 AI381541 AA768558 AI138798 AA432063 AA948713 AI869485 AI307419 AI336589 AI301672 BF055581 AI312785 AI521208 AI927918 AI989759 M78015 BF718621 AI927654 AI795909 AI335381 BF334524 AW007444 AA706797 AA975178 AA884739 AA443837 AA933897 AI826464 AI271737 AA053419 H79704 AI984483 BG952614 BF345358 AW083336 AA643660 AI478232 AA603071 BE714413 AW078660 AW070418 R02364 BG925951 AL568823 AA053459 AA446748 BG954446 BF760569 AY007099 AU150467 AI127583 BE735800 AI125772 AI373009 AI215670 AI769136 AA586848 AW451158 N50799 AA936337 AI355427 BE677905 AW338020 BG151557 AA657954 AI754947 AW467279 AI128755 BF448136 AI369247 BF439175 BE207948 AI089272 B911455 AA420720 F36980 AI494204 AA953319 AA155753 AI052675 AA044804 AI282678 BG741226 F25798 AA180204 AI682613 AI0152630 AA420766 AI373393 AI885767 T03896 BF939430 AA974325 AW072996 AW005963 BG252471 AI192002 AI918908 AA776144 BI834864 AI753954 BE908511 AW628731 AA034958 BF447074 AW194549 AI915192 AL567164 BF691569 AL565970 AW471137 AW276992 AL536717 BF591783 AI571746 BF939172 BG745029 BG575588 BI054960 H51485 AW799491 AI370437 H26413 AA585334 AU151276 AA074274 AA936883 AW131643 AI221650 AW105476 AW952294 H23835 BI035010 F22360 BF849322 BE873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 BF972860 BG119842 BI094093 AL538757 BE271653 BI856538 BE90573 BG109826 BE784430 BE899255 BI833973 BM010809 BE621321 BG684956 BE904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 BG472870 BE393697 N28533 AA316042 N42043 AW404246 AW892094 AA379896 AW801110 AW406977 AA379791 BG941889 BE076254 AA360459 AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AA494241 W32225 BF745937 AI383690 BG202360 NM_006156 D23662 BF038671 BI670321 BI603145 BI666956 BG176628 BG707476 BG768814 BE312007 BF125930 BF037916 BG942671 AI752472 AW009362 BE379126 BI198555 BF126026 N28289 BE388301 BG327102 AI571450 BF038400 AI884649 AI718962 AI742314 AA977058 AI150699 BG944784 AA187402 BG283893 AV712007 W01301 BG774109 W77840 C15672 BI670016 AI752473 AA484409 C14921 N41745 C15220 F30164 AA133181 BF768974 H30334 AA034968 AA384232 AA353297 AW407023 AA337516 F36177 AA374444 AA402758 AI41545 BI021470 AA973914 BE155647 BE155627 AA505535
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TABLE 65C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405121	8102330	Minus	35816-36004,36587-36684
401203	9743387	Minus	172961-173056,173868-173928
400494	9714719	Plus	169845-170272
402294	2282012	Minus	2575-3000
404730	8389582	Plus	119832-120016,124110-124275
403593	6862650	Minus	62554-62712,69449-69602
403710	6437516	Plus	27413-28978
401905	8671966	Plus	153965-154441,156599-156819
403108	8980955	Plus	93253-93667
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402315	7381741	Minus	30728-32065
401131	8699812	Minus	94802-94987,95804-95887,96323-96487,9759
401205	9743388	Plus	167373-167433,167936-168031
403105	8980016	Minus	145287-145744
401846	7712190	Minus	82775-82823,82912-83022
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406467	9795551	Plus	182212-182958
401429	8217890	Minus	86946-87579
404467	8077630	Minus	24951-25853
406587	8189273	Minus	120577-120718
404175	9931117	Minus	107420-107547,109625-109796

TABLE 66A. DISEASE INDICATIONS AND PREFERRED UTILITIES FOR SELECTED GENES

Table 66A provides disease indications and preferred utilities for about 439 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Primekey:	Unique Eos probeset identifier number
ExAccon:	Exemplar Accession number
UgID:	Unigene ID number
UgTitle:	Unigene title
Disease:	diseases indicated for selected gene as described in table 1 and abbreviated as follows: AWPC (androgen independent prostate diseases), arth (arthritic diseases), bph (benign prostatic hyperplasia), blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), gli0 (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrotic diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
Utility:	preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Primekey	Ex Accon	UgID	Ug Title	Disease	Utility
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	angio, blad, lung, cerv, ovar, headnk, esoph	mAb+diag+s.m.
400297	AI127076	Hs.305201	hypothetical protein DKFZp564O1278	breast, blad, colon, pros	mAb
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	breast, ovar, pros, stom, uter, blad, lung, headnk	mAb
400843			NM_003105:Homo sapiens sortilin-related	blad	s.m.
402075			ENSP00000251056:Plasma membrane calcium	blad, lung, headnk, cerv, mela, esoph	mAb+diag
402901			NM_025206:Homo sapiens hypothetical pro	blad	CTL
404287			FGENESH predicted novel CUB-domain conta	panc, lung, colon, uter, esoph	mAb+s.m.

5	404682		ortholog of mouse polydomain protein	panc	diag
	404875		NM_022819: Homo sapiens phosphatase A2	blad	CTL+s.m.
	404977		Insulin-like growth factor 2 (somatomedi	blad, ovar	mAb+diag
	405033		C1002652: gi544327 sp Q04799 FMO5_RABIT	blad	s.m.
	405547		NM_018833: Homo sapiens transporter 2, A	cerv, mela	mAb+s.m.
	406400		kallikrein 8 (neurosin/ovasin) (KLK8)	ovar, uter	diag
	406964	M21305	FGENES predicted novel secreted protein	angio, blad, fibro	diag
10	407603	AW955705	Homo sapiens, clone IMAGE:4299322, mRNA,	glio, blad	CTL
	407792	A1077715	putative secreted ligand homologous to f	ovar, uter, cerv, panc	mAb+diag
	407811	AW190902	cysteine knot superfamily 1, BMP antagon	blad, panc, stom, uter, lung, esoph	diag
	407836	T79340	B-cell CLL/lymphoma 6, member B, zinc fi	angio	CTL
	407975	X89426	endothelial cell-specific molecule 1	angio, renal	diag
	408243	Y00787	interleukin 8	blad, stom, headnk, cerv, lung, angio, esoph, panc	diag
15	408367	AK001178	Homo sapiens orphan neurotransmitter tra	mela	mAb+s.m.
	408369	R38438	SLC15A2 Solute carrier family 15 (H+pep	pros, lung, fibro, uter, glio, cerv, ovar	mAb
	408380	AF123050	diubiquitin	lung, blad, headnk, panc, stom, fibro, esoph, mela	CTL
	408482	NM_000676	adenosine A2b receptor	lung, esoph, headnk	mAb+s.m.
	408562	AJ435323	roundabout (axon guidance receptor, Dros	uter, fibro	mAb+s.m.
20	408790	AW580227	neurotrophic tyrosine kinase, receptor,	lung	mAb+s.m.
	408908	BE296227	serine/threonine kinase 15	lung, blad, headnk, stom	s.m.
	409041	AB033025	Hypothetical protein, XP_051860 (KIAA119	uter, ovar, lung, colon, stom, headnk, breast, panc	CTL+diag
	409079	W87707	interleukin 6 signal transducer (gp130,	breast, pros	mAb+s.m.
	409103	AF251237	XAGE-1 protein	lung	CTL
25	409178	BE393948	kallikrein 5	ovar, breast, mela	diag
	409220	BE243323	tumor necrosis factor receptor superfam	angio, renal, colon, stom	mAb+s.m.
	409348	A1401535	ESTs	renal, glio	mAb+s.m.+CTL
	409389	AB007979	Homo sapiens mRNA, chromosome 1 specific	glio	mAb+diag
	409420	Z15008	laminin, gamma 2 (nicein (100kD), kalini	lung, headnk, panc, stom, cerv, esoph, blad	diag
	409632	W74001	serine (or cysteine) proteinase inhibito	lung, blad, headnk	diag
30	409637	AA323948	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	renal	mAb+s.m.+CTL
	409663	A1743750	KIAA1862 protein	renal	CTL
	409745	AA077391	gb:7B14E12 Chromosome 7 Fetal Brain cDNA	ovar, renal	mAb+s.m.+CTL
	409757	NM_001898	cystatin SN	panc, stom, lung, blad,	diag
35	409893	AW247090	minichromosome maintenance deficient (S.	lung, cerv, blad, test, esoph	CTL+s.m.
	409956	AW103364	inhibin, beta A (activin A, activin AB a	breast, panc, ovar, colon, headnk, lung, blad, esoph	diag
	410001	AB041036	kallikrein 11	ovar, pros, uter, cerv, lung	diag
	410055	AJ250839	gene for serine/threonine protein kinase	renal	s.m.
	410153	BE311926	hypothetical protein FLJ12691	renal, blad	CTL
40	410274	AA381807	hypoxia-inducible protein 2	lung, renal	CTL
	410309	BE043077	alpha-2,8-sialyltransferase III	panc	s.m.
	410407	X66839	carbonic anhydrase IX	renal, lung, colon, stom, ovar, uter, blad	mAb+s.m.
	410418	D31382	transmembrane protease, serine 4	colon, blad, lung, ovar, panc, headnk	mAb+diag+s.m.
	411274	NM_002776	kallikrein 10	colon, ovar, uter, cerv, headk, panc	diag
45	411411	AA345241	ESTs, Weakly similar to KIAA1330 protein	renal	mAb+s.m.
	411773	NM_006799	protease, serine, 21 (testisin)	ovar	diag
	412078	X69699	paired box gene 8	ovar	CTL
	412140	AA219691	RAB6 interacting, kinesin-like (rabkines	lung, blad, headnk, breast, ovar, panc, angio, test, mela	s.m.
	412580	AA113262	similar to CABLES [Homo sapiens]	mela	mAb+s.m.+CTL
50	412609	Z48804	ocular albinism 1 (Nettleship-Falls)	mela	s.m.
	412628	AJ972402	hypothetical protein MGC2648	pros	diag
	412709	AL022327	KIAA0027 protein	glio	mAb+s.m.
	412719	AW016610	ESTs	lung, headnk, blad, glio, cerv	s.m.
	412959	D87458	KIAA0282 protein	glio	CTL+s.m.
55	412986	X81120	cannabinoid receptor 1 (brain)	glio	mAb+s.m.
	413048	M93221	mannose receptor, C type 1	fibro, panc	mAb
	413063	AL035737	chitinase 3-like 1 (cartilage glycoprote	glio, ovar, blad, lung	diag
	413278	BE563085	interferon-stimulated protein, 15 kDa	panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela, stom	CTL+s.m.
	413324	V00571	corticotropin releasing hormone	blad	diag
60	413385	M34455	indoleamine-pyrrole 2,3 dioxygenase	blad, lung, mela, fibro, uter	s.m.
	413554	AA319146	secretogranin II (chromogranin C)	panc, glio	diag
	413719	BE439580	small inducible cytokine subfamily A (Cy	panc, lung, headnk, cerv, colon, uter, stom, esoph	diag
	414577	A1056548	hypothetical protein FLJ20992 similar to	angio	CTL+diag
	414774	X02419	plasminogen activator, urokinase	lung, blad, headnk, panc, stom, ovar, esoph	diag
65	414812	X72755	monokine induced by gamma interferon	breast, blad, lung, fibro, panc, colon, headnk,	
				cerv, stom, renal, ovar, test, mela, esoph	diag
	414825	X06370	epidermal growth factor receptor (avian	glio, lung, renal, esoph, panc, headnk, arth	mAb+s.m.+CTL
	414883	AA926960	CDC28 protein kinase 1	lung, ovar, stom, colon, cerv, headnk, test	s.m.
	414907	X90725	polo (Drosophila)-like kinase	blad, lung, ovar, test	s.m.
70	414945	BE076358	lymphocyte antigen 6 complex, locus E	mela	mAb+s.m.
	415138	C18356	tissue factor pathway inhibitor 2	angio, panc, stom, lung, uter	CTL+diag
	415511	A1732617	ESTs	blad, ovar, renal	mAb+s.m.+CTL
	415539	AJ733881	BMP-R1B	breast, uter, pros	mAb+s.m.
	415668	AW957684	Homo sapiens lysyl oxidase-like 4 (LOXL4	mela	diag
75	415669	NM_005025	serine (or cysteine) proteinase inhibito	lung	mAb+diag+s.m.
	415817	U88967	protein tyrosine phosphatase, receptor-t	lung, glio, headnk, cerv, mela, esoph, fibro	mAb+s.m.
	415910	U20350	chemokine (C-X3-C) receptor 1	glio	mAb+s.m.
	415929	AA724373	Homo sapiens mucopolip-3 (MCOLN3)	mela	mAb
	415989	A1267700	ESTs	pros, ovar, blad, lung, headnk, panc, colon, stom	mAb+s.m.+CTL
	416091	AF295370	defensin, beta 3	headnk, esoph, mela	CTL+diag
80	416209	AA236776	MAD2 (mitotic arrest deficient, yeast, h	lung, headnk, colon, uter, stom	CTL+s.m.
	416250	AA581386	Kremen 2	esoph, lung, cerv, ovar	mAb+s.m.
	416350	AF188625	phospholipase A2, group IID	test, mela, fibro	CTL
	416530	U62801	kallikrein 6 (neurosin, zyme)	ovar, uter	diag

5	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	breast, panc, uter, mela	mAb+s.m.
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	lung, ovar, uter, blad, angio, test	diag
	416836	D54745	Hs.80247	cholecystokinin	pros, EWS, glio	diag
	416857	AA188775	Hs.292453	FGENES predicted TM containing protein	glio	mAb+s.m.
	417034	NM_006183	Hs.80962	neurotensin	lung, headnk, cerv	diag
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	blad, lung, headnk, cerv, esoph	diag
	417166	AA431323	Hs.42146	Paired box protein Pax-3	mela	CTL
	417355	D13168	Hs.82002	endothelin receptor type B	glio, mela	mAb+s.m.
10	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon	mAb+diag
	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal	mAb
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	lung, mela	mAb+diag
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	blad, cerv, panc, ovar	mAb
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	lung, panc, breast, ovar, headnk, stom	CTL
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	ovar, panc, stom, colon, uter, pros	diag
15	417933	X02308	Hs.82962	thymidylate synthetase	blad, lung, angio, colon, panc, esoph	s.m.
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela	mAb+diag+s.m.
	418030	BE207573	Hs.83321	neuromedin B	glio, panc	diag
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	mela	diag
20	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	uter, ovar	CTL+diag
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	lung, blad, ovar, headnk, panc, cerv, mela	s.m.
	418506	AA084248	Hs.372651	Unknown protein for MGC:29643 (formerly	angio, ovar, glio, uter, lung, blad, panc, mela	mAb+diag
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	lung, blad, renal, panc, stom, colon, ovar	mAb+s.m.
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	esoph, headnk	s.m.
25	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	lung, blad, stom, ovar, panc, esoph, cerv, mela	CTL
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	lung	CTL
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	blad	s.m.
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	leuk, ovar, breast, blad, renal	mAb+s.m.
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	renal, uter, lung	CTL
30	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	lung, esoph, headnk, blad	diag
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor I	lung	mAb+s.m.
	419172	AW338625	Hs.22026	ESTs; similar to TRANSMEMBRANE 4 SUPERF	angio, renal	mAb+s.m.
	419183	U06069	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	blad, lung, headnk, panc	CTL+s.m.
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	panc, lung, stom, cerv, pros, headnk, esoph	diag
35	419235	AW470411	Hs.288433	neurotrophin	panc, fibro, headnk, lung	mAb+diag
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	ovar, pros, lung, breast, uter, test, panc, stom	mAb+s.m.
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	glio, omuc, stom, lung, panc, colon, renal, uter	mAb+diag
	419556	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	lung, fibro, test	mAb+s.m.
	419704	AA429104	Hs.45057	ESTs	glio	CTL+s.m.
40	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	glio	mAb+diag
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	blad, lung, colon, ovar, test, esoph, mela	CTL+s.m.
	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	blad, stom	mAb
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	lung, mela	s.m.
	420208	BE276055	Hs.95972	silver (mouse homolog) like	mela	CTL
45	420370	Y13645	Hs.97234	uroplakin 2	blad	mAb
	420440	NM_002407	Hs.97644	mammaglobin 2	ovar, uter, cerv	diag
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	headnk, glio, cerv, mela	CTL+s.m.
	420610	A1683183	Hs.99348	disal-less homeo box 5	uter, endo, lung	CTL
	420737	L08096	Hs.99899	CD70 : tumor necrosis factor (ligand) s	renal	mAb+s.m.
50	420789	A1670057	Hs.199882	ESTs	renal	mAb+s.m.+CTL
	420876	AA918425	Hs.177744	FGENES predicted novel protein containin	panc, blad	s.m.
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mito	blad, lung	CTL+s.m.
	421110	AJ250717	Hs.1355	cathepsin E	blad, panc, stom, lung, fibro, ovar, esoph	sm+diag
55	421340	F07783	Hs.1369	decay accelerating factor for complement	angio, panc, stom	diag
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	breast, panc, headnk, lung, stom, blad, cerv, colon, fibro, test, mela, esoph	diag
	421471	U90545	Hs.327179	solute carrier family 17 (sodium phosph	renal	mAb+s.m.
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	lung	mAb+s.m.
	421508	NM_004833	Hs.105115	absent in melanoma 2	blad, esoph, lung, mela	mAb+s.m.+CTL
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	breast	mAb+s.m.
60	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	breast, ovar, panc, cerv, uter, pros, lung, stom, headnk	diag
	421574	AJ000152	Hs.105924	defensin, beta 2	headnk, lung	CTL+diag
	421582	A1910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	breast, panc, lung, omuc	diag
	421666	AL035250	Hs.1408	endothelin 3	mela	mAb+diag
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	lung	mAb+s.m.
65	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	lung, cerv, headnk, blad	mAb+s.m.
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	glio	mAb+s.m.
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	panc, pros	diag
	422109	S73265	Hs.1473	gastrin-releasing peptide	panc, lung, colon, fibro	diag
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	headnk, blad, lung, cerv, stom, esoph	diag
70	422163	AF027208	Hs.112360	prominin (mouse)-like 1	colon, breast, fibro	mAb+s.m.
	422192	AA305159	Hs.113019	fts485	mela	s.m.
	422260	AA315993	Hs.105484	regenerating gene type IV	colon, omuc, stom, panc	mAb+diag
	422282	AF019225	Hs.114309	apolipoprotein L	blad, lung, headnk, renal	diag
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	lung, blad, test, cerv, headnk, esoph	s.m.
75	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	mela	mAb+s.m.+CTL
	422330	D30783	Hs.115263	epiregulin	panc, colon, blad	mAb+diag
	422397	AJ223366	Hs.116051	MYEOV Myeloma overexpressed gene (in a	panc, stom, colon, esoph, renal, blad	CTL+s.m.
	422424	A1186431	Hs.296638	prostate differentiation factor	blad, panc, pros, angio, colon, stom, lung, mela	diag
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	colon, renal	mAb+diag
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	lung, blad	s.m.
80	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	blad, cer, lung, uter, angio, stom, test	s.m.
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	breast, ovar, pros, panc, lung, colon, uter	diag
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	ovar, blad, panc, lung, headnk, colon, stom	CTL+s.m.
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	renal, ovar, blad	mAb+s.m.

5	423184	NM_004428	Hs.1624	ephrin-A1	pros, panc, renal	mAb+s.m.
	423242	AL039402	Hs.125783	DEME-6 protein	breast, renal, ovar, pros, colon	CTL
	423422	AC005175	Hs.128425	NY-REN-24 antigen	glio	mAb
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	renal, colon	mAb
	423583	AL122055	Hs.129836	KIAA1028 protein	pros	s.m.
	423634	AW59908	Hs.1690	heparin-binding growth factor binding pr	lung, blad, headnk, panc	diag
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test	mAb+diag+s.m.
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	colon, stom, ovar	CTL
10	423961	D13666	Hs.136348	periosin (OSF-2os)	breast, colon, blad, lung, fibro, panc, headnk, ovar, mela	mAb+diag
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	blad, headnk, stom, cerv, esoph	mAb+s.m.
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	headnk, lung, cerv	diag
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	colon, stom	mAb+s.m.+CTL
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	mela, fibro	s.m.
15	424381	AA285249	Hs.146329	protein kinase Chk2 (CHEK2)	lung, colon, test	s.m.
	424411	NM_005209	Hs.146549	crystallin, beta A2	panc	s.m.
	424502	AF242388	Hs.149585	lensin	lung	s.m.
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	panc, pros, angio, blad, lung	mAb+s.m.
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	ovar	diag
20	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela	diag
	424735	U01875	Hs.272499	short-chain alcohol dehydrogenase family	blad, breast	CTL+s.m.
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	mela	CTL+s.m.
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	ovar, blad, lung, headnk, panc, stom	s.m.
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	renal, fibro	mAb+s.m.
25	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	pros, colon, stom, uter, cerv, headnk, esoph, panc	diag
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	glio, mela	mAb+s.m.+CTL
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	glio	mAb+s.m.
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph	mAb+diag+s.m.
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	lung, headnk	s.m.
30	425535	AB007937	Hs.158287	syndecan 3	mela, glio	mAb+s.m.
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	lung, headnk, cerv, esoph, blad	mAb
	425721	AC002115	Hs.159309	uroplakin 1A	blad	mAb
	425723	NM_014420	Hs.159311	dicdkopi (Xenopus laevis) homolog 4	endo, uter, colon	CTL+diag
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	lung	s.m.
35	425776	U25128	Hs.159499	parathyroid hormone receptor 2	ovar, uter, lung	mAb+diag
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	panc, glio	s.m.
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	blad, lung, headnk	mAb+s.m.
	425883	AL137708	Hs.161031	Homo sapiens mRNA: cDNA DKFZp434K0322 (f	blad, panc	mAb
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	stom, panc	mAb+s.m.
40	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	renal	mAb+s.m.
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	blad	mAb+diag
	426215	AW963419	Hs.155223	stanniocalcin 2	breast, lung, renal, colon, ovar, uter	mAb+diag
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	panc, lung, colon, esoph, stom	mAb+s.m.
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	panc, blad, stom	diag
45	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	glio	CTL+s.m.
	426427	M86699	Hs.169840	TTK protein kinase	ovar, lung, headnk, cerv, colon, uter, stom, test	CTL+s.m.
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	blad, breast	s.m.
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	ovar, colon, blad, lung, cerv	mAb+diag
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	mela	diag
50	426761	AI015709	Hs.172089	PORIMIN Pro-oncosis receptor inducing me	lung, esoph, pros, uter, panc, colon, ovar, headnk	mAb+s.m.
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	renal	mAb+s.m.
	426890	AA393167	Hs.41294	ESTs	renal, colon, ovar, uter, stom	CTL
	427239	BE270447	Hs.356512	ubiquitin carrier protein	lung, blad, test, mela	CTL+s.m.
55	427335	AA448542	Hs.251677	G antigen 7B	lung, headnk, blad, mela, esoph	CTL
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	glio	CTL+s.m.
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	colon, stom, panc	CTL
	427747	AW411425	Hs.180655	serine/threonine kinase 12	blad, lung, ovar, stom, test, esoph	s.m.
	427923	AW274357	Hs.301406	FGENESH predicted 11 TM protein	mela	mAb
60	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	panc	mAb+diag
	428093	AW594506	Hs.104830	ESTs	ovar, panc	CTL
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	glio	mAb+s.m.
65	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	breast	s.m.
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	ovar, uter, colon, stom	mAb+s.m.
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	ovar, panc, lung	diag
	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	renal	mAb+s.m.
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela, stom	mAb+diag+s.m.
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	headnk, stom, esoph, colon	diag
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	panc	diag
70	428450	NM_014791	Hs.184339	KJAA0175 gene product	ovar, cerv, panc, lung, blad, mela	s.m.
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	lung, blad, colon, uter, ovar	s.m.
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela	mAb+s.m.
	428486	AW583497	Hs.184604	pancreatic polypeptide	panc	diag
	428505	AL035461	Hs.2281	chromogranin B (secretogranin I)	panc, lung	diag
75	428513	BE220806	Hs.184697	plexin C1	mela, panc, stom, headnk	mAb
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	ovar, EWS, uter	mAb+s.m.
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	blad, ovar, pros, lung, stom, test	CTL+s.m.
	428698	AA852773	Hs.334838	KJAA1866 protein	breast, colon, lung, panc, stom, headnk, ovar, EWS	mAb
	428748	AW593206	Hs.98785	Ksp37 protein	lung	diag
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	ovar, cerv, lung, panc, stom, renal	diag
80	428778	AK000530	Hs.193326	fibroblast growth factor receptor-like 1	ovar	mAb+s.m.
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	glio, mela	mAb+s.m.
	428841	AM18430	Hs.104935	ESTs	renal	mAb+s.m.+CTL
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	cerv, panc, colon, stom, headnk, renal	mAb+diag
	428969	AF120274	Hs.194689	artemin	lung, cerv	diag

5	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	stom, panc, colon, ovar	
	429149	AW193360	Hs.197962	Homolog of mouse ADP-ribosylation factor	glio	mAb+s.m.
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	lung, blad, headnk, cerv, esoph, stom, mela	mAb+s.m.
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	lung	mAb+s.m.
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	angio, blad, glio	mAb+s.m.
	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	breast, pros	mAb+s.m.
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	panc, headnk, lung, ovar	mAb+s.m.
10	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	lung, fibro	diag
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	lung, mela	mAb+diag
	429910	NM_000867	Hs.2507	5-hydroxytryptamine (serotonin) receptor	leio	s.m.
	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	glio	mAb+s.m.
	430280	AA361258	Hs.237868	interleukin 7 receptor	mela, lung, panc, stom, esoph, headnk	s.m.
	430377	NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	mela	mAb+s.m.+CTL
15	430486	BE062109	Hs.241551	chloride channel, calcium activated, tam	lung, blad, headnk, cerv, esoph	CTL
	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	mela	mAb+s.m.
	430890	XS4232	Hs.2699	glypican 1	glio, lung, cerv, blad, esoph	s.m.
	431053	S40369	Hs.249141	Glutamate receptor subunit	glio	mAb+s.m.
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	ovar, uter	mAb
20	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	panc, lung, glio, test	diag
	431515	NM_012152	Hs.258583	EDG-7 (endothelial differentiation, lys	ovar, pros, lung, blad	diag
	431620	AA126109	Hs.264981	Z'-S'-oligoadenylate synthetase 2 (69-71	esoph, cerv	mAb+s.m.
	431629	AJ077025	Hs.265827	interferon, alpha-inducible protein (clo	panc, uter, cerv, stom, esoph, mela	CTL+s.m.
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	ovar, panc, blad, headnk, mela, renal	mAb+diag
25	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	test, renal, blad	mAb+s.m.
	431846	BE019924	Hs.271580	uroplakin 1B	lung, blad, headnk, uter, cerv, stom, ovar	CTL
	431870	AW449902	Hs.105500	ESTs	renal	mAb+diag
	431939	AW008061	Hs.231994	ESTs	renal, colon	mAb+s.m.+CTL
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela	mAb+s.m.+CTL
30	432196	AW300888	Hs.273230	hypothetical protein FLJ10830	renal	mAb+diag
	432201	AIS38613	Hs.298241	Transmembrane protease, serine 3	breast, colon, ovar, stom, panc, uter, cerv, lung	CTL
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	renal	mAb+diag+s.m.
	432596	AJ224741	Hs.278461	matrilin 3	panc, breast	CTL
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	renal, breast, lung, stom, hepC, fibro	diag
35	432800	BE391046	Hs.278962	AIM-1 protein	mela, pros	CTL
	432829	W60377	Hs.57772	ESTs	blad	mAb+s.m.
	432867	AW016936	Hs.233364	ESTs	stom, colon	CTL+s.m.
	432874	W94322	Hs.279651	melanoma inhibitory activity	panc, stom, mela	mAb+s.m.+CTL
40	432990	AL036071	Hs.279899	tumor necrosis factor receptor superfami	pros, renal	diag
	433001	AF127513	Hs.279905	clone HQ0310 PRO0310p1	colon, breast, lung, blad, cerv, uter, test, mela	mAb+s.m.
	433447	U29195	Hs.3281	neuronal pentraxin II	mela, esoph, colon, renal	s.m.
	433848	AF095719	Hs.93764	carboxypeptidase A4	headnk, esoph, lung	diag
	433867	AK000596	Hs.3618	hippocalcin-like 1	renal	s.m.
	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	stom, colon	CTL
45	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	mela	CTL+s.m.
	435013	H91923	Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	renal, lung	s.m.
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	glio	CTL
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	lung, headnk	mAb
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	angio, glio	diag
50	436456	AW292677	Hs.248122	melanin-concentrating hormone receptor (mela, glio	mAb
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	glio	mAb+s.m.
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	lung, blad, colon, ovar, uter, headnk, test	mAb+s.m.
	436576	AI458213	Hs.77542	ESTs	renal, panc, headnk, lung	s.m.
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	blad, lung	mAb+s.m.
55	436895	AF037335	Hs.5338	carbonic anhydrase XII	lung, headnk	CTL+s.m.
	436961	AW375974	Hs.156704	ESTs	breast, renal, ovar, glio	mAb+s.m.
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	lung, panc, renal, uter, colon	CTL
	437016	AL076916	Hs.5398	guanine monophosphate synthetase	ovar, fibro	diag
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	lung, blad, cerv, esoph, headnk	s.m.
60	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph	CTL
	437212	AI765021	Hs.210775	ESTs	panc, renal	mAb+s.m.+CTL
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	renal, uter, ovar	mAb+s.m.+CTL
	437852	BE001836	Hs.256897	putative GPCR	lung	CTL
65	437938	AI950087	Hs.369628	gb:wq05c02.x1 NCL CGAP_Kid12 Homo sapien	blad, lung	mAb+s.m.
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	renal, ovar, uter, cerv, blad, renal	mAb+s.m.+CTL
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	glio, mela	diag
	438859	AI593626	Hs.93522	Homo sapiens mRNA for KIAA1647 protein,	mela	mAb
	438929	AW195515	Hs.253177	ESTs	renal	CTL+diag
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Ho	renal	mAb+s.m.+CTL
70	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	renal	mAb+s.m.+CTL
	439223	AW238299	Hs.250618	UL16 binding protein 2	uter, stom, pros, fibro	mAb+s.m.+CTL
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	lung, headnk, cerv, esoph, blad, colon	mAb
	439569	AW602166	Hs.222399	CEGP1 protein	lung	mAb
	439606	W79123	Hs.58561	G protein-coupled receptor 87	breast, AWPC, pros, blad	mAb+s.m.
75	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig)	lung, blad, headnk, cerv, esoph	diag
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	blad, lung, cerv, renal	mAb+s.m.
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	colon, stom, panc, lung	mAb+s.m.
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-ti	renal, cerv, pros, headnk, colon, test	mAb+s.m.+CTL
	440065	W03476	Hs.266331	Homo sapiens Fc receptor homolog express	blad, ovar, lung, headnk, test	mAb
80	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	mela	s.m.
	440304	BE159984	Hs.125395	hepatitis A virus cellular receptor 1	glio	diag
	440311	AI733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN	renal, colon, blad	mAb
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	renal	mAb+s.m.
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	glio, ovar, uter, renal, hepC	mAb+s.m.+CTL
					mela	mAb+diag
						s.m.

5	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	lung, blad, headnk, test, mela, esoph	s.m.
	441392	AW451831	Hs.222119	ESTs, Weakly similar to S30433 keratin 1	renal	mAb+s.m.-CTL
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypothe	fibro, angio	mAb
	442117	AW654964	Hs.128899	ESTs: hypothetical protein for IMAGE:447	breast, lung, blad, panc, headnk, stom, ovar, pros	mAb+s.m.
	442133	AW874138	Hs.129017	ESTs; type Ia transmembrane protein	ovar, uter	mAb
	442438	AA995998		gbrs26b03.s1 NCI_CGAP_Kid5 Homo sapiens	uter, ovar, renal	mAb+s.m.-CTL
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	mela	mAb+diag
	443211	AI128388	Hs.143655	ESTs	blad, ovar, lung, headnk, stom	mAb+s.m.-CTL
10	443247	BE614387	Hs.333893	c-Myc target JPO1	colon, lung, blad, panc	CTL
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	colon, lung, blad, stom, test, mela	CTL
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	renal	diag
	443646	AI085198	Hs.164226	Thrombospondin 1	angio, panc, uter	diag
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	gio, uter, ovar	mAb+s.m.-CTL
15	443859	NM_013409	Hs.9914	folistatin	lung, cerv, headnk, blad, esoph	diag
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	renal	mAb+s.m.
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv	mAb
	444371	BE540274	Hs.239	forkhead box M1	lung, headnk, blad, gio, test, mela	s.m.
	444381	BE387335	Hs.283713	hypothetical protein BC014245	breast, colon, blad, lung, panc, headnk, ovar, stom, uter,	
					renal, angio, test, mela, esoph	diag
20	444488	AW192879	Hs.355660	ancient conserved domain protein 4	renal	mAb+s.m.
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	fibro, esoph	diag
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	lung, blad, headnk, cerv	mAb+diag
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph	CTL+s.m.
	444809	BE207568	Hs.208219	oculostriatin	mela	mAb+s.m.
25	445070	NM_000677	Hs.258	adenosine A3 receptor	gio, renal	mAb+s.m.
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	panc, headnk, stom, lung, esoph	diag
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv	mAb+diag
	445891	AW391342	Hs.199460	DPCR1 protein	stom, panc, esoph, omuc, esoph	mAb
30	445895	D29954	Hs.13421	KIAA0056 protein	pros	CTL
	446051	BE048061	Hs.37054	ephrin-A3	colon, breast	mAb+diag
	446163	AA026880	Hs.25252	prolactin receptor	breast, cerv, uter	mAb+s.m.
	446232	AI281848	Hs.194691	retinoic acid induced 3	stom, panc, colon, ovar	mAb+s.m.
	446341	AI040763	Hs.310735	FGENESH prediction similar to multidrug	mela	diag
35	446619	AU076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter	mAb+s.m.
	446650	AB016625	Hs.15813	solute carrier family 22 (organic cation	renal	diag
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	breast, panc, headnk, lung, fibro, mela	mAb+diag
	447004	AW296968	Hs.157539	FGENESH predicted secreted protein	colon	CTL+diag
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	gio, pros, fibro, breast, ovar, lung, panc	CTL+s.m.
40	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	gio, panc	CTL+s.m.
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazar	renal, breast, stom, lung, mela, ovar	CTL+diag
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	esoph, stom, colon	CTL
	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenylylsulfate)	renal	CTL
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	colon, blad, pros, lung, stom, AWPC, ovar	CTL
45	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	colon, pros, stom, uter	CTL
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	mela	s.m.
	447835	AW591623	Hs.164129	ESTs, Weakly similar to I38022 hypothe	renal, ovar, uter	mAb+s.m.-CTL
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	mela	mAb+s.m.
	448105	AW591433	Hs.298241	Transmembrane protease, serine 3	breast, panc, colon, lung, ovar, stom	mAb+s.m.-CTL
50	448243	AW369771	Hs.367688	integrin, beta 8	ovar, uter, lung, stom, headnk, gio, panc	mAb+s.m.
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	gio	mAb+s.m.-CTL
	448499	BE613280	Hs.77550	p53-regulated DDA3	gio	CTL+s.m.
	448595	AB014544	Hs.21572	KIAA0644 gene product	breast, gio	mAb+s.m.
	448610	NM_006157	Hs.21602	nel (chicken)-like 1	mela	diag
55	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	lung, renal	mAb+s.m.
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	panc, lung, stom, omuc	mAb+s.m.
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	panc, ovar, uter, gio, headnk, lung	mAb
	449444	AW818436	Hs.351306	solute carrier family 16 (monocarboxylic	renal, panc	mAb+s.m.
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	lung, panc, renal, stom, hepC, fibro, mela	mAb+s.m.
60	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	colon	CTL
	449722	BE280074	Hs.23960	cyclin B1	headnk, blad, lung, panc, angio, test, mela, esoph	s.m.
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	renal	mAb+s.m.
	450375	AA009647	Hs.352537	a disintegrin and metalloproteinase doma	breast, ovar, headnk, panc, lung, esoph, colon	mAb+diag+s.m.
65	450531	AW301032	Hs.203800	(BC017500) Similar to hypothetical prote	colon	CTL
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	lung, headnk, panc, breast, stom, ovar, esoph, colon	mAb+diag
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	fibro, lung	s.m.
	450931	N25156	Hs.25648	tumor necrosis factor receptor superfam	lung, renal	mAb+s.m.
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	blad, lung, ovar, panc	diag
70	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	gio, fibro, mela	mAb+s.m.
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	colon, panc	CTL
	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	renal	mAb
	451537	RS6631	Hs.26550	retinoid X receptor, gamma	mela	CTL+s.m.
	451668	Z43948	Hs.326444	cartilage acidic protein 1	blad, ovar, lung	mAb+diag
	451939	U08046	Hs.27311	single-minded (Drosophila) homolog 2	pros	CTL
75	451979	BF0972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	angio	CTL+s.m.
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	renal	CTL
	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (ovar	mAb+s.m.+diag
	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	breast, stom, panc	mAb
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	stom, panc, renal, colon, mela, fibro	mAb+s.m.
80	452203	X57522	Hs.352018	transporter 1, ATP-binding cassette, sub	cerv, esoph, blad, stom, mela, renal	mAb+s.m.
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	breast, headnk, panc, stom, lung, esoph, fibro	diag
	452355	NS4926	Hs.29202	G protein-coupled receptor 34	gio, fibro, panc	mAb+s.m.
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	blad, breast, panc, headnk, stom, lung, arth, renal, esoph	diag
	452431	U88879	Hs.29499	tol-like receptor 3	renal, hepC	mAb

5	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	breast, blad, lung, headnk, ovar, stom, uter, panc	mAb	
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	renal, headnk, colon, lung, panc	mAb+s.m.-CTL	
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	lung, ovar, breast, mela, test, esoph, renal	CTL	
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	headnk, breast, colon, arth, lung, blad, esoph, stom	mAb+diag	
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	renal	CTL	
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	renal, pros	mAb+s.m.	
	453642	AJ370936	Hs.34074	dipeptidylpeptidase VI	glio	mAb+s.m.	
10	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	renal, mela	s.m.	
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	glio, lung, uter, headnk, cerv, panc, pros	mAb+s.m.	
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	lung, uter, blad, test	CTL+s.m.	
	456546	AI690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	ovar	mAb+s.m.	
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	uter, ovar	CTL	
15	456759	BE259150	Hs.127792	della (Drosophila)-like 3	glio, lung	mAb+s.m.	
	457133	M54968	Hs.351221	v-Ki-ras2 Kirsten rat sarcoma 2 viral on	panc	s.m.	
	457489	AI693815	Hs.127179	cryptic gene	panc, pros, lung	diag	
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	glio	mAb+s.m.	
	458079	AI796870	Hs.54277	Homo sapiens similar to RIKEN cDNA 28100	mela, fibro	mAb	
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypothesi	glio	mAb+s.m.-CTL	
20	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	ovar, uter, test	CTL	
25	TABLE 66B:						
	Pkey:	Unique Eos probeset identifier number					
	CAT number:	Gene cluster number					
	Accession:	Genbank accession numbers					
30	Pkey	CAT Number	Accession				
	409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AJ361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625				
			BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377				
			AA150780 BI033518 BI027818 BG015789 BI033807 AA341445				
	438966	1242593_1	AW979074 AA834841 AA828650				
	442438	24590_1	AK022175 AU147222 AI124945 AU121400 F07756 AW979025 AA828595 AA828577 BE935573 AA829588 AI743616 BE315309 BE047365 AI761053				
			AW168960 AA833900 BG679419 BE171071 BF034368 BF754297 R61781 F08149 F07647 T77332 AA897461 AI829714 AJ376820 AI809991				
			AW661854				
35	TABLE 66C:						
	Pkey:	Unique number corresponding to an Eos probeset					
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA					
40	Strand:	sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.					
	NI_position:	Indicates DNA strand from which exons were predicted.					
		Indicates nucleotide positions of predicted exons.					
45	Pkey	Ref	Strand	NI_position			
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,			
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416			
	402901	8894222	Minus	175426-175667			
	404287	2326514	Plus	53134-53281			
	404682	9797231	Minus	40977-41150			
	404875	9801324	Plus	96588-96732,97722-97831			
50	404977	3738341	Minus	43081-43229			
	405033	7107731	Minus	142358-142546			
	405547	1054740	Plus	124361-124520,124914-125050			
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077			
55	TABLE 67:						
	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigeneID:	Unigene number					
60	Unigene Title:	Unigene gene title					
	Seq ID No:	Sequence Identification Number linking the information in Table 67 to the sequences in Table 68					
65	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No		
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No 1 & 199		
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No 2 & 200		
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	Seq ID No 3 & 201		
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Seq ID No 4 & 202		
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No 5 & 203		
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fts, clone PL	Seq ID No 6		
70	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No 7 & 204		
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	Seq ID No 8 & 205		
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No 9 & 206		
	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No 10 & 207		
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No 11 & 208		
75	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No 12 & 209		
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	Seq ID No 13 & 210		
	443211	AI128388	Hs.143655	ESTs	Seq ID No 14		
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	Seq ID No 15 & 211		
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	Seq ID No 16 & 212		
80	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No 17 & 213		
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No 18 & 214		
	408380	AF123050	Hs.44532	diubiquitin	Seq ID No 19 & 215		
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	Seq ID No 20 & 216		
	409757	NM_001898	Hs.123114	cystatin SN	Seq ID No 21 & 217		

5	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	Seq ID No 22 & 218
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 23 & 219
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 24 & 220
	444783	AK001468	Hs.62180	anillin (Drosophila Scars homolog), act	Seq ID No 25 & 221
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	Seq ID No 26 & 222
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No 27 & 223
	415989	AI267700	Hs.351201	ESTs	Seq ID No 28
	415989	AI267700	Hs.351201	ESTs	Seq ID No 29
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 30 & 224
10	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 31 & 225
	432867	AW016936	Hs.233364	ESTs	Seq ID No 32
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	Seq ID No 33
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	Seq ID No 34 & 226
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	Seq ID No 35 & 227
15	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	Seq ID No 36 & 228
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	Seq ID No 37 & 229
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	Seq ID No 38 & 230
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	Seq ID No 39 & 231
	452203	X57522	Hs.352018	transporter 1, ATP-binding cassette, sub	Seq ID No 40 & 232
20	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	Seq ID No 41 & 233
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	Seq ID No 42 & 234
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	Seq ID No 43 & 235
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	Seq ID No 44 & 236
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	Seq ID No 45 & 237
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	Seq ID No 46 & 238
	415511	AI732617	Hs.182362	ESTs	Seq ID No 47
	440304	BE159984	Hs.125395	hepatitis A virus cellular receptor 1	Seq ID No 48 & 239
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	Seq ID No 49 & 240
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	Seq ID No 50
30	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 51 & 241
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 52 & 242
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 53 & 243
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 54 & 244
	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 55 & 245
35	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 56 & 246
	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	Seq ID No 57 & 247
	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	Seq ID No 58 & 248
	426890	AA393167	Hs.41294	ESTs	Seq ID No 59 & 249
	437212	AI765021	Hs.210775	ESTs	Seq ID No 60
40	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo	Seq ID No 61
	440311	AI733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN !	Seq ID No 62
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fs, clone H	Seq ID No 63
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fs, clone H	Seq ID No 64
45	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	Seq ID No 65 & 250
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	Seq ID No 66 & 251
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	Seq ID No 67 & 252
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	Seq ID No 68
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No 69 & 253
50	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	Seq ID No 70 & 254
	420737	L08096	Hs.99899	CD70; tumor necrosis factor (ligand) s	Seq ID No 71 & 255
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	Seq ID No 72 & 256
	420789	AI670057	Hs.199882	ESTs	Seq ID No 73
	420789	AI670057	Hs.199882	ESTs	Seq ID No 74
55	441392	AW451831	Hs.222119	ESTs, Weakly similar to S30433 keratin 1	Seq ID No 75 & 257
	452431	U88879	Hs.29499	toll-like receptor 3	Seq ID No 76 & 258
	431870	AW449902	Hs.105500	ESTs	Seq ID No 77
	431870	AW449902	Hs.105500	ESTs	Seq ID No 78
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	Seq ID No 79 & 259
60	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	Seq ID No 80
	438859	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 protein,	Seq ID No 81
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 82 & 260
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 83
	409348	AI401535	Hs.146090	ESTs	Seq ID No 84
65	447269	NM_004861	Hs.17958	cerebroside (3'-phosphoadenylylsulfate:g	Seq ID No 85 & 261
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	Seq ID No 86 & 262
	428841	AI418430	Hs.104935	ESTs	Seq ID No 87
	428841	AI418430	Hs.104935	ESTs	Seq ID No 88
	428841	AI418430	Hs.104935	ESTs	Seq ID No 89
	409663	AI743750	Hs.98306	KIAA1862 protein	Seq ID No 90 & 263
70	409663	AI743750	Hs.98306	KIAA1862 protein	Seq ID No 91 & 264
	431939	AW008061	Hs.231994	ESTs	Seq ID No 92 & 265
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	Seq ID No 93 & 266
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	Seq ID No 94 & 267
75	433867	AK000596	Hs.3618	hippocalcin-like 1	Seq ID No 95 & 268
	433867	AK000596	Hs.3618	hippocalcin-like 1	Seq ID No 96 & 269
	437938	AI950087	Hs.369628	gb:wq05c02.x1 NCL CGAP_Kid12 Homo sapien	Seq ID No 97
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	Seq ID No 98 & 270
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxyic	Seq ID No 99 & 271
80	432196	AW300888	Hs.273230	hypothetical protein FLJ10830	Seq ID No 100 & 272
	432196	AW300888	Hs.273230	hypothetical protein FLJ10830	Seq ID No 101 & 273
	438929	AW195515	Hs.253177	ESTs	Seq ID No 102
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	Seq ID No 103 & 274
	446650	AB016625	Hs.15813	solute carrier family 22 (organic cation	Seq ID No 104 & 275

5	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chloride)	Seq ID No 105 & 276
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (Izaro)	Seq ID No 106 & 277
	449444	AW818436	Hs.351306	solute carrier family 16 (monocarboxylic)	Seq ID No 107 & 278
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No 108 & 279
	444488	AW192879	Hs.355660	ancient conserved domain protein 4	Seq ID No 109 & 280
	450931	N25156	Hs.25648	tumor necrosis factor receptor superfamily	Seq ID No 110 & 281
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfamily	Seq ID No 111 & 282
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfamily	Seq ID No 112 & 283
10	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	Seq ID No 113 & 284
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	Seq ID No 114 & 285
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor type	Seq ID No 115 & 286
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	Seq ID No 116 & 287
	436576	AL036071	Hs.279899	tumor necrosis factor receptor superfamily	Seq ID No 117 & 288
15	451527	AF022813	Hs.77542	ESTs	Seq ID No 118 & 289
	448733	NM_005629	Hs.26518	transmembrane 4 superfamily member 7	Seq ID No 119 & 290
	410274	AA381807	Hs.61762	solute carrier family 6 (neurotransmitter)	Seq ID No 120 & 291
	125218	H91923	Hs.110024	hypoxia-inducible protein 2	Seq ID No 121 & 292
20	436961	AW375974	Hs.156704	Empirically selected from AFFX single pass	Seq ID No 122 & 293
	431630	NM_002204	Hs.265829	ESTs	Seq ID No 123
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha)	Seq ID No 124 & 294
	419508	AW997938	Hs.90786	integrin, alpha 3 (antigen CD49C, alpha)	Seq ID No 125 & 295
	431840	AA534908	Hs.2860	ATP-binding cassette, sub-family C (CFTR)	Seq ID No 126 & 296
25	442438	AA995998		POU domain, class 5, transcription factor	Seq ID No 127 & 297
	447835	AW591623		gbr:os26b03.s1 NCL CGAP_Kd5 Homo sapiens	Seq ID No 128
	429276	AF056085	Hs.164129	ESTs, Weakly similar to I38022 hypothetical	Seq ID No 129
	448595	AB014544	Hs.21572	G protein-coupled receptor 51	Seq ID No 130 & 298
	440516	S42303	Hs.161	KIAA0644 gene product	Seq ID No 131 & 299
30	456759	BE259150	Hs.127792	cadherin 2, type 1, N-cadherin (neuronal)	Seq ID No 132 & 300
	447004	AW296968	Hs.157539	delta (Drosophila)-like 3	Seq ID No 133 & 301
	425088	AA663372	Hs.169395	FGENESH predicted secreted protein	Seq ID No 134 & 302
	409389	AB007879	Hs.301281	hypothetical protein FLJ12015	Seq ID No 135 & 303
	448321	NM_005883	Hs.20912	Homo sapiens mRNA, chromosome 1 specific	Seq ID No 136 & 304
35	426344	H41821	Hs.322469	adenomatous polyposis coli like	Seq ID No 137 & 305
	419704	AA429104	Hs.45057	transcriptional activator of the c-fos p	Seq ID No 138 & 306
	412959	D87458	Hs.75090	ESTs	Seq ID No 139 & 307
	448499	BE613280	Hs.77550	KIAA0282 protein	Seq ID No 140 & 308
40	458435	AI418718	Hs.144121	p53-regulated DDA3	Seq ID No 141 & 309
	443785	AW449952	Hs.190125	ESTs, Weakly similar to T46916 hypothetical	Seq ID No 142 & 310
	427343	AI880044	Hs.176977	basic-helix-loop-helix-PAS protein	Seq ID No 143 & 311
	416857	AA188775	Hs.292453	protein kinase C binding protein 2	Seq ID No 144 & 312
	429149	AW193360	Hs.197962	FGENESH predicted TM containing protein	Seq ID No 145 & 313
	418030	BE207573	Hs.83321	Homolog of mouse ADP-ribosylation factor	Seq ID No 146 & 314
45	457561	AA331517	Hs.286055	neuromedin B	Seq ID No 147 & 315
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	Seq ID No 148 & 316
	430147	R60704	Hs.234434	chimerin (chimaerin) 2	Seq ID No 149 & 317
	453642	AI370936	Hs.34074	hair/finhancer-of-split related with YRP	Seq ID No 150 & 318
	453857	AL080235	Hs.35861	dipeptidylpeptidase VI	Seq ID No 151 & 319
50	449048	Z45051	Hs.22920	Ras-induced senescence 1 (RIS1)	Seq ID No 152 & 320
	418506	AA084248	Hs.372651	similar to S68401 (cattle) glucose induc	Seq ID No 153 & 321
	416636	N32536	Hs.42645	Unknown protein for MGC:29643 (formerly)	Seq ID No 154 & 322
	421508	NM_004833	Hs.105115	solute carrier family 16 (monocarboxylic)	Seq ID No 155 & 323
	421379	Y15221	Hs.103982	absent in melanoma 2	Seq ID No 156 & 324
55	428784	Y12851	Hs.193470	small inducible cytokine subfamily B (Cy)	Seq ID No 157 & 325
	431958	X63629	Hs.2877	purinergic receptor P2X, ligand-gated ion	Seq ID No 158 & 326
	417542	J04129	Hs.82269	cadherin 3, type 1, P-cadherin (placenta)	Seq ID No 159 & 327
	418678	NM_001327	Hs.167379	progesterone-associated endometrial prote	Seq ID No 160 & 328
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No 161 & 329
60	420208	BE276055	Hs.95972	cancer/testis antigen (NY-ESO-1)	Seq ID No 162 & 330
	430377	NM_001922	Hs.301865	silver (mouse homolog) like	Seq ID No 163 & 331
	438549	BE386801	Hs.21858	dopachrome tautomerase (dopachrome delta	Seq ID No 164 & 332
	412580	AA113262	Hs.17901	trinucleotide repeat containing 3	Seq ID No 165 & 333
	417166	AA431323	Hs.42146	similar to CABLES [Homo sapiens]	Seq ID No 166 & 334
65	428513	BE220806	Hs.184697	Paired box protein Pax-3	Seq ID No 167 & 335
	447937	AL109716	Hs.20034	plexin C1	Seq ID No 168 & 336
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 169 & 337
	446341	AL040763	Hs.310735	Homo sapiens mRNA full length insert cDN	Seq ID No 170 & 338
	446341	AL040763	Hs.310735	FGENESH prediction similar to multidrug	Seq ID No 171 & 339
70	458079	AI796870	Hs.54277	FGENESH prediction similar to multidrug	Seq ID No 172 & 340
	415668	AW957684	Hs.306814	Homo sapiens similar to RIKEN cDNA 28100	Seq ID No 173 & 341
	447674	BE270640	Hs.19192	Homo sapiens lysyl oxidase-like 4 (LOXL4)	Seq ID No 174 & 342
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	Seq ID No 175 & 343
	440065	W03476	Hs.266331	cyclin-dependent kinase 2	Seq ID No 176 & 344
75	414945	BE076358	Hs.77667	Homo sapiens Fc receptor homolog express	Seq ID No 177 & 345
	440672	AF083811	Hs.7345	lymphocyte antigen 6 complex, locus E	Seq ID No 178 & 346
	412609	Z48804	Hs.74124	MAD1 (mitotic arrest deficient, yeast, h	Seq ID No 179 & 347
	453837	AL138387	Hs.256126	ocular albinism 1 (Nettleship-Falls)	Seq ID No 180 & 348
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv	Seq ID No 181 & 349
80	434276	AF123659	Hs.93605	baculoviral IAP repeat-containing 7 (liv	Seq ID No 182 & 350
	408367	AK001178	Hs.44424	leucine zipper, putative tumor suppresso	Seq ID No 183 & 351
	444809	BE207568	Hs.208219	Homo sapiens orphan neurotransmitter tra	Seq ID No 184 & 352
	415929	AA724373	Hs.304950	oculospasmin	Seq ID No 185 & 353
	421666	AL035250	Hs.1408	Homo sapiens mucopolin-3 (MCPOLN3)	Seq ID No 186 & 354
				endothelin 3	Seq ID No 187 & 355

424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	Seq ID No 188 & 356
425535	AB007937	Hs.158287	syndecan 3	Seq ID No 189 & 357
451537	R56631	Hs.26550	retinoid X receptor, gamma	Seq ID No 190 & 358
430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No 191 & 359
418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	Seq ID No 192 & 360
448610	NM_006157	Hs.21602	nel (chicken)-like 1	Seq ID No 193 & 361
432800	BE391046	Hs.278962	A1M-1 protein	Seq ID No 194 & 362
416350	AF188625	Hs.189507	phospholipase A2, group IID	Seq ID No 195 & 363
405545			Target Exon	Seq ID No 196 & 364
414812	X72755	Hs.77367	monokine induced by gamma interferon	Seq ID No 197 & 365
432874	W94322	Hs.279651	metanoma inhibitory activity	Seq ID No 198 & 366

Table 68 lists sequences as described in Table 67

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

	1	11	21	31	41	51	
20	ATGCACAGCT	TTCTCCCACT	GCTGCTGCTG	CTGTCTCTGG	GTGTGGTGTG	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACATCA	AGAGCAAGAT	GTGGACCTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAACC	TGAAGAACAGA	TGGCGAGCAA	GTGGAAGAAC	GGAGAAATAG	TGGCCCACTG	180
	GTTGAAAAAT	TGAAGCAAAAT	CAGCAAAATC	TTTGGGCTGA	AAGTGAACCTG	AGCCACAGAT	240
25	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	GAATGTGGAG	TGCCTGATGT	GCGTCGATGT	300
	GCTCTCACT	AGGGGAACCC	TGCTGGGGAG	CAACACATCT	GACTCTACAG	GATTGAAAAAT	360
	TACACGCCAG	ATTTGCCAAAT	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	TTTCCAACCT	420
	TGGAGTAGAT	TCACCACTGT	GACATTCAAC	AAGTCTCTCC	AGGGCTCAAG	AGCATCATCG	480
	ATATCTTTTG	TACGGGGAGA	TGATCGGGAC	AAGTCTCTCT	TTGATGGACC	TGGAGGAAAT	540
30	CTTGCTCATG	CTTTTCAACC	AGGCCAGAGT	ATTGGGGGGG	ATGCTCATTT	TGATGAAGAT	600
	GAAAGGTGGA	CAACAATAAT	CAGAGGACAT	AAGTTACATC	GTGTTGCGCG	TCATGAACCT	660
	GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAAGT	GTGATGTTCA	CGAGCTTCAG	GATGACATTC	ATGGCATCCA	AGCCATATAT	780
	GGAGCTTCCC	AAAACTCTGT	CACGCCCATC	CGGCACAAA	CCCCAAAAGC	ATTGTGACAGT	840
35	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
	TTCTACATGC	GCACAAATCC	CTTCTAACCG	GAGGTGAGAC	CAATTTCATC	TTCTGTTTCT	960
	TGGCCCAAC	TGCCAAATGG	CTGTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
	CGGTTTTFCA	AAGGGAATTA	GTACTGGGCT	GTTCAAGGAC	AGAAATGTGT	ACACGGATAT	1080
	CCCCAAGACA	TCTACAGTAA	TTTGGGCTTC	CTCAGAAGCT	TGAAGCATAT	CGATGCTGCT	1140
40	CTTTCCTAGG	AAAACTCTGG	AAAAACCTAC	TTCTTTGTGT	CTAACAAATA	CTGGAGGATAT	1200
	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCCAAT	TGATAGACACA	TGACTTTCTCT	1260
	GGAAATTTGCC	ACAAAGTTCT	TGCAAGTTTC	ATGAAAGAAAT	GATTTTTCTA	TTTCTTTTCAT	1320
	GGAAACAAGC	AAATACAAAT	TGATCTTAAA	ACGAAGAGAA	TTTTTGACTCT	CCAGAAAGCT	1380
	AATAGCTGGT	TCAACTCGAG	GAAAAATTAG				

Seq ID NO: 2 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

	coding sequence: 1-1495									
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50	ATGCACAGCT	TTCTCCCACT	GCTGTCTGCT	CTGTCTCTGGG	GTGTGGTGTCT	ACACAGCTTC				60
	CCAGCGCACT	TAGAAAACATA	AGAGCAAGAT	GTGGCACTTAG	TCCAGAAAT	CCTGGAAAAA				120
	TACTACAACC	TGAAGACATG	TGGGAGGCCAA	TTTGGAAAAG	GGAGAAATAG	TGGCCCAAGT				180
	GTTGAAAAAT	TGAAGCAAAAT	CAGGAGAAATC	TTTGGGCTGA	AAGTGACTGG	GAAGCAAGCT				240
55	GCTCTAACCC	TGAAGGTGAT	GAAGCAAGCCC	AGATGTGGAG	TCCGCTAGAT	GGCTCAAGTT				300
	GTCTTCACT	AGGGGAGACC	TGCTTGGGAG	CAACAACTAC	TGACCTACAG	GATGTAAAT				360
	TACACGCCAG	ATTTGCCAAG	AGCAAGTGTG	GACCAATGCCA	TTGAGAAAGC	CTTCCAACCT				420
	TGGAGTAATG	TCACACCTCT	GACATTCACC	AAGTCTCTCT	AGGGTCAAGC	AGACATCATG				480
	ATATCTTTTG	TACGGGAGGA	TCATCGGGAC	AACCTCTCCT	TTGATGGAAC	TGGAGGAAAT				540
60	CTTGTCTATG	CTTTTCAACC	AGGCCGCAAT	ATTGGAGAGG	ATGCTCAATT	TGATGAAGAT				600
	GAAAGGTGGA	CCAAACAATT	CAGAGAGTAC	AACCTACGCT	GTGTGCGGG	TCATGCCCTC				660
	GGCCATTCTC	TTGACTCTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC				720
	ACCTTTCAGT	GTGATGTTCT	GCTAGCTCAG	GATGACATTA	ATGGCATCTCA	AGGCATATAT				780
	GGAGCTTCCC	AAAACTCTGA	CCAGGCCATC	GGGCCACAAG	CCCCAAAAGC	ATTGTGACAGT				840
65	AAAGTCAACT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTCTCT	TAAAGACAGA				900
	TTCTACATCT	GCACAAATTC	CTTCTACCCG	GAAAGTGAAG	TCAATTTTCA	TTCTGTGTTCT				960
	TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC				1020
	CGGTTTTC	AAAGGGAATG	ATACTTGGCT	GTTACGGGAC	AGAAATGTGT	ACACGGATAT				1080
	CCCAAGGACA	TCTACAGCTC	CTTTGGCTTC	CTTAGAAGCT	TGAAGCATAT	CGATGTCTGT				1140
70	CTTTCTGAGG	AAAAACACTGG	AAAAACCTAC	TTCTTTGTGT	CTAACAAAT	TCTGGAGGAT				1200
	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAGT	TAGATGACAC	TGACTTTCTCT				1260
	GGAAATGGCC	ACAAAGTTGA	TGCAAGTTTC	ATGAAACAAAT	GATTTTCTTA	TTTCTTTTCA				1320
	GGAAACAAGC	AATACAAATT	TGATCTTAAA	ACGAAGAGAA	TTTGTACTCT	CCAGAAAGCT				1380
	AATAGCTTGT	TCAACTTCGAC	GAAAATATAG							

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_002422.2
Coding sequence: 64..1497

80

coding sequence: 84...1497

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ACAAGGAGGC	AGGCAAGACA	GCAAGGCATA	GAGACAACAT	AGAGCTAAGT	AAAGCCAGTG	60
GAAATGAAGA	GTCTTCCAAT	CCTACTGTGT	CTGTGCGTGG	CAGTTTGCTC	AGCCTATCCA	120
TGGATGTGAG	CTCAAGAGGTC	TGAGGACACC	AGCATGAACC	TTGTTTCAGAA	ATATCTAGAA	180
AACCTACAGC	ACCTCAAAAA	AGATGTGAAA	CAGTTTGTGA	GGAGAAAGGA	CAGTGGCTCT	240

	GTGTGTTAAAA	AAATCCGAGA	AATGCAGAAG	TTCTTTGGAT	TGGAGGTGAC	GGGGAAGCTG	300
	GACTCCGACA	CTCTGGAGGT	GATGCGCAAG	CCCAGGTGTG	GAGTTCTCTGA	TGTTGGTCCAC	360
	TTCAGAACCT	TTCTTGGCAT	CCCGAAGTGG	AGGAAAAACC	ACCTTACATA	CAGGATTGTG	420
5	AATTATACAC	CAGATTGTGC	AAAAGATGCT	GTGTATTCTG	CTGTTGAGAA	AGCTCTGAAA	480
	GTCTGGGAAG	AGGTGACTCC	ACTCATTTC	TCCAGGCTGT	ATGAAGGAGA	GGCTGATATA	540
	ATGATCTCTT	TTGCAGTTAG	AGAACATGGA	GACTTTTACC	CTTTTGATGG	ACCTGGAAT	600
	GTTTTGGCCC	ATGCCATATG	CCCTGGGCCA	GGGATTAATG	GAGATGCCCA	CTTTGATGAT	660
	GATGAACAA	GGACAAAGGA	TACAACAGGG	ACCAATTAT	TTCTGTTGC	TGCTCATGAA	720
10	ATTGGCCACT	CCCTGGGTCT	CTTTCACTCA	GCCAACACTG	AAGCTTTGAT	GTACCCACTC	780
	TATCACTCAC	TCACAGACCT	GACTCGGTTT	CGCTGTCTC	AAGATGATAT	AAATGGCATT	840
	CAGTCCCTCT	ATGGACCTCC	CCCTGACTCC	CCTGAGACCC	CCCTGGTACC	CACGGAACCT	900
	GTCCCTCCAG	AACCTGGGAC	GCCAGCCAAC	TGTGATCCTG	CTTTGTCTCT	TGATGCTGTC	960
	AGCACTCTGA	GGGGAGAAAT	CCTGATCTTT	AAAGACAGGC	ACTTTTGGCG	CAATCCCTC	1020
15	AGGAAGCTTG	AACCTGAAT	GCATTTGATC	TCTTCATTTT	GGCCATCTCT	TCCTTCAGGC	1080
	GTGGATGCCG	CATATGAAGT	TACTAGCAAG	GACCTCGTTT	TCATTTTAA	AGGAAATCAA	1140
	TTCTGGGCCA	TCAGAGGAAA	TGAGGTACGA	GCTGGATACC	CAAGAGGCAT	CCACACCTTA	1200
	GGTTTCCCTC	CAACCGTGAG	GAAATCGAT	GCAGCCATTT	CTGATAAGGA	AAAGAACAAA	1260
	ACATATTCTT	TTGTAGAGGA	CAAAATCTGG	AGATTGATG	AGAAGAGAAA	TTCCATGGAG	1320
20	CCAGGCTTTC	CCAAGCAAT	AGCTGAAGAC	TTTCCAGGGA	TTGACTCAAA	GATTGATGCT	1380
	GTTTTGAAG	AATTTGGGTT	CTTTTATTTT	TTTACTGGAT	CTTCACAGTT	GGAGTTTGAC	1440
	CCAAATGCAA	AGAAAGTGAC	ACACACTTTG	AAGAGTAACA	GCTGGCTTAA	TTGTTGAAAG	1500
	AGATATGTAG	AAGGCACAA	ATGGGCACCT	TAAATGAAGC	TAATAATTCT	TCACCTAAGT	1560
	CTCTGTGAAT	TGAAATGTTT	GTTTCTCTCT	GCCTGTGCTG	TGACTCGAGT	CACACTCAAG	1620
25	GGAACTTGAG	CGTGAATCTG	TATCTTGGCG	GTCAATTTTA	TGTTAATTACA	GGGCATTCAA	1680
	ATGGGCTGCT	GCTTAGCTTG	CACCTTGCTA	CATAGAGTGA	TCCTTCCCAA	GAGAAGGGGA	1740
	AGCACTCGTG	TGCAACAGAC	AAGTGACTGT	ATCTGTGTAG	ACTATTGTCT	TATTTAATAA	1800
	AGACGATTGG	TCAGTTGTTT	T				
30	Seq ID NO: 4 DNA Sequence						
	Nucleic Acid Accession #: NM_001854						
	Coding sequence: 162..5582						
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35	AACCATCAAA	TTTGAAGAA	AAAGCCCTTT	GACTTTTTC	CCCTCTCCCT	CCCAATGGC	60
	TGTGTAGCAA	ACATCCCTTG	CGATACCTTG	GAAAGGACGA	AGTTGGTCTG	CAGTCGCAAT	120
	TTCTGGGGTT	GAGTTTCACG	TTGTGAGTGC	GGGGCTCGGA	GATGGAGCCG	TGTCCTCTA	180
	GGTGAAAC	GAAACGGTGG	CTCTGGGATT	TCACCGTAAC	AACCTCTCGA	TTGACCTTCC	240
40	TTCTCCAGC	TAGAGAGGTC	AGAGGAGCTG	CTCCAGTTGA	TGTAATAAAA	GCACATAGATT	300
	TTCACAATTC	TCAGAGGGGA	ATATCAAAAA	CAACGGGATT	TTGCACAAAC	AGAAAGAAAT	360
	CTAAAGGCTC	AGATACTGCT	TACAGAGTTT	CAAGCAAGC	ACAACCTCAGT	GCCTCAACAA	420
	AACAGTATT	TCCAGGTGGA	ACTTTCCTCC	AAGACTTTTC	AATACTATT	ACAGTAAAC	480
	CAAAAAAGG	AATTCAGTCT	TTCTTTTAT	CTATATATA	TGAGCATGGT	ATTGAGCAAA	540
	TTGGTGTGA	GGTTGGGAGA	TCACCTGTTT	TTCTGTTTGA	AGACCACACT	GGAAAACTTG	600
45	CCCCAGAGA	CTATCCCTTC	TTCAAGACTG	TAAACATCCG	TGACGGGAAG	TGGCATCGGG	660
	TAGCAATCAG	CGTGGAGAAG	AAAACGTGTA	CAATGATTGT	TGATTGTAA	AAGAAAAACCA	720
	CGAAACCACT	TGATAGAAGT	GAGAGAGCAA	TTGTTGATAC	CAATGGAAATC	ACGGTTTTTG	780
	GAAACAAGAT	TTTGGATGAA	GAGGTTTTTG	AGGGGGACAT	TCAGCAGTTT	TTGATCAGAG	840
	GTGATCCCAA	GGCAGCATAT	GACTACTGTG	AGCATTATAG	TCCAGACTGT	GACTCTTCAG	900
50	CACCCAGGCG	TGCTCAAGCT	CAGGAACCTC	AGATAGATGA	GTATGCACCA	GAGGATATAA	960
	TGGAATATGA	CTATGAGTAT	GGGGAAGCAG	AGTATAAAGA	GGCTGAAAGT	GTAACAGAGG	1020
	GACCCACTGT	AATCTAGGAG	ACAATAGCAC	AGACGGAGGC	AAACATCGTT	GATGATTTTC	1080
	AAGAATACAA	CTATGGAACA	ATGGAAGATT	ACCAGACAGA	AGCTCCTAGG	CATGTTTCTG	1140
55	GGACAATGA	GCCAAATCCA	GTTGAAGAAA	TATTTACTGA	AGAATATCTA	ACGGGAGAGG	1200
	ATTATGATT	CCAGAGGAAA	AATCTGAGG	ATACACTATA	TGAAAACAAA	GAAATAGAGG	1260
	GCAGGGATT	TGATCTTCTG	GTAGATGGAG	ATTTAGGCGA	ATATGATTTT	TATGAATATA	1320
	AAGAATATGA	AGATAAACCA	ACAAGCCCCC	CTAATGAAGA	ATTTGGTCCA	GGTGATACCA	1380
	CAGAACTGA	TATTACAGAA	ACAAGCATAA	ATGGCCATGG	TGCATATGGA	GAGAAAGGAC	1440
	AGAAAGGAGA	ACCAGCAGTG	GTGAGCCCTG	GTATGCTTGT	CGAAGGACCA	CCAGGACCCAG	1500
60	CAGGACCTGC	AGGTATTATG	GGTCTCCAG	GTCTACAAGG	CCCCACTGGA	CCCCCTGGTG	1560
	ACCCTGGCGA	TAGGGGCCCC	CCAGGACGTC	CTGGCTTACC	AGGGGGCTGAT	GGTCTACCTG	1620
	GTCTCTCTGG	TACTATGTTG	ATGTTACCGT	TCCGTTATGG	TGGTGATGGT	TCCAAAGGAC	1680
	CAACCATCTC	TGCTCAGGAA	GCTCAGGCTC	AAGCTATTCT	TCAGCAGGCT	CGGATTGCTC	1740
	TGAGAGGCC	ACCTGGCCCA	ATGGGTCTAA	CTGGAAGACC	AGGTCTCTGT	GGGGGGCTGT	1800
65	GTTCATCTGG	GGCCAAAGGT	GAGAGTGGTG	ATCCAGGTCC	TCAGGGCCCT	CGAGGTGCTC	1860
	AGGGTCCCC	TGGTCCAACG	GGAAAACTG	GAAAAAGGGG	TGTTCCAGGT	GCAGATGGAG	1920
	GAAGAGGAAT	GCCAGGAGAA	CCTGGGGCAA	AGGGAGATCG	AGGGTTTATG	GGACTTCCGG	1980
	GTCTGCCAGG	TGACAAAGGT	CACAGGGGTG	AACGAGGTCC	TCAAGGTCTC	CCAGGTCTCT	2040
	CTGGTGATGA	TGGAATGAGG	GGAGAAGATG	GAGAAATTGG	ACCAAGAGGT	CTTCCAGGTG	2100
70	AAGCTGGCCC	ACGAGGTTTG	CTGGGTCCAA	GGGGAACCTC	AGGAGCTCCA	GGGCAGCCTG	2160
	GTATGGCAGG	TGTAGATGGC	CCCCCAGGAC	CAAAAGGGAA	CATGGGTCCC	CAAGGGGAGC	2220
	CTGGGCTTCC	AGGTCAACAA	GGGAATCCAG	GACCTCAGGG	TCTTCTGGT	CCACAAGGTC	2280
	CAATTGGTCC	TCCTGGTGAA	AAAGGACCA	AAGGAAACCC	AGGACTTGCT	GGACTTCTCT	2340
	GTGCTGATGG	GCCTCTGGT	CATCTGGGA	AAGAAGGCCA	GTCTGGAGAA	AAGGGGGCTC	2400
75	TGGTCCCCC	GCTTCCACAA	GCTCTATTG	GATNNCCGGG	CCCCCGGGGA	GTAAGGGGAG	2460
	CAGATGGTGT	CAGAGGTCTC	AAGGGATCTA	AAGGTGAAAA	GGGTGAAGAT	GTTTTCAG	2520
	GATTCAAAGG	TGACATGGGT	CTAAAAGGTG	ACAGAGGAGA	AGTTGGTCAA	ATTGGCCCAA	2580
	GAGGNAAGA	TGGCCCTGAA	GGACCAAGAG	GTGAGCAGG	CCCACTGGA	GACCCAGGTC	2640
	CTTCAGGTCA	AGCAGGAGAA	AAGGGAAC	TTGGAGTTCC	AGGATTACCA	GGATATCCAG	2700
80	GAAGACAAGG	TCCAAGGGT	TCCAAGGAT	TCCCTGGGTT	TCCAGGTGCC	AATGGAGAGA	2760
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Seq ID NO: 10 DNA Sequence

Nucleic Acid Accession #: AK092195

Coding sequence: 1..2034

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Seq ID NO: 11 DNA Sequence

Nucleic Acid Accession #: NM_032044

Coding sequence: 182..658

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Seq ID NO: 12 DNA Sequence

Nucleic Acid Accession #: XM_051860.2

Coding sequence: 261..4346

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	CTATGACGCT	GACTCTTGGC	AGCAGACCCAG	TGGGGGATGG	CTGGGTCCCC	CAGCCCTGTC	4440
75	CAGCAGCTGC	CTGGGAAGGC	CGTGTTCAG	CCCTGATGGG	CCAAGGGAAG	GCTATCAGAG	4500
	ACCCTGGTGC	TGCCACCTGC	CCCTACTCAA	GTGTCTACCT	GGAGCCCTCTG	GGGCGGTGCT	4560
	GGCCAATGCT	GGAAACATTC	ACTTTCCTGC	AGCCTCTTGG	GTGCTTCTCT	CCTATCTGTG	4620
	CCTCTTCAGT	GGGGGTTTGG	GGACCATATC	AGGAGACCTG	GGTTGTGCTG	ACAGCAAGA	4680
80	TCCACTTTGG	CAGGAGCCCT	GACCCAGCTA	GGAGGTAGTC	TGGAGGGCTG	GTCAATCACA	4740
	GATCCCCATG	GTCTTCAGCA	GACAAGTGAG	GGTGGTAAAT	GTAGGAGAAA	GAGCCTTGGC	4800
	CTTAAGGAAA	TCTTTACTCC	TGTAAGCAAG	AGCCAACTCT	ACAGGATTAG	GAGCTGGGGT	4860
	AGAACTGGCT	ATCCTTGGGG	AAGAGGCAAG	CCCTGCCCTCT	GGCGGTGTCC	ACCTTTCAGG	4920
	AGACTTTGAG	TGGCAGGTTT	GGACTTGGAC	TAGATGACTC	TCAAAGGCCCT	TTTGTAGTCT	4980
	GAGATTCCAG	AAATCTGCTG	CATTTACAT	GGTACCTGGA	ACCCAAACAGT	TCATGGATAT	5040
	CCACTGATAT	CCATGATGCT	GGGTGCCCCA	GCGCACACGG	GATGGAGAGG	TGAGAACTAA	5100

	TGCCTAGCTT	GAGGGGTCTG	CAGTCCAGTA	GGGCAGGCAG	TCAGGTCCAT	GTGCACTGCA	5160
	ATGCCAGGTG	GAGAAATCAC	AGAGAGGTAA	AATGGAGGCC	AGTGCCATTT	CAGAGGGGAG	5220
	GCTCAGGAAG	GCTTCTGTCT	TACAGGAATG	AAGGCTGGGG	GCATTTTGCT	GGGGGGAGAT	5280
	GAGGCAGGCT	CTGGAATGGC	TCAGGGATTG	AGCCCTCCCT	GCGCTGCCT	GCTGAAGCTG	5340
5	GTGACTACGG	GGTCGCCCTT	TGCTCACGTC	TCTCTGSCCC	ACTCATGATG	GAGAAGTGTG	5400
	GTGAGAGGGG	AGCAATGGGC	TTTGCTGCTT	ATGAGCACAG	AGGAATTCAG	TCCCCAGGCA	5460
	GCCCTGCGCT	TGACTCCAAG	AGGGTGAAGT	CCACAGAAAT	GAGCTCCTGC	CTTAGGGCCT	5520
	CATTGTGCTT	TCATCCAGGG	AACTGAGCAC	AGGGGGCCTC	CAGGAGACCC	TAGATGTGCT	5580
	CGTACTCCCT	CGCCCTGGGA	TTTCAGAGCT	GGAAATATAG	AAAATATCTA	GCCCAAAGCC	5640
10	TTCAATTTAA	CAGATGGGGA	AAGTGAGCCC	CCAAGATGGG	AAAGAACACC	ACAGCTAAGG	5700
	GAGGGCTGGG	GGAGCCCCAC	CCTAGCCCTT	GCTGCCACAC	CACATTGCCT	CAACAACCGG	5760
	CCCCAGATTG	CCCAGGCACT	CCTGAGGTAG	CTTCTGGAAA	TGGGGACAAG	TCCCTCGAA	5820
	GGAAAGGAAA	TGACTAGAGT	AGAATGACAG	CTAGCAGATC	TCTTCCCTCC	TGCTCCACGC	5880
	GCACACAAAC	CCGCCCTCCC	CTTGGTGTG	GCGTCCCTG	TGGCTTCAC	TTTGTTCAC	5940
15	ACCTGTGAGC	CCAGCCTGGG	TGCACAGTAG	CTGCAACTCC	CCATTGGTGC	TACCTGGCTC	6000
	TCCCTGTCTT	GCAGCTCTAC	AGGTGAGGCC	CAGCAGAGGG	AGTAGGGCTC	GCATGTGTTT	6060
	TGGTGAGCCA	ATTTCGCTGA	TCTTGGGTGT	CTGAACAGCT	ATTGGGTCCA	CCCCAGTCCC	6120
	TTTCAGCTGC	TGCTTAATGC	CCTGCTCTCT	CCCTGGCCCA	CCTTATAGAG	AGCCCAAAGA	6180
20	GCTCCTGTAA	GAGGGAGAAC	TCTATCTGTG	GTTTATAATC	TTGCACGAGG	CACCAGAGTC	6240
	TCCCTGGGTC	TTGTGATGAA	CTACATTTAT	CCCTTTCTCT	GCCCAACCCA	CAAACTCTTT	6300
	CCTTCAAAGA	GGGCCCTGCT	GGCTCCCTCC	ACCCAAGTGC	ACCCATGAGA	CTCGGTCCAA	6360
	GAGTCCATTG	CCCAGGTGGG	AGCCAAGTGT	CAGGGAGGTC	TTTCCACCA	AACATCTTTC	6420
	AGCTGCTGGG	AGGTGACCAT	AGGGCTCTGC	TTTTAAAGAT	ATGGCTGCTT	CAAGGCCAG	6480
25	AGTCACAGGA	AGGACTTCTT	CCAGGGAGAT	TAGTGGTGTG	GGAGAGGAGA	GTTAAATGA	6540
	CCTCATGTCC	TTCTGTGCA	CGGTTTTGTT	GAGTTTTTAC	TCTTCTAATG	CAAGGGTCTC	6600
	ACACTGTGAA	CCAATTAGGA	TGTGATCACT	TTGAGGTGGC	CAGGAATGTT	GAATGTCTTT	6660
	GGCTCAGTTC	ATTTAAAGAA	GATATCTATT	TGAAAGTTCT	CAGAGTTGTA	CATATGTTTC	6720
	ACAGTACAGG	ATCTGTACAT	AAAAGTTTCT	TTCTAAACCC	ATTACCAAG	AGCCAATATC	6780
30	TAGGCATTTT	CTTGGTAGCA	CAAAATTTCT	TATTGCTTAG	AAAATTGTCC	TCCTTGTTAT	6840
	TTCTGTTTGT	AGAGCTTAAG	TGAGTTAGGT	CTTTAAGGAA	AGCAACGCTC	CTCTGAAATG	6900
	CTTGTCTTTT	TTCTGTGCCC	GAAGTAGCTG	GTCTTTTTC	GGGAGTTAGA	TGTATAGAGT	6960
	GTTTGTATGT	AAACATTTCT	TGTAGGCATC	ACCATGAACA	AAGATATATT	TTCTATTAT	7020
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	AAAGCTCTTA	TTCTATGAT	GCCCCCTGG	ATTTTCATCA	TTTTTCATCC	TTGGATGATG	180
	AAGGAGATAC	TCAAACATA	GATTTCATGT	TTGAGGAGAA	GGCCAATTTG	GAGAATAAGT	240
45	TACTGGGGAA	GAATGGAAGT	GGAGGGCTTT	TTGAGGGCAA	AACTCCCTTG	AGAAAGGCTA	300
	ATCTTCAGCA	AGCTATTGTC	ACACCTTTGA	AACCAAGTGA	CAACACTTAC	TACAAAGAGT	360
	CAGAAAAAGA	AAATCTTTGT	GAACAATCCA	TTCCGTCAAA	TGCTTGTCT	TCCTTGGGAG	420
	TTGAGGCAGC	CATATCAAGA	AAAACCTCCAG	CCCAGCCTCA	GAGAAAGTCT	CTTAGGCTTT	480
	CTGCTCAGAA	GGATTGGGAA	CAGAAAGAAA	AGCATCATGT	AAAAATGAAA	GCCAAGAGAT	540
50	GTGCCACTCC	TGTAATCATC	GATGAAATTC	TACCCTCTAA	GAAAATGAAA	GTTTCTAACA	600
	ACAAAAGAAA	GCCAGAGGAA	GAAGGCAGTG	CTCATCAAGA	TACTGCTGAA	AAGAATGCAT	660
	CTTCCCAAGA	GAAAGCCAAG	GGTAGACATA	CTGTGCTTGT	TATGCCACCT	GCAAAGCAGA	720
	AGTTTCTAAA	AAGTACTGAG	GAGCAAGAGC	TGGAGAAGAG	TATGAAAATG	CAGCAAGAGT	780
	TGGTGGAGAT	GCGGAAAAAG	AATGAAGAAT	TCAAGAAACT	TGCTCTGGCT	GGAATAGGGC	840
55	AACTGTGAAA	GAATCAGTGT	AGCCAGGTCA	CCAAATCAGT	TGACTTCCAC	TTCCGACACG	900
	ATGAGCGAAT	CAAAACAAT	CTGAGAACCC	AGGAGGAATG	TAAGGAAGTG	AACTTTACAT	960
	CTGAATCTAG	AAAGACTCCT	TCATCTCCTG	CCCGAGTGAC	TAAGGAGTGT	ACCATTTGTA	1020
	AGCCTTTCAA	CCTGTCCCAA	GAAAGAAAAA	GAACATTGTA	TGAAACAGTT	TCTACATATG	1080
	TGCCCTTGGC	ACAGCAAGTT	GAAGACTTCC	ATAACGAAC	CCCTAACAGA	TATCATTTGA	1140
60	GGAGCAAGAA	GGATGATATT	AACTGTTTAC	CCTCCAAATC	TTCTGTGACC	AAGATTGACA	1200
	GAGACCCACA	GACTCCTGTA	CTGCAAAACA	AACACCGTGC	ACGGGCTGTG	ACCTGCAAAA	1260
	GTACAGCAGA	GCTGGAGGCT	GAGGAGCTCG	AGAAATTGCA	ACAATACAAA	TTCAAAGCAC	1320
	GTGAACCTGA	TCCCAAGAAT	CTTGAAGGTG	GGCCCATCTT	GCCCAAGAAA	CCACCTGTGA	1380
	AACCACCCAC	CGAGCCTATT	GGCTTTGATT	TGGAAATTGA	GAAAAGAATC	CAGGAGCGAG	1440
65	AATCAAGAAA	GAAAACAGAG	GATGAACACT	TTGAATTTCA	TTCCAGACCT	TGCCCTACTA	1500
	AGATTTTGGG	AGATGTTGTG	GGTGTTCCTG	AAAAGAAGGT	ACTTCCAATC	ACCGTCCCCA	1560
	AGTCACCGAG	CTTTGCTATT	AAGAACAGAA	TTGGAATGCC	CACCAAGAAA	GATGAGGAAG	1620
	AGGACGAACC	GGTAGTGATA	AAAGCTCAAC	CTGTGCCACA	TTATGGGGTG	CCTTTTAAGC	1680
	CCCAATCCCC	AGAGGCAAGA	ACTGTGAAAA	TATGCCCTTT	CTCCTTTGAT	TCTCGAGACA	1740
70	AAGAACGTCA	GTTACAGAAG	GAGAAAGAAA	TAAAAGAACT	GCAGAAAGGG	GAGGTGCCCA	1800
	AGTTCAAGGC	ACTTCCCTTG	CCTCATTTTG	ACACCATTTA	CCTGCCAGAG	AAGAAGGTAA	1860
	AGAATGTGAC	CCAGATTGAA	CCTTCTGCT	TGGAGACTGA	CAGAAAGAGT	GCTCTGAAGG	1920
	CACAGACTTG	GAAGCACCAG	CTGGAAGAAG	AACTGAGACA	GCAGAAAGAA	GCAGCTTGT	1980
	TCAAGGCTCG	TCCAAACACC	GTCACTCTCT	AGGAGCCCTT	TGTTCCCAAG	AAAGAGAAGA	2040
75	AATCAGTTGC	TGAGGGCCTT	TCTGGTTCTC	TAGTTAGGGA	ACCTTTTCAG	CTGGCTACTG	2100
	AGAAAGAGGC	CAAAAGACGG	CAGGAGCTGG	AGAAGAGAA	GGCTGAGGTA	GAAGCCGAGA	2160
	AAGCCACGCA	GTTGGAGGAG	GCCAGACTAC	AGGAGGAAGA	GCAGAAAAAA	GAGGAGCTGG	2220
	CCAGGCTACG	GAGAGAACTG	GTGCATAAGG	CAAAATCAAT	ACGCAAGTAC	CAGGGTCTGG	2280
	AGATAAAGTC	AAGTAGCCAG	CCTCTGACTG	TGCCTGTATC	TCCCAAAATC	TCCACTCGAT	2340
80	TCCACTGTCTA	AACTCAGCTG	TGAGCTGCGG	ATACCGCCCG	GCAATGGGAC	CTGCTCTTAA	2400
	CCTCAAACT	AGGACCGCTC	TGCTTTGTCA	TTGGGCATGG	AGAGAAACCA	TTTCTCCAGA	2460
	CTTTTACCTA	CCCGTGCCCTG	AGAAAGCATA	CTTGACAACT	GTGGACTCCA	GTTTGTGTTA	2520
	GAATTGTTTT	CTTACATTAC	TAAGGCTAAT	AATGAGATGT	AACTCATGAA	TGCTCTGATT	2580
	AGACTCCATG	TAGTTACTTC	CTTTAAACCA	TCAGCCGGCC	TTTTATATGG	GTCTTCACTC	2640
	TGACTAGAAT	TAGTCTCTG	TGTCAGCACA	GTGTAATCTC	TATTGCTATT	GCCCTTACGC	2700

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 ACTCTCACCC TCTCCCAAC TTTTAAAA AATTTAAACC AGAAAAATAA GATAGTTAAA 2760
 TCCTAAGATA GAGATTAAGT CATGTTTAA ATGAGGAACA ATCAGTAAAT CAGATTCTGT 2820
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 Nucleic Acid Accession #: Eos sequence
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 CTTTGAAGAG CAGTCAGACT CTTGCTTGGC TCTTCAGACT TAATTGGGGG GTTTAACAGG 240
 TGAGGTGTCT GGGGGAACCT TTTTACAACA TCTCTCTGAA AGAATCCGGG CTGCCAGTTT 300
 CATTTGGTTT GGGTGTCTAG AGCATGATGG AAAGACAAA AAACACAACT TGACATCTGC 360
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 AGAAATGGGT TCAAAATTTTA CTGCAACTC ACCAATTTCT TGGCTTGGT TCAGCAATTA 420
 AACTCCCTAA AATTCAAGTTT TTTCTTTGTA AAATGGGGTT ATGAACAGTA CCTACTTCAA 480
 AATGTGTTTG TGAAGATTAA AAAAGTTAAC ATAAAGAGTT TAGAAGAGTG TCTGGCATAT 540
 TGTGCTCAAT AAGTGTATT TATTATTATG CTGAATAAAC CAGTAATTTA ATTAGTAT 598

25
 Seq ID NO: 15 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 63..3224
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 CCAATGTGAG GCGCAAGCAG GCGAAACCCC AGCACATCAA CTGGGAGGAG GACCAGGGCG 120
 AGCAGACGAG GCGAGCAGAG ACCCGGAGT TTGCAGATGC GCGCCACGCG GCGCCCGCGG 180
 CGGGGGAGCT GGGTGTCTCA GTGAACACC CAGGGAATGA CGAGGTGGCG AGTGAGGATG 240
 AAGCCACACT AAAGCGGCTT CTTGCGGAGG AGACGCACGT CTGTGAGAAA TGCTGTGCGG 300
 35
 AGTTCCTCAG CATCTCTGAG TTCTTGAAC ATAAGAAAAA TTGCACTAAA AATCCACCTG 360
 TCCTCATCAT GAATGACAGC GAGGGGCGCTG TGCTTTCAGA AGACTTCTCC GGAGCTGTAC 420
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 CAGAGGACAT GAAGGAGAAG CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG 540
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 CACTCCCTGC CCGCTGTCTT GGTGCCAACA GCATCCCGTG GGTCTCTGAG CAGATCTTGT 720
 GTCTGACAGA CAGCAGATCC AGCTCACCGA GCAGATCCGC ATCCAGGTGA 780
 ACATGTGGGC CTCCACGCCC CTCCACTCAA GCGGGCAGG GCGCGACACT CTGAAGACCT 840
 TGGGAGCCCA CATGTCTCAG CAGGTTTCTG CAGCTGTGGC TTGCTCAGC CAGAAAGCTG 900
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 GAAGCCAAAG TCTGTCTCTG GATGCCCTGA AACAAGCCAA GCTACCTCAC GCCAACATCC 960
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 GCTCGGTGCT CTTCAGAGC CCTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA 1140
 AGGGGAAGCC ACCGAACATC TCCGCGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT 1200
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 ACAAGCACAA GTGTAAGTAC TGTAGCAAGG TTTTGGGAC TGATAGCTCC TTGCAGATCC 1260
 ACCTCGCTC CCACACTGGA GAGAGACCCT TCGTGTGCTC TGCTGTGGT CATCGCTTCA 1320
 CCACCAAGGG GTGCTCAAG GTGCACTTTC ACCGACATCC CCAGGTGAAG GCAAAACCCC 1380
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 GGACCCCTGA GCCAGGGTCA GAGACCTTGA AATTGCAGCA GTTGTGGAG AACATTGACA 1740
 AGGCCACCAC TGATCCCAAC GAATGTCTCA TTTGCCACCG AGTCTTAAGC TGTGAGAGCT 1800
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 CCTCAAGAT GCATTATGCG ACCCACACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG 1860
 GCGAGCCTT TTCTACCAAA GGTAACTTGA AGACACACCT TGGGTTTCC CAAACCAACA 1920
 CATCCATTAA GAGCGAGCAT TCGTGCCCA TCTGCCAGAA GAAGTTCACT AATGCCGTGA 1980
 TGCTGCAGCA ACATATTGCG ATGCACATGG GCGGTGAGT TCCCAACACG CCTCTGCCAG 2040
 AGAATCCCTG TGACTTTACG GGTCTGAGC CAATGACCGT GGGTGAGAAC GGCAGCACCG 2100
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 GCGCTATCTG CCATGATGAT GTCATCGAAA GCATCGATGT AGAGGAAGTC AGCTCCAGG 2160
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 80
 TGGCGGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGTTCTCT ACCCTCCCGG 3060
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 AAGGAGCAAT GCAGACACAG TGAATCTCT AGAATCTGCT TTGTTTGTGA AAGACTCATC 3300
 TCTCTGTGTT TCTTTTTTCT TACTGATATG CAAATGATGT TTACTAGGTT GGTGTGAGC 3360

ACAACCTCAG GCAAGTGCTA CAATCAGAT TGTGCTATG CTGCTTTGCA AAAAGTTG 3418

Seq ID NO: 16 DNA Sequence

Nucleic Acid Accession #: NM_005101

Coding sequence: 76..573

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CCACAGCCCA	CAGCCATGGG	CTGGGACCTG	ACGGTGAAGA	TGCTGGCGGG	CAACGAATTC	120
CAGGTGTCCC	TGAGCAGCTC	CATGTCCGGT	TCAGAGCTGA	AGGCCGAGAT	CACCCAGAAG	180
ATTGGCGTGC	ACGCTTCCCA	GCAGCGTCTG	GCTGTCCACC	CGAGCGGTGT	GGCGCTGCAG	240
GACAGGGTCC	CCCTTGCCAG	CCAGGGCCTG	GGCCCTGGCA	GCAAGGTCTT	GCTGGTGGTG	300
GACAAATGCG	ACGAACCTCT	GAGCATCTCT	GTGAGGAATA	ACAAGGGCCG	CAGCAGCACC	360
TACGAGGTCC	GGCTGACGCA	GACCGTGGCC	CACCTGAAGC	AGCAAGTGAG	CGGCTGGAG	420
GGTGTGCAGG	ACGACCTGTT	CTGGCTGACC	TTGAGGGGGA	AGCCCCTGGA	GGACCAGCTC	480
CGCGTGGGGG	AGTACGGCCT	CAAGCCCCCT	AGCACCGTGT	TCATGAATCT	GGCGCTCGGG	540
GGAGGCGGCA	CAGAGCCTGG	CGGGCGGAGC	TAAGGGCCTC	CACCAGCATC	CGAGCAGGAT	600
CAAGGGCCCG	AAATAAAGGC	TGTTGTAAGA	GAAT			634

Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 62..895

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TATGATCATC	TTAATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
CAAGGATGGA	ATTTTTTCAT	ACTCCATATG	GCTTGAAACG	GCAGCCGGTG	TGTACCACAG	180
AGAAGCACGG	TCTGGCAAA	ACAAGCTCAC	CTACGCAGAA	GCTAAGGCGG	TGTGTGAATT	240
TGAAGGCGGC	CATCTCGCAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGGATTTC	300
TGTCGTGTCT	CTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTT	TGAAGCCAGG	360
GCCCAACTGT	GGATTGGGAA	AAACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
TGAAAGATGG	GATGCTTATT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GGCTCTTTAC	480
AGATCCAAAG	CAATTTTATA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAT	540
CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTTAGATT	600
TGACCTTGAA	GATGACCCAG	GTTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
TGATGTCCAT	GGCTTTGTGG	GAAGATACTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
TACAGGAATG	GTCAATGACT	TGAAGTTTCT	AAGTGATGCT	TCAGTGACAG	CTGGAGGTTT	780
CCAAATCAAA	TATGTTGCAG	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAATACAAG	840
TACTACTTCT	ACTGGAAATA	AAAACTTTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAAA	900
AAAAAAAGGA	TGATCAAAAC	ACACAGTGTT	TATGTTGGAA	TCCTTTGGAA	CCCTTTGAT	960
CTCACTGTTA	TTATTAACAT	TTATTTATTA	TTTTTCTAAA	TGTGAAAGCA	ATACATAATT	1020
TAGGGAATAT	TGGAAATAT	AGGAACTTT	AAACGAGAAA	ATGAAACCTC	TCATAATCCC	1080
ACTGCATAGA	AATAACAGC	GTAAACATT	TCATATTTTT	TTCTTTCACT	CATTTTTCTA	1140
TTTGTGGTAT	ATGTATATAT	GTACCTATAT	GTATTTGCAT	TTGAAATTTT	GGAAATCCTG	1200
TCATATGACA	GTTTGTGATT	ATACTTTTTA	AATCTTGAAC	TTTATAAACA	TTTTCTGAAA	1260
TCATTGATTA	TTCTACAAAA	ACATGATTTT	AAACAGCTGT	AAAATATTCT	ATGATATGAA	1320
TGTTTTATGC	ATTATTTAAG	CCTGTCTCTA	TTGTTGGAAT	TTCAGTTCAT	TTTCATAAAT	1380
ATTGTTGCAA	TAAATATCCT	TGAACACACA	AAAAAAAAAA	AA		

Seq ID NO: 18 DNA sequence

Nucleic Acid Accession #: NM_007115.1

Coding sequence: 69..902

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CTGACGATAT	GATCATCTTA	ATTACTTTAT	TTCTCTTGCT	ATGGGAAGAC	ACTCAAGGAT	120
GGGGATTCAA	GGATGGAATT	TTTCATAACT	CCATATGGCT	TGAACGAGCA	GCCGGTGTGT	180
ACCACAGAGA	AGCACGGTCT	GGCAAAATCA	AGCTCACCTA	CGCAGAAGCT	AAGGCGGTGT	240
GTGAATTTGA	AGGCGGCCAT	CTCGCAACTT	ACAAGCAGCT	AGAGGCAGCC	AGAAAAATTG	300
GATTTCTATG	CTGTGCTGCT	GGATGGATGG	CTAAGGGCAG	AGTTGGATAC	CCCATTTGTA	360
AGCCAGGGCC	CAACTGATGA	TTTGGAAAAA	CTGGCATTAT	TGATTATGGA	ATCCGTCTCA	420
ATAGGAGTGA	AAGATGGGAT	GCCTATTGCT	ACAACCCACA	CGCAAAGGAG	TGTGGTGGCG	480
TCCTTACAGA	TCCAAAGCGA	ATTTTTAAAT	CTCCAGGCTT	CCCAATGAG	TACGAAGATA	540
ACCAAACTCT	CTACTGGCAC	ATTAGACTCA	AGTATGGTCA	GCGTATTTC	CTGAGTTTTT	600
TAGATTTTGA	CCTTGAAGAT	GACCCAGGTT	GCTTGGCTGA	TTATGTTGAA	ATATATGACA	660
GTTACGATGA	TGTCATGGC	TTTGTGGGAA	GATAGTGTGG	AGATGAGCTT	CCAGATGACA	720
TCATCAGTAC	AGGAAATGTC	ATGACCTTGA	AGTTTCTAAG	TGATGCTTCA	GTGACAGCTG	780
GAGGTTTCCA	AATCAAATAT	GTTCGAATGG	ATCCTGTATC	CAATCCAGT	CAAGGAAAAA	840
ATACAAGTAC	TACTTCTACT	GGAAATAAAA	ACTTTTTAGC	TGGAAGATTT	AGCCACTTAT	900
AAAAAAAGAA	AAGGATGATC	AAAAACACACA	GTGTTTATGT	TGGAATCTTT	TGGAACCTCT	960
TTGATCTCAC	TGTTATTATT	AACATTTATT	TATTATTTTT	CTAATGTGTA	AAGAAATACA	1020
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ATCCCACTGC	ATAGAAATAA	CAAGCGTTAA	CATTTTCATA	TTTTTTTCTT	TCAGTCATTT	1140
TGTATTTTGT	GGTATATGTA	TATATGTACC	TATATGTATT	TGCATTTGAA	ATTTTGGAA	1200
CCTGCTCTAT	GTACAGTTTT	GTATTATACT	TTTTAAATCT	TGAACCTTAT	GAACATTTTC	1260
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ATGAATGTTT	TATGCATTAT	TTAAGCCTGT	CTCTATTGTT	GGAATTTTCA	GTCATTTTCA	1380
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Seq ID NO: 19 DNA Sequence

Nucleic Acid Accession #: NM_006398.1

Coding sequence: 19..516

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	GAACATGTCC	GGTCTAAGAC	CAAGGTTCCCT	GTGCAGGACC	AGGTTCTTTT	GCTGGGCTCC	180
5	AAGATCTTAA	AGCCACGGAG	AAGCCTCTCA	TCTTATGGCA	TTGACAAAGA	GAAGACCATC	240
	CACCTTACCC	TGAAAGTGGT	GAAGCCCACT	GATGAGGAGC	TGCCCTTGTT	TCTTGTGGAG	300
	TCAGGTGATG	AGGCAAGAG	GCACCTCCTC	CAGGTGCGAA	GGTCCAGCTC	AGTGGCACAA	360
	GTGAAAGCAA	TGATCGAGAC	TAAGACGGGT	ATAATCCCTG	AGACCCAGAT	TGTACTTTCG	420
	AATGGAAGA	GACTGGAAGA	TGGGAAGATG	ATGGCAGATT	ACGGCATCAG	AAAGGGCAAC	480
10	TTACTCTTCC	TGGCATCTTA	TGTATTGGA	GGGTGACCAC	CCTGGGGATG	GGGTGTTGGC	540
	AGGGGTCAAA	AAGCTTATTT	CTTTTAACTC	CTTACTCAAC	GAACACATCT	TCTGATGATT	600
	TCCCAAAAT	AATGAGAATG	AGATGAGTAG	AGTAAGATTT	GGGTGGGATG	GGTAGGATGA	660
	AGTATATTGC	CCAACCTCTAT	GTTTCTTTGA	TTCTAACACA	ATTAATTAAG	TGACATGATT	720
	TTTACTAATG	TATTACTGAG	ACTAGTAAAT	AAATTTTTAA	GGCAAAATAG	AGCATTTC	777
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	Nucleic Acid Accession #: NM_002358.2						
	Coding sequence: 75..692						
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	GGCGCGAAT	CGTGGCCGAG	TTCTTCTCAT	TCGGCATCAA	CAGCATTTTA	TATCAGCGTG	180
	GCATATATCC	ATCTGAAACC	TTTACTCGAG	TGCAGAAATA	CGGACTCACC	TTGCTTTGTA	240
25	CTACTGATCT	TGAGCTCATA	AAATACCTAA	ATAATGTGGT	GGAACTCACTG	AAAGATTGGT	300
	TATACAAGTG	TTCACTTCAG	AACTGGTTTG	TAGTTATCTC	AAATATTGAA	AGTGGTGAGG	360
	TCCTGGAAG	ATGGCAGTTT	GATATTGAGT	GTGACAAGAC	TGCAAAAGAT	GACAGTGCAC	420
	CCAGAGAAA	GTCTCAGAAA	GCTATCCAGG	ATGAAATCCG	TTCACTGATC	AGACAGATCA	480
	CAGCTACGGT	GACATTTCTG	CCACTGTTGG	AAGTTTCTTG	TTCAITTTGAT	CTGCTGATTT	540
30	ATACAGACAA	AGATTGTGGT	GTACCTGAAA	AATGGGAAGA	GTCCGGACCA	CAGTTTATTA	600
	CCAATTCTGA	GGAGTCCCGC	CTTCGTTTCT	TTACTACTAC	AATCCACAAA	GTAAATAGCA	660
	TGGTGGCCTA	CAAAATTCCT	GTCAATGACT	GAGGATGACA	TGAGGAAAAT	AATGTAATTG	720
	TAATTTTGAA	ATGTGGTTTT	CCTGAAATCA	GGTCATCTAT	AGTTGATATG	TTTATTTTCA	780
	TTGGTTAATT	TTTACATGGA	GAAAACCAAA	ATGATACTTA	CTGAACTGTG	TGTAATTGTT	840
35	CCTTTATTTT	TTTGGTACCT	ATTTGACTTA	CCATGGAGTT	AACATCATGA	ATTTATTGCA	900
	CATTGTTCAA	AAGGAACCCG	GAGGTTTTTT	TGTCAACATT	GTGATGTATA	TTCTTTTGAA	960
	GATAGTAACT	GTAGATGGAA	AAACTTGTGC	TATAAGGCTA	GATGCTTTCC	TAAATCAGAT	1020
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	AAAGGAAGTC	TAAATATTCA	GAATCTTTGT	TAAAGTCTGT	AAAGTAACCT	ATAATCTATA	1140
40	AACAATGAAA	TATTGCTGTA	TAGCTCCTTT	TGACCTTCAT	TTCAATGATA	GTTTTCCCTA	1200
	TTGAATCAGT	TTCCAATTAT	TTGACTTTAA	TTTATGTAA	TTGAACCTAT	GAAGCAATGG	1260
	ATATTTGTAC	TGTTTAAATG	TCTGTGATAC	AGAACTCTTA	AAAATGTTTT	TTCAATGTTT	1320
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	AAAAAAAAAA						1390
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	GGCCCAAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAACGCGAGC	CTCAATGATG	180
	AGTGGGTACA	GGTGGCCCTT	CACTTCGCCA	TCAGCGAGTA	TAACAAGGCC	ACCAAGATG	240
55	ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
	ATTACTTCTT	CGAGCTAGAG	GTGGGCGGCA	CCATATGTAC	CAAGTCCGAG	CCCAACTTGG	360
	ACACCTGTGC	CTTCTATGAA	CAGCCAGAAC	TGCAGAGAA	ACAGTTGTGC	TCTTTGAGAA	420
	TCTACGAAGT	TCCTGGGAG	AACAGAAAGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAACTCT	480
	AGGGATCTGT	GCCAGGCCAT	TCCGACCAGC	CACCAACCC	TCCCAACCCC	TGTAGTGCTC	540
60	CCACCCCTGG	ACTGGTGGCC	CCCACCCCTG	GGGAGGCGCT	CCCATGTGCG	TGGCCCAAGA	600
	GACAGACAGA	GAAGGCTGCA	GGAGTCTCTT	GTTGCTCAGC	AGGGCGCTCT	GCCTCCCTC	660
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	GAGGCGGAGC	CAGCCGAGGG	AGTGAACCAT	GGACAAGTTG	AAATGCCCGA	GTTTCTTCAA	120
	GTGCAAGGAG	AAGGAGAAAG	TGTGGGCTTC	ATCAGAGAA	TTCCATGTTG	GTGAAAATGA	180
	TGAGAATCAG	GACCGTGGTA	ACTGGTCCAA	AAAATGGGAT	TATCTTCTAT	CTATGATTGG	240
	ATACGCACTG	GGATTAGGAA	ATGTGTGGAG	ATTTCCATAT	CTGACCTACA	GCAATGGTGG	300
75	AGGCGCCTTC	TTGATACCTT	ATGCAATTAT	GTTAGCATTG	GCTGGTTTAC	CTTTGTCTTT	360
	TCTGGAGTGT	TCACTGGGAG	AATTTGTAG	CTTAGGTCCA	GTTTCAGTTT	GGAGGATTCT	420
	TCCATTGTTT	CAAGGTGTGG	GAATTACAA	GGTCTGTATC	TCCATTTTGT	TGACAACTCA	480
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	ACCATGGAAA	AATTTGTTCT	CGTGGTTCAG	TAAAAACTGT	AGCAGATCAC	CAATAGTAAC	600
80	TCACTGTAAT	GTGAGTACAG	TGAATAAAGG	AATACAAGAG	ATCATCCAAA	TGAATAAAG	660
	CTGGGTAGAC	ATCAACAATT	TTACCTGCAT	CAACGGCAGT	GAAATTTATC	AGCCAGGGCA	720
	GCTTCCAGT	GAAACAATTT	GGAATAAAGT	GGCGCTCCAA	CGGTCAAGTG	GAATGAATGA	780
	GACTCGAGTA	ATTGTTTGGT	ATTAGCACT	TTGTCTTCTT	CTGGCTTGGC	TCATAGTTGG	840
	AGCAGCACTA	TTTAAAGGAA	TCAAATCGTC	TGGCAAGGTG	GTATATTTTA	CAGCTCTTTT	900
	CCCTATGTG	GTCCTACTCA	TCTGTTAGT	ACGAGGTGCA	ACTCTGGAGG	GTGCTTCAAA	960

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 60 GAGATAATT ATGTTATTGT ATTGTAAACC ATTAATGAAA ACTTTTTCAC AGTTGAGTGA 4500
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Seq ID NO: 23 DNA sequence
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 Coding sequence: 19..516

65 1 11 21 31 41 51
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 80 TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAGAAATAG AGCATTC

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5	AACTCGGCGC	TGGTGTCTGT	GGCGGTGCGC	GACCGCGGCC	TGCACACGCC	CATGTACTAC	180
	TTCTCTTGCC	ACCTGGCCTT	GGTAGACGCG	GGCTTCACTA	CTAGCGTGGT	GCGCGCGCTG	240
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	TGCGCATCGC	TGGTCTGGG	TTGGGCGGAA	TGGTCTCTCC	TGGCGGTGAT	GGCTCTGGAC	360
	CGCGGGGCGC	CAGTGTGCGC	CCGCTGCGC	TATGCGGGGC	TGCTCTCCCC	GCGCTATGT	420
10	CGCAGCTGG	CCAGCGCCTC	CTGGCTAAGC	GGCTCACCAC	ACTCGGTTGC	GCAAAACCGC	480
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	GAGCCCGCGC	AGCGCTACAA	CCAGGCACGG	GGCAAGTTCT	TATCGCTCTT	CTACACCGTG	840
	GTCAACCTCG	CTCTCAACCC	GCTCATCTAC	ACCCTCAGGA	ATAAGAAAGT	GAAGGGGGCA	900
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	CGTTTCCATC	GTCTCTGTAT	CCGACGCGCT	GGGCGATGGA	TCCGTTTACG	GAGAAACTGC	180
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	CACCTCTTCT	ACCAATGCCA	TCAGAGGAAA	AGGCTGCTTC	CCCTCCCAAA	CCTCTGCTTT	720
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	GTTGTGAGGG	ACAAAATCCT	GAGCTACTTC	CAAAAACCTCC	TATTAGTCCT	CTGAAAACGG	1140
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	GTCCAGCTCG	TAGCACAACC	CACAGAACCC	CCATTATTAC	TCCAAATACA	AAGGCCATCC	1380
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	AGGCAAAATC	CTTAAAGATG	ACATCAGACC	CAAAGGTTGA	GCAGAAAATT	GAAGTGATAC	1800
55	GTGAAATTTG	GATGAGTGTG	GATGATGATG	ATATCAATAG	TTGCAAGATA	ATTAATGACC	1860
	TCTTCAGTGA	TGTCCTAGAG	GAAGGTGAAC	TAGATATGGA	GAAGAGCCAA	GAGGAGATGG	1920
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	CTTTACTTGC	ACCATTTGCA	CAAAACAGTT	GTGTGGTAAG	TCCAGAGAGT	TTAGTGTTCA	2040
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	TGCAAGATGT	ATCCAATGAC	TTTGAATAAA	ATATTGAAGT	TTACAGCTTG	GTGCAAAAGA	2820
	AAGATCCCTC	AGGCCTTGAT	AAGAAGAAAA	AAACATCCAA	GTCCAAGGCT	ATTACTCCAA	2880
	AGCGACTCCT	CACATCTATA	ACCACAAAAA	GCAACATTCA	TTCTTCAGTC	ATGGCCAGTC	2940
	CAGGAGGTCT	TAGTGCTGTG	CGAACCAGCA	ACTTCGCCCT	TGTTGGATCT	TACACATTAT	3000
75	CATTGTCTTC	AGTAGGAAAT	ACTAAGTTTG	TTCTGGACAA	GGTCCCTTTT	TTATCTTCTT	3060
	TGGAAGGTCA	TATTATTTTA	AAAATAAAAT	GTCAAGTGAA	TTCCAGTGTT	GAAGAAAGAG	3120
	GTTTTCTAAC	CATATTTGAA	GATGTTAGTG	GTTTGTGTGC	CTGSCATCGA	AGATGGTGTG	3180
	TTCTTTCTGG	AAACTGTATA	TCTTATTGGA	CTTATCCAGA	TGATGAGAAA	CGCAAGAAATC	3240
	CCATAGGAAG	GATAAATCTG	GCTAATTGTA	CCAGTGTGCA	GATAGAACCA	GCCACACAGG	3300
	AATTTTGTGC	AAGACGCAAC	ACTTTTGAAT	TAATTAATGT	CCGACCACAA	AGAGAAGATG	3360
80	ACCGAGAGAC	TCTTGTGAGC	CAATGCAGGG	ACACACTCTG	TGTTACCAAG	AACTGCTGTG	3420
	CTGCAGATAC	TAAAGAAGAG	CGGATCTCTT	GGATGCAAAA	ACTCAATCAA	GTTCTTGTGG	3480
	ATATTTCGCT	TGGCAACCTT	GATGCTTGCT	ACAAACCTAT	TGGAAAGGCT	TAAACCGGGA	3540
	AATTTCCATG	CTATCTAGAG	GTTTTTGAAT	TCACTTAAG	AAACACACTT	AAGAGCATCA	3600
	GATTTACTGA	TTGCATTTTA	TGCTTTAAGT	ACGAAAGGGT	TTGTGCCAAT	ATTCACTACG	3660

	TATTATGCAG	TATTTATATC	TTTTGTATGT	AAAACCTTAA	CTGATTTCCTG	TCATTTCATCA	3720
	ATGAGTAGAA	GTAAATACAT	TATAGTTGAT	TTTGCTAAAT	CTTAATTTAA	AAGCCTCATT	3780
	TTCCTAGAAA	TCTAATTATT	CAGTTATTCA	TGACAATATT	TTTTTAAAG	TAAGAAATTC	3840
	TGAGTTGTCT	TCTTGGAGCT	GTAGGTCTTG	AAGCAGCAAC	GTCTTTCAGG	GGTTGGAGAC	3900
5	AGAAACCCAT	TCTCCAATCT	CAGTAGTTTT	TTGGAAGGC	TGTGATCATT	TATTGATCGT	3960
	GATATGACTT	GTACTAGGG	TACTGAAAA	AATGTCTAAG	GCCTTTACAG	AAACATTTTT	4020
	AGTAATGAGG	ATGAGAACTT	TTTCAAATAG	CAAAATATATA	TTGGCTTAAA	GCATGAGGCT	4080
	GTCTTCAGAA	AAGTGATGTG	GACATAGGAG	GCAATGTGTG	AGACTTGGGG	GTTCATATT	4140
	TTATATAGAA	GAGTTAATA	GCACATGGTT	TACATTTACT	CAGCTACTAT	ATATGCAGTG	4200
10	TGGTGACAT	TTTCACAGAA	TTCTGGCTTC	ATTAAGATCA	TTATTTTTCG	TGCGTAGCTT	4260
	ACAGACTTAG	CATATTAGTT	TTTTCTACTC	CTACAAGTGT	AAATGAAAA	ATCTTTATAT	4320
	TAAAAAGTA	AACTGTTATG	AAGCTGCTAT	GTACTAATAA	TACTTTGCTT	GCCAAAGTGT	4380
	TTGGGTTTTC	TTGTTGTTTG	TTTGTGTTT	TGTTTTGGT	TCATGAACAA	CAGTGTCTAG	4440
	AAACCCATT	TGAAAGTGG	AAATTAATA	GTACCTATC	ACCTTTAAAC	GCCTTTTTTT	4500
15	AAAAATTATA	AATATTGTAA	AGCAGGGTCT	CAACTTTTAA	ATACACTTTG	AACCTCTTCT	4560
	CTGAATTATT	AAAGTTCTTT	ATGACCTCAT	TTATAAACAC	TAAATTCGT	CACCTCCTGT	4620
	CATTTTATT	TTTATTCT	CAAAATGATT	TTTTCTGTG	CATATTATAA	AAATATATT	4680
	TATGAGCTCT	TACTCAAATA	AATACCTGTA	AATGCTAAAA	GG		4720
20	Seq ID NO: 26 DNA Sequence						
	Nucleic Acid Accession #: NM_018098.4						
	Coding sequence: 29..2680						
	1	11	21	31	41	51	
25	AGAGTGCTGA	TTTGAAGAA	TACAAATCAT	GGCTGAAAT	AGTGATTATA	CATCCACTAC	60
	TGGGAGGACT	AGCTTGGCAG	ACTCTTCCAT	TTTTGATTCT	AAAGTTACTG	AGATTTCCAA	120
	GGAAACTCTA	CTTATTGGAT	CTACTTCATA	TGTAGAAGAA	GAGATGCCTC	AGATTGAAAC	180
	AAGAGTGATA	TTGGTTCAAG	AAGCTGGAAA	ACAAGAAGAA	CTTATAAAG	CCTTAAAGGA	240
	CATTAAAGTG	GGCTTTGTAA	AGATGGAGTC	AGTGAAGAA	TTTGAAGGTT	TGGATTCTCC	300
30	GGAAATTGAA	AATGTATTGT	TAGTCACGGA	CTTTCAGGAT	TCTGTCTTTA	ATGACCTCTA	360
	CAAGGCTGAT	TGTAGAGTTA	TTGGACCCAC	AGTTGTATTA	AATTGTTTCA	AAAAAGGAGA	420
	GCCTTTCGCA	TTTTCATGTC	GCCGTTGTA	TTGTACAAGT	ATGATGAATC	TAGTACTATG	480
	CTTTACTGGA	TTTAGGAAAA	AAGAAGAACT	AGTCAGGTTG	GTGACATTGG	TCCATCACAT	540
	GGGTGGAGTT	ATTGCGAAAG	ACTTTAAATC	AAAAGTTACA	CATTTGGTGG	CAAAATGTAC	600
35	ACAAAGGAGAA	AAATTTCAGG	TTGCTGTGAG	TCTAGTACT	CCAATTATGA	AGCCAGAATG	660
	GATTATATAA	GCTTGGGAAA	GGCGGAATGA	ACAGGATTTC	TATGCAGCAG	TTGATGACTT	720
	TAGAAATGAA	TTTAAAGTTC	TCCCAATTCA	AGATTGTATT	TTAAGTTTCC	TGGGATTTTC	780
	AGATGAAGAG	AAAACCAATA	TGGAAGAAAT	GACTGAAATG	CAAGGAGGTA	AATATTATCC	840
	GCTTGGAGAT	GAAAGATGCA	CTCACCTTGT	AGTTGAAGAG	AATATAGTAA	AAGATCTTCC	900
40	CTTTGAACCT	TCAAAGAAAC	TTTATGTTGT	CAAGCAAGAG	TGGTTCTGGG	GAAGCATTCA	960
	AATGGATGCC	CGAGCTGGAG	AAACTATGTA	TTTATATGAA	AAGGCAATA	CTCTGAGCT	1020
	CAAGAATACA	GTGCTCAATG	TTTCTCTAAA	TACCCTAAC	AGCAATCGCA	AACGACGTGG	1080
	TTTAAAGAA	ACACTTGCTC	AGCTTTCAAG	AGAGACAGAC	GTGTCACCAT	TCCACCCCG	1140
	TAAGCCGCCA	TCAGCTGAGC	ATTCCTTTTC	CATAGGGTCA	CTCCTAGATA	TCTCCAACAC	1200
45	ACCAGAGTCT	AGCATTAACT	ATGGAGACAC	CCCAAAGTCT	TGTACTAAGT	CTTCTAAAG	1260
	CTCCACTCCA	GTTCCTTCAA	AGCAGTCAG	AAGGTGGCAA	GTTCGAAAAG	AGCTTTATCA	1320
	AACTGAAAGT	AATTATGTTA	ATATATTGGC	AACAATTATT	CAGTATTATC	AAGTACCATT	1380
	GGAAAGAGGAA	GGACAACGTG	GTGGACCTAT	CCTTGACCCA	GAGGAGATTA	AGACTATTTT	1440
50	TGGTAGCATC	CCAGATATCT	TTGATGTACA	CACTAAGATA	AAGGATGATC	TTGAAGACCT	1500
	TATAGTTAAT	TGGATGAGA	GCAAAAGCAT	TGGTGACATT	TTTCTGAAAT	ATTCAAAAGA	1560
	TTTGGTAAAA	ACCTACCTCT	CCTTTGTAAA	CTTCTTTGAA	ATGAGCAAGG	AAACAATTAT	1620
	TAAATGTGAA	AAACAGAAAC	CAAGATTTC	TGCTTTTCTC	AAGATAAAC	AAGCAAAACC	1680
	AGAAATGTGA	CGGCAGAGCC	TTGTTGAAC	TCTTATCCGA	CCAGTACAGA	GGTTACCCAG	1740
55	TGTTGCATTA	CTTTAAATG	ATCTTAAGAA	GCATACAGCT	GATGAAAATC	CAGACAAAAG	1800
	CACCTTAGAA	AAAGCTATTG	GATCACTGAA	GGAAAGTAAT	ACGCATATTA	ATGAGGATAA	1860
	GAGAAAACA	GAGCTCAAA	AGCAAAATTT	TGATGTTGTT	TATGAAGTAG	ATGGATGCC	1920
	AGCTAATCTT	TTATCTTCTC	ACCGAAGCTT	AGTACAGCGG	GTGAAACAA	TTTCTCTAGG	1980
	TGAGCACCCC	TGTGACAGAG	GAGAACAAGT	AATCTCTTCT	CTCTTCAATG	ATTGCCCTAGA	2040
60	GATAGCAAGA	AAACGGCACA	AGGTTATTGG	CACCTTTAGG	AGTCCTCATG	GCCAAACCCG	2100
	ACCCCCAGCT	TCTCTTAAGC	ATATTACCT	AATGCCCTCT	TCTCAGATTA	AGAAGGTATT	2160
	GGACATAAGA	GAGACAGAAG	ATTGCCATAA	TGCTTTTGCC	TTGCTTGTA	GGCCACCAAC	2220
	AGAGCAGGCA	AATGTGCTAC	TCAGTTTCCA	GATGACATCA	GATGAACCTC	CAAAAGAAAA	2280
	CTGGCTAAAG	ATGCTGTGTC	GACATGTAGC	TAACACCATT	TGTAAGCAG	ATGCTGAGAA	2340
65	TCTTATTTAT	ACTGCTGATC	CAGAATCCTT	TGAAGTAAAT	ACAAAAGATA	TGGACAGTAC	2400
	ATTGAGTAGA	GCATCAAGAG	CAATAAAAAA	GACTTCAAAA	AAGGTTACAA	GAGCAATCTC	2460
	TTTCTCCAAA	ACTCCAAAAA	GAGCTCTTCG	AAGGGCTCTT	ATGACATCCC	ACGGCTCAGT	2520
	GGAGGGAAGA	AGTCTTCCA	GCAATGATAA	GCATGTAATG	AGTCGTCTTT	CTAGCACATC	2580
	ATCATTAGCA	GGTATCCCTT	CTCCCTCCCT	TGTCAGCCTT	CCTTCCTTCT	TTGAAAGGAG	2640
70	AAGTCATACG	TAAAGTAGAT	CTACAATCA	TTGATATGA	AGCGTTACCA	AAATCTTAAA	2700
	TTATAGAAAT	GTATAGACAC	CTCATACTCA	AATAAGAAAC	TGACTTAAAT	GGTACTTGTA	2760
	ATTAGCACTT	GGTGAAGCT	GGAAGGAAGA	TAAATAACAC	TAAACTATGC	TATTTGATTT	2820
	TTCTTCTTGA	AAGAGTAAGG	TTTACCTGTT	ACATTTTCAA	GTAAATTCAT	GTAAAAATG	2880
	ATAGTGATT	TGATGTAATT	TATCTCTTGT	TTGAATCTGT	CATTCAAAGG	CCAATAATTT	2940
	AAGTTGCTAT	CAGCTGATAT	TAGTAGCTTT	GCAACCCCTG	TAGAGTAAAT	AAATTTTATG	3000
75	GGCGGGTGCC	AAATCTGCT	GTGAATCTAT	TTGTATAGTA	TCCATGAATG	AATTTATGGA	3060
	AATAGATATT	TGTGCAGCTC	AATTTATGCA	GAGATTAAAT	GACATCATAA	TACTGGATGA	3120
	AAACTTGCAAT	AGAAATCTGA	TTAAATAGTG	GCTGCTGTTT	ACATGTGCAG	TTTGAAGTAT	3180
	TTAAATAACC	ACTCCTTTCA	CAGTTTATTT	TCTTCTCAAG	CGTTTTCAAG	ATCTAGCATG	3240
	TGGATTTTAA	AAGATTGCCC	CTCATTAACA	AGAATAACAT	TTAAAGGAGA	TTGTTTCAAA	3300
80	ATATTTTTCG	AAATTGAGAT	AAGGACAGAA	AGATTGAGAA	ACATTGTATA	TTTTGCAAAA	3360
	ACAAGATGTT	TGTAGCTGTT	TCAGAGAGAG	TACGGTATAT	TTATGGTAAAT	TTTATCCAAT	3420
	AGCAAAATCTT	GATTTAGTTT	GATAGTGTGT	GGAATTTTAT	TTTGAAGGAT	AAGACCATGG	3480
	GAAAAATTGTG	TGAAAGACTG	TTTGTACCTT	TCATGAAATA	ATTCTGAAGT	TGCCATCAGT	3540
	TTTACTAATC	TTCTGTGAAA	TGCATAGATA	TGCGCATGTT	CAACTTTTAA	TTTGGTCTT	3600

5 ATAATTAAT GTAAATTTGA AATTTCATTT GCTGTTTCAA AGTGTGATAT CTTTCACAAT 3660
 AGCCTTTTTT TAGTCAGTAA TTCAGAATAA TCAAGTTTCA ATGGATAAAT GCATTTTTAT 3720
 TTCCTATTTT TTTAGGGAGT GCTACAAATG TTTGTCACTT AATTTTCAAG TTTCTGTTTT 3780
 AATAGTTAAC TGACTATAGA TTGTTTTCTA TGCCATGTAT GTGCCACTTC TGAGAGTAGT 3840
 AATGACTCT TTGCTACATT TTAAGAGCAA TTGTATTAGT AAGAACTTTG TAAATAAATA 3900
 CCTAAACCC AAGTGT 3916

Seq ID NO: 27 DNA Sequence

Nucleic Acid Accession #: NM_002497.1

Coding sequence: 135..1472

10
 15
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1 11 21 31 41 51
 | | | | |
 GGCACGAGTA GGGGTGGCGG GTCAGTGTCT CTCGGGGGCT TCTCCATCCA GGTCCCTGGA 60
 GTTCTTGCTC CTTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG GCGCACTCTG 120
 GCGACTGGCC GGCCATGCCT TCCCGGGCTG AGGACTATGA AGTGTGTAC ACCATTGGCA 180
 CAGGCTCCTA CGGCGCTGCG CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT 240
 GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTCTGAAG 300
 TGAATTTGCT TCGTGAACCT AAACATCCAA ACATCGTTCT TTAATATGAT CGGATTATTG 360
 ACCGGACCAA TACAACACTG TACATTGTAA TGAATATTG TGAAGGAGGG GATCTGGCTA 420
 GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTCGAG 480
 TGATGACTCA GTTGACTCTG GCGCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA 540
 CCGTATTGCA TCGGATCTT AAACAGCCA ATGTTTTCCT GGATGGCAAG CAAAACGTCA 600
 AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTT GCAAAACAT 660
 TTGTTGGCAC ACCTTATTAC ATGTCTCCTG AACAAATGAA TCGCATGTCC TACAATGAGA 720
 AATCAGATAT CTGGTCAATT GGCTGCTTGC TGTATGAGT ATGTGCATTA ATGCTCCAT 780
 TTACAGCTT TAGCCAGAAA GAACCTGCTG GGAATACTAG AGAAGGCAAA TTCAGGCGAA 840
 TTCCATACCG TTACTCTGAT GAATTGAATG AATATTATAC GAGGATGTTA AACTTAAAGG 900
 ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACC TTTAATAGCA GATTGCTGTT 960
 CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGCGGACA ATTAGGAGAG CCAGAAAAT 1020
 CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAACCTGAA GGAATTCAG TTACAGGAGC 1080
 GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTTG 1140
 TTCGTGAGAG ACTAGCAGAG GACAACTGG CTAGAGCAGA AAATCTGTTG AAGAAGTACA 1200
 GCTTGCTAAA GGAACGGAAG TTCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC 1260
 CATCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA 1320
 GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA 1380
 GGCTTCAACG TGCCAGCTG CGGCTCAAG CCCTGTGAGA TATTGAGAAA AATTACCAAC 1440
 TGAAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC 1500
 AGGATGTAAT ATTACCAACC TTTAAGACT GATATTCAAA TGCTGTAGTG TTGAATACTT 1560
 GGCCCATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTGGAAAT GGTTTTACTG 1620
 TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TTTTCTTTC TTTTAAAGAA 1680
 ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTAATC CTGTGTGTGA TTAAGTAGT 1740
 GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAT AATATTAGGA AAAAAATATT 1800
 TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT 1860
 TGTCATGTCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTGTAG CTTGAAAAAC 1920
 CCAGTTAGAT GCAATTTGGT CATTAAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC 1980
 TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT 2040
 TTTTCTCTG TTTAACAGAA TATGAGCTGT CTGTCAATTA CTTACTTCTT TCCCACTAAA 2100
 TAAAGAATT CTTCACTTA 2119

Seq ID NO: 28 DNA Sequence

Nucleic Acid Accession #: Eos sequence

55
 60
 65
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1 11 21 31 41 51
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 GGGAGCTACA ATGTTTGTG ATTATTCAT CTGATGTGAA AAAGGCAGTG AATTTAATAG 60
 AAAATAACTT CGTAGAGCAA AATCTCAGGT GTGTTTTTTT AGTGCCGAG TCTTGGATGA 120
 TGGGTTCTTA GAAGCTCTCA ACATCTCTTC TTAATTGGAG AAAGTGTAA GCCCCAAAGT 180
 AGCTGGAGCA GTACATCTTC AATTTTGTAC AAGAAAAACAG GAACCTGATT ACTTTGAGTG 240
 CTATTCAATTA GTTCTGCTT TCAATTGAGAA TGCAACAAAA GCCAACTAGG CTGCTGTCAA 300
 CTCCTTGCMN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 360
 CTAGGAGTCT TTTTCATCTG AGTGAGTCT GCACAAATGA TCTTCAAAGC ATTTAGCCA 420
 CCAGAGGAAT TCTCTGAAA TACCCAAAAT CCATCAGTAT CTTGAATCAT GCTGGATTTT 480
 GAAGAATTCT TAACAAGCCA TGTAAGGGG GCTCTCTGGC CTGAAATAG TGATGTTTTT 540
 TATACAGAAA GGAGAATGCA GAATGGTCAG ACTACCATGC ACTGTTAAAT TTGATTTCAA 600
 GAAATTACAG GAAAACTTTC CAAAGTTCCA TCTCACAGAA ATTATTTTAA CAAAGAAATC 660
 CAAGATAAGT TTAGTTTTAT GGAAGACTTT TATGTGGTTT TTAATCACTC TTAATCTCAG 720
 ACATCAACAG ATGATTACAT CACTTATTTA GCTAGTAAAT TTATTAATAT AAAAACTCAG 780
 AGACATTCOA ATATCCACAT TGCTTACACC ATTAGGCATA GATTCAAGTG CAGCTATGAC 840
 AATTGAAAAA AAGCTGTTTT GTGATTTAAA GGTTTAAAT TCTCTAACCA AACTGCTTGA 900
 TCCAGATGCA GGACTGCAAA TGTTAATATT TGTCTGGAA GAACAATCAA ATAAGACTTA 960
 AGAGGAAAAG GAATGGCCAC AATCCACCTG AATTTTTTTT TTAAGAAAGT TGCAGCTTAC 1020
 TAAATCAGAA TGAATAAGTA AGTACAAGAT TATAACAAA ATGCAATCAA ACTTTTCTTA 1080
 AGCTTACCTA AAGTTATTTT ATCTGAAAAT TTCAAGCAAC TTTGTTCAAC ATTAATTTGA 1140
 CAATCTAAAC TAACAAGTCT TTTGAATTTA TGCAATGTTG TAAACATCT CTCTATTAAAC 1200
 TGTATTACCT AAGGCTAAAC CTAAAATTTT TAAGCAAAAT TAGAAAAATA GTCTTCACTC 1260
 ATCAAAAAAT AAAGTTTGTG ACATTTAGTA TTTTCCCAAG AAAAAAATAA GTCTTCACTC 1320
 AAAAAAATAA AGAGTCTGTG CAAAATGTCA TTTTCCCAAG AAAAAAATAA GTCTTCACTC 1380
 CTAATATCCA AAAAAAATAA AAATTTGAGA TGGGTTTCCC AAGGAAAAA CAGCAATCA 1440
 AACACAAAAA ACAAGAACAA AAAAAAATA GACAAAAAGA 1480

Seq ID NO: 29 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 TCCCTGCAGC TGTGTTTGA CAGGTCAATT ACCATGCTGT CCTCCAGGTT CAACAGTATG 60

5 GCTCCAAAGG ATGAAATTTT ATTCTGATTT TCTGGCTGAA GACTATTCTC TTTGTGTATG 120
 TCCACCACAG TTACTTTATC CCTTCATCTG TGGATGGGCA GGAAGCTCCA AACTGTCCAA 180
 GGAGATAGTT CTGTTGTGAT TACTTCATTG AGAAATTTAA CTTATGAGCA GTTGAAAGGA 240
 ATGCAAGTTG CTGCAAAATC AGAATGAAGA GTGCAAAACG ASSRAGCTAC AATGTTTGT 300
 CATTATTCAC TCTGATGTGA AAAAGGCAGT GAATTTAATA GAAATAACT TCGTAGAGYA 360
 AAATCTCAGG TGTGTTTITT TAGTGCCGCA GTCTTGGATG ATGGGTCTCT AGAAGCTCTC 420
 AAACATCTCT TCTTAATTGG AGAAAGTGTT AAGCCCCAAA GTAGCTGGAG CAGTACATCT 480
 TCAATTTTGT ACAAGAAAGC AGGAACTTGA TTACTTTGAG TGCTATTCTAT TAGTTTCTGC 540
 10 TTTCAATTGAG AATGCAACAA AAGCCAATA GGCTGCTGCT AACTCCTTGC TGGACTTCTT 600
 CTGCCATGT CACAGGAATC GTAATCTCAC TGGACAATTA ACTAGGGAGT CTTTCATCTT 660
 GAGTGACTGC TGCACAAATG ATCTTCAAGG CATTTTAGCC ACCAGAGGAA TTCTCTTGAA 720
 ATACCCAAAG TCCATCAGTA TCTTGAATCA TGCTGGATTT TGAAGAATTC TTAACAAGCC 780
 ATGTAAAGGG GGCTCTCTGG CCTTGAATA GTGATGTTTT TTATACAGAA AGGAGAATGC 840
 15 AGAATGGTCA GACTACCATG CACTGTTAAA TTTGATTTC AGAAATTACA GGAAGAACTT 900
 CCAAGTTTCC ATCTCACAGA AATTATTTTT ACAAGAATT CCAAGATAAG TTTAGTTTTA 960
 TGGAGAGACT TTAATGTGTT TTTACTCACT CTTCATCTCA GACATCAACA GATGATTACA 1020
 TCACTTATTT AGCTAGTAAA TTTATTAATA TAAAACTCA GAGACATTCC AATATCCACA 1080
 TTGCTTACAC CATTAGGCAT AGATTCACTG TCAGCTATGA CAATTGAAAA TAAGCTGTTT 1140
 20 TGTGATTAAA AGGTTTAAAT TTCTTAACC AAAGTCTTG ATCCAGATGC AGGACTGCAA 1200
 ATGTTAATAT TTGTTCTGGA AGAACAAATCA AATAAGACTT AAGAGGAAAA GGAATGGCCA 1260
 CAATCCACCT GAAAAATTTT TTTTAAAAAG TGTGCAGCCT ACTAAATCAG AATGAAAAATA 1320
 GAAGTACAGG ATTATAAACA AAATGCAATC AAACCTTTCT TAAGCTTACC TAAAGTTATT 1380
 TCATCTGAAA ATTTCAAGCA ACTTGTCTCA ACATTAAATT GACAATCTAA ACTAACAAGT 1440
 25 CTTTGAATT TATGCAATGT AGTAAACATT CTCTCTATTA ACTTTATTAC CTAAGGCTAA 1500
 ACCTAAATTT TTTAAGCAAA ATTAGAAAAA TAGTCTTCTC TCATCAAAAA ATAAAGTTTG 1560
 TTACATTAG TATTTTCCCA AT 1582

Seq ID NO: 30 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..817

30 1 11 21 31 41 51
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 AGATATATCA TACGAAAAATG AAAATTATAA TTCTTCTTGG ATTCTCTGGG GCCACATTGT 60
 35 CAGCCCCAGT TTACTTCTTA ATCTTAATAA TGGTCAACTT TTGCCACTAC AACTTCAGGG 120
 CCCACTTAAT TCATGGAATTC CACTTTCTC TGGAAATTTA CAACAGCAGC AGCAGGCTCA 180
 AATTCCAGGA CTCTCCAGT TCTCTTATC AGCTCTAGAC CAGTTTGCTG GACTGTCTCC 240
 AAATCAGATA CCCTTAAACAG GAGAGGCCAG TTTTGCCCAA GGAGCCCAAG CAGGCCAAGT 300
 TGATCCCTTA CAGCTTCAAA CACCGCTCA GACACAACCA GGCCCCAGTC ACGTGATGCC 360
 40 CTATGTATTC TCCTTCAAAA TGCTCAAGA GCAAGGACAG ATGTTTCAAT ACTATCCAGT 420
 TTACATGGTC CTACCTGGG AACAACCTCA GCAAAACAGT CCAAGGTAC CTCAACAAAC 480
 AAGACAGCAA CAGTATGAGG AGCAGATACC ATTCTATGCT CAATTGGAT ACATTCCACA 540
 ACTAGCAGAA CCTGCTATAT CAGGAGGACA GCAGCAACTA GCTTTGATC CCCAACTAGG 600
 CACAGCTCCT GAAATGCTG TGATGTCAAC AGGAGAAGAG ATACCATATT TACAAAAAGA 660
 AGCGATCAAC TTTAGACATG ACAGTGACAG AGTTTTCATG CCCTCAACTT CACCAAAACC 720
 45 CAGCACAACC AATGTTTTCA CTTCTGCTGT AGACCAAACT ATTACCCAG AGCTCCCAAG 780
 AGAGAAGGAC AAGACTGACA GCCTAAGGGA ACCATAA 817

Seq ID NO: 31 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..917

50 1 11 21 31 41 51
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 AGAGAGGAAA AGAACACAGA TCTCGCATGG TTCAGATTTT TCTTTTATAG TCCAGGAGTA 60
 55 AGATATATCA TACGAAAAATG AAAATTATAA TTCTTCTTGG ATTCTCTGGG GCCACATTGT 120
 CAGCCCCACT TATCCACAG CGTCTCATGT CTGCCAGCAA TAGCAATGAG TTACTTCTTA 180
 ATCTTAATAA TGGTCAACTT TTGCCACTAC AACTTCAGGG CCCACTTAAT TCATGGATTC 240
 CACCTTTCTC TGGAAATTTA CAACAGCAGC AGCAGGCTCA AATTCAGGA CTCTCCAGT 300
 60 TCTCTTATC AGCTCTAGAC CAGTTTGCTG GACTGTCTCC AAATCAGATA CCCTTAACAG 360
 GAGAGGCCAG TTTTGCCCAA GGAGCCCAAG CAGGCCAAGT TGATCCCTTA CAGCTTCAAA 420
 CACCGCTCA GACACAACCA GGCCCCAGTC ACGTGATGCC CTATGTATTC TCCTTCAAAA 480
 TGCTCAAGA GCAAGGACAG ATGTTTCAAT ACTATCCAGT TTACATGGTC CTACCTGGG 540
 65 AACAACTCA GCAACAGTT CCAAGGTAC CTCAACAAAC AAGACAGCAA CAGTATGAGG 600
 AGCAGATACC ATTCTATGCT CAATTGGAT ACATTCCACA ACTAGCAGAA CCTGCTATAT 660
 CAGGAGGACA GCAGCAACTA GCTTTGATC CCCAACTAGG CACAGCTCCT GAAATGCTG 720
 TGATGTCAAC AGGAGAAGAG ATACCATATT TACAAAAAGA AGCGATCAAC TTTAGACATG 780
 ACAGTGACAG AGTTTTCATG CCCTCAACTT CACCAAAACC CAGCACAACC AATGTTTTCA 840
 80 CTTCTGCTGT AGACCAAACT ATTACCCAG AGCTCCCAAG AGAGAAGGAC AAGACTGACA 900
 GCCTAAGGGA ACCATAA 917

Seq ID NO: 32 DNA Sequence

Nucleic Acid Accession #: Eos sequence

70 1 11 21 31 41 51
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 TTTTITTTTT TTTTGTAGA GATGGGGTCT CACTTTGTTG CCCATGCTTT GGCTGCTCTT 60
 75 CAAGATTTAG CACTTCTGAG CTGTTGCTTT TGTCTCCAGT CTACCTGAG CAGTTCCTTA 120
 GGTGTTGAA GCAGAAGAAA GAGAAAAGAG GCTTAGGTTA TACTGCTTAG AACCTCTCT 180
 TCACTAACC TACCGACCA CCTACCCATA AATCCATACC TACACACACA CCCCCTTCT 240
 TTCTCTGCC CTGCTTTTGC CTGCGCTGCT TTCAATTGCA CGTGTGTTGA GTATAGCCTT 300
 80 TGCTCTGCC TACTCAGCT CTGGAAGTGA GGGTGAATTT GAGACCCAGA GGAATGGGAT 360
 TTACAGCTTC TTGCTTTCTT CTTGCTTGT CTTAGAACTG AAGTACAAAT GGGAGAAGC 420
 TTTGATGAAG GAAGACCCCC ATCCAAGAAC ATCTAGTTTT CAGGTGCCAT AACAGCAGAG 480
 CAAGTTCA 488

Seq ID NO: 33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
5	CTCCCAGAGT	GCTAGGATTA	CAGGCATGAG	CCACTGCTCC	CAGCCTTCCA	GAGGAATTTT	60
	AAGCCCATGT	CCAAACATTC	TGTTTGTATA	AATATATTCT	AATTTTAA	TAAATAGTTT	120
	CTACTTTTCT	GAACCTTATA	TTTTTCTTG	CTATAATGGA	TTTTCATAAT	CAGAAAAGAT	180
	TAAATTAGTA	ATCATGAATT	GCCTTCAATA	TTTGGCAGTA	AGTCAATGAA	ATAATAAGGC	240
	ACTTATATAC	CATCTTTGAC	ATCATTAAAA	GTATCAAAATC	CCATTAACT	AAAACTTCTT	300
10	TAAGCATTTT	GAAGACAGAA	AATGTTTACA	TGTTTCTTTC	AGTTCTCTAG	GCTTTTGTGC	360
	TAATGATGCG	TGACTTAGGA	TAAAGATTGA	ATTAAGTGCC	CAGCTTGAAA	CATAATAATT	420
	TTTCTGTATA	AGCCACAGAT	CCTCTACCTC	CTTTGTGTTA	AAGCCTTTAT	ATGAAACAAT	480
	TAAGTAGAAG	CATTCAATAG	TGTGTCAATTA	ACTGTTTATA	CTAATAAATG	GATACAGCAC	540
	ATTTTCATGG	CCTGTAATGT	AGAACATAC	ATATAAAGTT	CTCAGTTTGG	GGATGACTAG	600
15	GTITCTGGAA	GGAATAGAAT	GCTAAATCAA	TGGATGGCAT	TGGGCTGAGA	AACACTGCTG	660
	CTACTAATCA	GCCTTGAATG	TGTAATGTGA	ACATGCAAAA	GAGAACATGC	ATACACTCAA	720
	ATTGTIACAA	TGCTATAACT	GGAAGTTGAA	GGACTTGAAT	TTTTATATTG	TGCTATTGTT	780
	ATGTTTCTG	TAATTTGTTA	TATCTAAGGA	ATTTTGTAGG	TAATATAAAA	GAAAAAGAGA	840
	ATAATGAACA	ATGATGTCAC	TGGAGGGTTT	TTACATTAAA	TTAGATCATT	TTTCTTCTTA	900
20	TTCAACAATA	TAATCTTAAT	CTTTAAGAAT	TAATATAAAT	TTAATATTAT	AATTCATAAT	960
	CTTTAAGAAT	TAATAATTAT	AATTTAATAT	TATAATTAAT	AATCTTAAAG	AATTAATAAT	1020
	ATAATTTAAT	ATTATAATTA	ATAATCTTTA	AGAATTAAAT	ATTACAATTA	ATAATTAATA	1080
	ATAATCTTAA	TCCTTAAGAA	TTAATAATAA	TCCTTAATCG	CAATAAATAAT	CGCAAGGAGG	1140
	AGAAGTAAGT	CCCTCTCTCT	TCTGTATGAA	CTTTTCTCCC	ACATGCTGCT	GTATGGTTTA	1200
25	GTGAGAGTGA	AGTTCTAAAG	AACATCAATA	TGATTGGTGG	GATAATCCAA	AGACATTTT	1260
	TCAGAAATCAA	ATGCAATGTC	GAAGGTTTGT	TTCTTGATCA	TGTATTACT	GGTCCACAGC	1320
	ACAAAATAAA	GTGACCAAT	ATACATAGGA	AAGTTGAATT	TGTACACATA	CAGCATCTGA	1380
	AATGTATCTG	ATGTTACAGA	TCAAGATTTC	ACTGAACATT	GTAGAAATGT	GTATCTTTTG	1440
	CATGTATATT	TTACATTGAT	TTTCTATTTA	TGTACATCTA	GAAAGTTTAA	ACCCTAATAA	1500
30	ATAGTTTGT	AATTTTGAAT	AATAGTGTCA	GTTTATATGT	GAGGGAGTAG	AGACAGAGAG	1560
	GTTAGCACTG	GATAAATAAT	AGTAAGGCCA	AAGGAGAAAA	TTTCATAGAA	AATATTGTTG	1620
	TGTCTAAT	GAGTACAGCA	TGAAAGGCTT	CCTCTACAAG	ACACTAGTCA	AAGAGTTGAG	1680
	AGCTGCGGTT	TCTAATCTTT	GTCCATTACT	CCCTTACTCC	CTATGAGACT	GTGGACCTGT	1740
	CACITGGGCT	CTCTGGTCTT	CAGTTTCTTC	ACCAGTAAAA	CAAGGAACCTT	GAACCAAAATG	1800
35	ACCTCTAGTG	TTCCCTTGG	GTTTAAATGT	CTATAAATGT	TCAATGACTA	GAATGTATTG	1860
	CGTTTTTCTT	TATTCTTTTT	GCTTTGAGAA	AAGAGAATGT	GATTTAAGAG	TAATAATTG	1920
	AATACCAATT	ATCCACATTA	AAATTGTGTC	CTCTATGTGT	AAGGCATAGC	ACATTATAGCA	1980
	CACATACATA	AGCACACTAA	GCACCTTACA	AATATCTCTA	TTTATTCTTT	ACATAATCTT	2040
	TTGAAATTGA	TTATGTAATA	CACACTGTTT	TTGAACAATT	GGTGACTTCC	AGCTGTTTAA	2100
40	AACAACTAC	AGTATGTTGC	TTGAGTACTG	ACTTAGGAGG	TCAGCAATTGG	TTTCACTAGG	2160
	AGCTTCTCAA	AGCACGCTGC	CAACATGCT	CCAGTCTCAT	TGTCAAGGCC	TTAGACCAGG	2220
	CAATCAATTAC	GAGTACGTTG	CTTCAACTTC	AGCAGCAGCA	AAACGATCTG	GCGGGGCTT	2280
	GGTGAAACAG	ACTGCTGGGC	TGCACCACTA	GAATTTCTCA	TTCAGAGGGT	CTGGCCTGAT	2340
	CACITGGCATT	TCTAATCACT	TCCAGGTGA	TGCAGATGTT	TCTGGTCCAG	GGACCCCAAT	2400
45	TTGAGAACCA	CTGTATTAAA	ATTTCTTCA	TCTCTATAGA	AATGGAAAGA	TTTTTTATAA	2460
	GGCTCTAAT	TGCTTTAAG	ATAAATGAGA	TTTCACTTAA	TTCTGTTGGA	GAAATTTGTT	2520
	TAAAAATTAT	GTAAAGAAG	CGAAATCAC	TTTATGTTAA	GGCTCTATT	ATAGCAAGTG	2580
	AACITTTTCA	GAGTTAATAA	AGGCTTACAA	AAATAATTTT	GACTGTGAAA	CTAATTAATA	2640
	TCTCTGTGTT	TCAATTAAG	CATAAACATA	TTTGAATAAA	AATAGGTTAA	CAATAATTG	2700
50	GGACATGTAT	TCAGTATAAT	TTTAAGATAA	TTTACAAAA	TATATGTAAC	ATTGCAATTG	2760
	TTTCTGTAAA	ATATCTTCGG	AAAAAGCCTT	GTTTTCCCTA	GTGTGTTATT	TGTTGAATTT	2820
	CTTGTTAAT	GTATTTTCT	CCATTGAAAA	AAATGTTTTT	AATCAATGTG	ATCAATACAG	2880
	CTATCTATAT	GCCTGCTTT	CACGTGA				2907

Seq ID NO: 34 DNA Sequence
Nucleic Acid Accession #: NM_003979.2
Coding sequence: 254..1357

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60	ATAACAGCAT	GAAGTGCCGT	GGAACGTGAA	TAGGCGTGTC	CTCTCCCTCG	ACCCTCCCCC	60
	TCCTTGTCCC	TCTGCTCACC	CCTCGCTCGT	TCCTTCCCTC	CGGCGAGGGC	CGCCTTTATA	120
	ACAACTGCTC	AGAGTGGGAG	GGCGGGATAG	CTGTCCAAGG	TCTCCCCCAG	CAGTGAGGAG	180
	CTCGCTGCT	GCCTCTTGC	GCGCGGGAAG	CAGCACCAAG	TTCAAGGCCA	ACGCTTGGC	240
	ACTAGGGTCC	AGAAATGGCTA	CAACAGTCCC	TGATGGTTGC	CGCAATGGCC	TGAAATCCAA	300
65	GTAATACAGA	CTTTGTGATA	AGGCTGAAGC	TTGGGGCATC	GTCTAGAAA	CGGTGGCCAC	360
	AGCCGGGGTT	GTGACCTCGG	TGGCCTTCAT	GCTCACTCTC	CCGATCCCTG	CTGCAAGGT	420
	GCAGGACTCC	AACAGGCGAA	AAATGCTGCC	TACTCAGTTT	CTCTTCTCTC	TGGGTGTGTT	480
	GGGCATCTTT	GGCTCACTT	TGCGCTTCAT	CATCGGACTG	GACGGGAGCA	CAGGGCCAC	540
	AGCTTCTTTC	CTCTTTGGGA	TCTCTTTTC	CATCTGCTTC	TCTGCTCTGC	TGGCTCATGC	600
70	TGTGAGTCTG	ACCAAGCTCG	TCCGGGGGAG	GAAGCCCTTT	TCCCTGTGTT	TGATTTCTGG	660
	TCTGGCCGTG	GGCTTCAGCC	TAGTCCAGGA	TGTTATCGCT	ATTGAATATA	TTGTCTTGAC	720
	CATGAATAGG	ACCAACGTCA	ATGTCTTTTC	TGAGCTTTCC	GCTCTCTGTC	GCAATGAAGA	780
	CTTTGTCTCT	CTGCTCACTT	ACGTCCTCTT	CTTGATGGCG	CTGACCTTCC	TCAATGCTCT	840
	CTTCACTTTC	TGTGGTTTCT	TCAAGGGCTG	GAAGAGACAT	GGGGCCCA	TCTACCTCAC	900
75	GATGCTCTCT	TCCATTGCCA	TCTGGGTGGC	CTGGATCACC	CTGCTCATGC	TTCTTGACTT	960
	TGACCGCAGG	TGGGATGACA	CCATCTCAG	CTCCGCTTGG	GCTGCCAATG	GCTGGGTGTT	1020
	CTGTGTGGCT	TATGTTAGTC	CCGAGTTTGG	GCTGCTCACA	AAGCAACGAA	ACCCCATGGA	1080
	TTATCTGTTT	GAGGATGCTT	TCTGTAACCC	TCAACTCGTG	AAGAAGAGCT	ATGGTGTGGA	1140
	GAACAGAGCC	TACTCTCAAG	AGGAAATCAC	TCAAGTTTTC	GAAGAGACAG	GGGACACGCT	1200
80	CTATGCCCCC	TATTCACAC	ATTTTCAGCT	GCAGAACCCG	CCTCCCCCAA	AGGAATTCTC	1260
	CATCCACGG	GCCACGCTT	GGCCGAGCCC	TTACAAAGAC	TATGAAGTAA	AGAAAGAGGG	1320
	CAGCTAACTC	TGTCCTGAGT	AGTGGGACAA	ATGCAGCCGG	GCGGCAGATC	TAGCGGGAGC	1380
	TCAAGGGGAT	GTGGGCGAAA	TCTTGAGTCT	TCTGAGAAAA	CTGTACAGA	CACTACGGGA	1440
	ACAGTTTGCC	TCCCTCCAG	CCTCAACCAC	AATTCTTCCA	TGCTGGGGCT	GATGTGGGCT	1500
	AGTAAGACTC	CAGTTCTTAG	AGGCGCTGTA	GTATTTTTTT	TTTTTTGTCT	CATCCTTGG	1560

	ATACCTCTTT	TAAGTGGGAG	TCTCAGGCAA	CTCAAGTTTA	GACCCCTTACT	CTTTTGTGTT	1620
	GTTTTTTGAA	ACAGGATCTT	GCTCTGTAC	CCAGGCTTGA	GTGCAGTGGT	GCGATCACAG	1680
	CCAGTGCAG	CCTCGACCAC	CTGTGCTCAA	GCAATCCTCC	CATCTCCATC	TCCCAAAGTG	1740
	CTGGGATGAC	AGGCGTGAGC	CACAGCTCCC	AGCCTAGGCC	CTTAATCTTG	CTGTTATTTT	1800
5	CCATGGACTA	AAGGTCTGGT	CATCTGAGCT	CACGCTGGCT	CACACAGCTC	TAGGGGCCCTG	1860
	CTCCTCTAAC	TCACAGTGGG	TTTTGTGAGG	CTCTGTGGCC	CAGAGCAGAC	CTGCATATCT	1920
	GAGCAAAAT	AGCAAAAGCC	TCTCTCAGCC	CACTGGCCTG	AATCTACACT	GGAAGCCAAAC	1980
	TGCTGGCAC	CCCGCTCCC	CAACCTTCT	TGCTGGGTA	GGAGAGGCTA	AAGATCACCC	2040
	TAAATTTACT	CATCTCTCTA	GTGCTGCCTC	ACATTGGGCC	TCAGCAGCTC	CCCAGCACCA	2100
10	ATTACAGAGT	CACCCCTCTC	TTCTTGCACT	GTCCCCAAAC	TTGCTGTCAA	TTCCGAGATC	2160
	TAATCTCCCC	CTACGCTCTG	CCAGGAATTC	TTTCAGACCT	CACCTAGACA	AGCCCGGTG	2220
	CTCCTTGTC	AGAGAATTGG	TAGATCATT	TCACCTTCAA	TTCTGGGGC	TGATACTTCT	2280
	CTCATCTTGC	ACCCCAACCT	CTGTAAATAG	ATTACCGCA	TTTACGGCTG	CATTCTGTAA	2340
	GTGGGCATGG	TCTCTAATG	GAGGAGTGT	CATTGTATAA	TAAATTATTC	ACCTGAGTAT	2400
15	GCAATAAAG	TGTGTGGCC	ACTCTTCAT	GGTGGTGGA	GCAAAAAA	AAAAA	2456

Seq ID NO: 35 DNA Sequence

Nucleic Acid Accession #: NM_032957.1

Coding sequence: 1..4203

20	1	11	21	31	41	51	
	ATGCCCAAGA	TAGTCTGTAA	TGGTGTGACC	GTAGACTTCC	CTTTCCAGCC	CTACAAATGC	60
	CAACAGGAGT	ACATGACCAA	GGTCTGTGAA	TGTCTGCAGC	AGAAGGTGAA	TGGCATCTCG	120
25	GAGAGCCCTA	CGGGTACAGG	GAAGACGCTG	TGCTGTCTGT	GCACCACGCT	GGCCTGGGGA	180
	GAACACCTCC	GAGACGGCAT	CTCTGCCGCG	AAGATTGCOG	AGAGGGCGCA	AGGAGAGCTT	240
	TTCCCGGATC	GGGCTTGTG	ATCTGGGGG	AACGCTGCTG	CTGCTGTGGG	AGACCCATA	300
	GCTTGCTACA	CGGACATCCC	AAAGATTATT	TACGCTCCA	GGACCCACTC	GCAACTCACA	360
	CAGGTACATCA	ACGAGCTTCG	GAACACCTCC	TACCGGCTA	AGGTGTGTGT	GCTGGGCTCC	420
30	CGGGAGCAGC	TGTGCATCCA	TCTTGAGGTG	AAGAAACAAG	AGAGTAACCA	TCTACAGATC	480
	CACCTTGTGCT	GTAAGGAGGT	GGCAAGTGGC	TCCTGTCTAT	TCTACAACAA	CGTAGAAGAA	540
	AAAAGCCTGG	AGCAGGAGCT	GGCCAGCCCC	ATCCTGGACA	TTGAGGAGCTT	GGTCAAGAGC	600
	GGAGGCAAGC	ACAGGGTGTG	CCCTTACTAC	CTGTCCCGGA	ACCTGAAGCA	GCAAGCCGAC	660
	ATCATATTCA	TGCCGTACAA	TTACTTGTG	GATGCCAAGA	GCCGAGAGC	ACACAACATT	720
	GACCTGAAGG	GGACAGTCTG	GATCTTTGAC	GAAGCTCACA	ACGTGGAGAA	GATGTGTGAA	780
35	GAATCGGCT	CCCTTGAGCT	GACTCCCAT	GACCTGGCTT	CAGGACTGGA	CGTCATAGAC	840
	CAGGTGCTGG	AGGAGCAGAC	CAAGGCAGCG	CAGCAGGGTG	AGCCCCACCC	GGAGTTGAGC	900
	GGGACTCCC	CCAGCCAGGG	GCTGAACATG	GAGCTGGAAG	ACATTGCAAA	GCTGAAGATG	960
	ATCCTGCTGC	GCCTGGAGGG	GGCCATCGAT	GCTGTTGAGC	TGCTTGAGAA	CGACAGCGGT	1020
40	GTACCAAGC	CAGGGAGCTA	CATCTTTGAG	CTGTTTGTCT	AAGCCAGAT	CACGTTTCAG	1080
	ACCAAGGGCT	GCAATCTGGA	CTCGCTGGAC	CAGATCATCC	AGCACCTGGC	AGGACGTGCT	1140
	GGAGTGTCCA	CCAACACGGC	CGGACTGCAG	AAGCTGGGGG	ACATTATCCA	GATTGTGTTT	1200
	AGTGTGGAAC	CCTCCGAGGG	CAGCCCTGGT	TCCCGAGCAG	GGCTGGGGGC	CTTACAGTCC	1260
	TATAAGGTGC	ACATCCATCC	TGATGCTGGT	CACCGGAGGA	CGGCTCAGCG	GTCTGATGCC	1320
	TGGAGCACCA	CTGCAGCCAG	AAAGCGAGGG	AAGGTGCTGA	GCTACTGGTG	CTTCAGTCCC	1380
45	GGCCACAGCA	TGCACGAGCT	GGTCGCGCAG	GGGCTCCGCT	CCCTCATCCT	TACCAAGGCG	1440
	AGCTGGCCCC	CGGTGTCTCT	CTTTGCTCTG	GAGATGCAGA	TCCCTTTCCC	AGTCTGCCTG	1500
	GAGAACCCAC	ACATCATCGA	CAAGCACCAAG	ATCTGGGTGG	GGGCTGCTCC	CAGAGGCCCC	1560
	GATGGAGGCC	AGTTGAGCTC	CGGTTTGAC	AGACGGTTTT	CCGAGGAGTG	CTTATCTCTC	1620
	CTGGGGGAAG	CTCTGGGCAA	CATCGCCCGC	GTGGTGCCTT	ATGGGCTCCT	GATCTTCTTC	1680
50	CTTCTCTATC	CTGTCAATGA	GAAGAGCCTG	GAGTTCTGGC	GGGCGCGCGA	CTTGGCCAGG	1740
	AAGATGGAGG	CGCTGAAGCC	GCTGTTTGTG	GAGCCAGGGA	GCAAGGCGAG	CTTCTCGAG	1800
	ACCATCAGTG	CTTACTATGC	AAGGGTTGCC	GCCCTGGGT	CCACCGGCGC	CACCTTCTCT	1860
	GGCGTCTGCC	CGGGCAAGGC	CAGCGAGGGG	CTGGACTTCT	CAGACACGAA	TGGCCGTGGT	1920
55	GTGATTGTCA	CGGGCTCCCC	GTACCCCCCA	CGCATGGACC	CCCGGTTGCT	CCTCAAGATG	1980
	CAGTTCTGGG	ATGAGTAGAA	GGGCCAGGGT	GGGCTGGGG	GCCAGTTCTC	CTCTGGGCAG	2040
	GAGTGGTACC	GGCAGCAGGC	GTCCAGGGCT	GTGAACGAGG	CCATCGGGCG	AGTATCCGG	2100
	CACCGCCAGG	ACTACGGAGC	TGTCTTCTCT	TGTGACCACA	GGTTCGCTT	TGCGGACGCA	2160
	AGAGCCCAAC	TGCCCTCTGT	GGTGGTCCCC	CAGTCAAGG	TGTATGACAA	CTTTGGCCAT	2220
60	GTCTCCGAG	ACGTGGCCCA	GTTCTTCCGT	GTGCGGAGC	GAACATGACC	AGCGCCGGCC	2280
	CCCCGGGCTA	CAGCACCCAG	TGTGCTGGA	GAAGATGCTG	TCAGCGAGGC	CAAGTCGCTC	2340
	GGCCCCCTCT	TCTCCACCAG	GAAAGCTAAG	AGTCTGGACC	TGCATGTCCC	CAGCCTGAAG	2400
	CAGAGGTCTT	CAGGGTCACC	AGCTGCCGGG	GACCCGAGGA	GTAGCCTGTG	TGTGGAGTAT	2460
	GAGCAGGAGC	CAGTTCTCTG	CCGGCAGAGG	CCAGGGGGGC	TGCTGGCCGC	CCTGGAGCAC	2520
65	AGCGAACAGC	GGGCGGGGAG	CCCTGGCGAG	GAGCAGGCC	ACAGCTGCTC	CACCTGTGCC	2580
	CTCCTGTCTG	AGAAGAGGCC	GGCAGAAGAA	CCGCGAGGAG	GGAGGAAGAA	GATCCGGCTG	2640
	GTCCAGCAC	CGGAGGAGCC	CGTGGCTGGT	GCACAGACGG	ACAGGGCCAA	GCTCTTCATG	2700
	GTGGCCGTGA	AGCAGGAGTT	GAGCCAAGCC	AACCTTGCCA	CCTTCACCCA	GGCCCTGCAG	2760
	GACTACAAGG	GTCCGATGGA	CTTCGCGGCC	CTGGCCGCTT	GTCTCGGCC	CCTCTTGTCT	2820
70	GAGGACCCCA	AGAAGCACAA	CCTGCTCCAA	GGCTTCTACC	AGTTTGTGCG	GGCCACCAT	2880
	AAGCAGCAGT	TTGAGGAGGT	CTGTATCCAG	CTGACAGGAC	GAGGCTGTGG	CTATCGGCTT	2940
	GAGCACAGCA	TTCCCGAAG	GCAGCGGGCA	CAGCCGGTCC	TGGACCCAC	TGGAAGAAAG	3000
	GGCCCGGATC	CCAAGCTGAC	CGTGTCCAG	GCTGCAGCCC	AGCAGCTGGA	CCCCCAAGAG	3060
	CACCTGAACC	ACAGGAGGCC	CCACCTGTGC	CCAGGCCAC	CCCCAACAGG	AGACCTGTGC	3120
	AGCCAAACAC	AGTGGGGGTC	TGGAGTGCCC	AGAGCAGGGA	AGCAGGGCCA	GCACCGCTG	3180
75	AGCGCTTACC	TGGCTGATGC	CCGCAAGGCC	CTGGGGTCCG	CGGGCTGTAG	CCAACCTTGT	3240
	GCAGCGCTGA	CAGCCTATAA	GCAAGACGAC	GACCTGACCA	AGGTGCTGGC	TGTGTTGGCC	3300
	GCCTGACCA	CTGCAAGGCC	AGAGGACTTC	CCCTCTGTGC	ACAGGTTTCT	CATGTTTGTG	3360
	CGTCCACACC	ACAGGAGCGG	CTTCTCACAG	ACGTGACAGG	ACCTGACCGG	CCGGCCCTAC	3420
	CCGGGCTAGG	AGCCACCGGG	ACCCAGGAG	GAGAGGCTTG	CCGTGCTCTC	TGTGCTTACC	3480
80	CACAGGGCTC	CCCAAGCAGG	CCCTCACGG	TCCGAGAAGA	CCGGGAAGAC	CCAGAGCAAG	3540
	ATCTCGTCTT	TCCTTAGACA	GAGGCCAGCA	GGGAGTGTGG	GGGCGGGCGG	TGAGGATGCA	3600
	GGTCCAGAGC	AGTCTCTCAG	ACCTCCACAC	GGGCTGTGAG	CATCTGAGTG	GGGTGAGCCT	3660
	CATGGGAGAG	ACATGCTGTG	GCAGGAGGCC	ACGGGAGGCT	CGGGCGGGCC	CCTCTCAGCA	3720
	GGCTGTGTGT	GCCAGGGCTG	TGGGGCAGAG	GACGTGGTGC	CCTTCCAGTG	CCCTGCTGTG	3780

5	GACTTCCAGC	GCTGCCAAGC	CTGCTGGCAA	CGGCACCTTC	AGGCCTCTAG	GATGTGCCCA	3840
	GCCTGCCACA	CCGCTCCAG	GAAGCAGAGC	GTCTATGAGC	TCTTCTGGCC	AGAGCCCCAC	3900
	AAGGACCATG	AGGGCCGTGG	AGGGGCCAGG	CCTGTGCTGT	CTGTGCTGG	TGTTGGCGCT	3960
	GCCTGCCCTG	CTGCCGGTGC	CGCTGTACG	CGGAGTGGCA	GAAACACCCA	CCTACCCCTG	4020
	GCGGGAAGCA	GAGACAGGGG	AGCGGCTGGT	GTGTGCCAGC	TGCCCCCCAG	GCACCTTTGT	4080
	GCAGCGGCGG	TGCCGCGGAG	ACAGCCCCAC	GACGTGTGGC	CGGTGTCCAC	CGGCCCACTA	4140
	CACGAGTTTC	TGGAATACCT	TGGAGCGCTG	CCGCTACTGC	AACGTCCTCT	GCGGGGAGCG	4200
	TGAGGAGGAG	GCACGGGCTT	GCCACGCCAC	CCACAACCGT	GCCTGCGGCT	GCGCACCGCG	4260
10	CTTCTTGGCG	CACGCTGGTT	TCTGCTTGA	GCACGATCG	TGTCCACCTG	GTGCCGGCGT	4320
	GATTGCCCGG	GGCACCACCA	GCCAGAACAC	GCAGTGCCAG	CGGTGCCCCG	CAGGCACCTT	4380
	CTCAGCCAGC	AGCTCCAGCT	CAGAGCAGTG	CCAGCCCCAC	CGCACTGCA	CGCCCTGGG	4440
	CCTGGCCCTC	AATGTGCCAG	GCTCTTCTCT	CCATGACACC	CTGTGCACCA	GCTGCACTGG	4500
	CTTCCCCCTC	AGCACCAGGG	TACCAGGAGC	TGAGGAGTGT	GAGCGTGGCG	TGATCGACTT	4560
15	TGTGGCTTTC	CAGGACATCT	CCATCAAGAG	GCTGCAGCGG	CTGCTGCAGG	CCCTCGAGGC	4620
	CCCGGAGGGC	TGGGGTCCGA	CACCAAGGGC	GGGCCCGCGG	GCCTTGACAG	TGAAGCTGGG	4680
	TGCGCGGCTC	TGGGGAGCTCC	TGGGGGCGCA	GGAAGGGGCG	CTGCTGGTGC	GGCTGCTGCA	4740
	GGCGCTGGCG	GTGGCCAGGA	TGCCCGGGCT	GGAGCGGAGC	GTCCGTGAGC	GCTTCTCTCC	4800
	TGTGCACTGA	TCTTGGCCCC	CTCTATTATTA	TCTACATCC	TGGCACCC	ACTTGCACTG	4860
20	AAAGAGGCTT	TTTTTTAAAT	AGAAGAAATG	AGGTTTCTTA	AAGCTTATTT	TTATAAAGCT	4920
	TTTTCATAAA	ACTGGTGTGA	GTTGC				4945

Seq ID NO: 36 DNA Sequence

Nucleic Acid Accession #: NM_016434.1

Coding sequence: 828..4487

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	ACTGCGGGAC	AGTGAGCCGA	GCAGAAGCTG	GAACGCAGGA	GAGGAAGGAG	AGGGGGCGGT	120
30	CAGGGCTCTC	AGGAGCCGGG	TCCTGGGCAA	GGCGCAGCGG	TTTTCAAATT	TTACAGAAAG	180
	CGGTGCGCTC	ACACTCGAGC	AGTAAAAAGA	TGCTCTCTGG	GAGGAGGGCC	GTGCAGCTCT	240
	CGGGGCAATG	TGTGTGGCTC	GGCTTAGAGA	GGCGGTAGTG	GAACGCAGAC	CTGTGGTGGG	300
	GAATGACATC	AAGGGAGGAG	ACGGGCGGGA	CCCCAGATT	CTGCTGTGG	GCGATGGAAG	360
	TGAGGTTTAC	TGGCCAGCGG	AGCCGACAC	AGAAGCGCA	AAACGCCGTG	TAGGCTTGGG	420
35	GGAGCCGAG	AGCAGGCGGA	CCCTCTCGC	GGGGAAACAG	TTTCGCGCG	GAGCACAAAG	480
	CAACGGACCG	GAAGTGGGGG	CGGGAAGTGC	AGTGGGCTCA	GCGCGGAGCT	GCGCCCTCTG	540
	CCCGCGAATA	CTCTGAGCTC	GCTGACAGCT	GGGACCGGGT	GCGCGCCCTC	GACTGGAGTC	600
	GGTTGAGTTC	CTGAGGGACC	CGGTTCTGG	AAGGTTCCGC	CGGAGACAA	GTGAGCAGTC	660
	TGTGCCATAG	GGATTCTCGA	AGAGAACAGC	GTTGTGTCCC	AGTGACATG	CTCGCATCGC	720
40	TTACCAAGAG	TGCCCGAGAC	CCTAAGATGT	TGGAGTGGT	TTTTTCGCAC	AGACCCGAAT	780
	AGCCTGCCCC	TCAGCCACGC	TCTGTGCCCT	TCTGAGAAAC	GGCTGATATG	CCCAAGATAG	840
	TCTCTGAATG	TGTGACCTTG	GACTTCCCTT	TCCAGCCCTA	CAATGCCAA	CAGGAGTACA	900
	TGACCAAGGT	CCTGGAATGT	CTGCAGCAGA	AGGTGAATGG	CATCTGGAG	AGCCCTACGG	960
	GTACAGGGAA	GAGCTGTGCG	CTGCTGTGCA	CCACGCTGGC	CTGGGAGAA	CACCTCCGAG	1020
45	ACGGCATCTC	TGCCCGCAAG	ATTGCGGAGA	GGGCGCAAGG	AGAGCTTTTC	CCGATCGGGG	1080
	CCTGTGATC	CTGGGGCAAC	GCTGTGCTG	CTGCTGGAGA	CCCATAGCT	TGCTACACGG	1140
	ACATCCCAAA	GATTATTATC	GGCTCCAGGA	CCCACTCGCA	ACTCACACAG	GTATCAACG	1200
	AGCTTCGGAA	CACCTCTTAC	CGGCTTAAGG	TGTGTGTGCT	GGGCTCCCGG	GAGCAOCTGT	1260
	GCATCCATCC	TGAGGTGAAG	AAACAAGAGA	GTAACCATCT	ACAGATCCAC	TTGTGCCGTA	1320
50	AGAAGGTGGC	AAGTGCCTCC	TGTCATTTCT	ACAACAACGT	AGAAGAAAAA	AGCCTGGAGC	1380
	AGGAGCTGGC	CAGCCCCATC	CTGGACATTT	AGGACTTGGT	CAAGAGCGGA	AGCAAGCACA	1440
	GGGTGTGCCC	TACTACCTG	TCCCGGAACC	TGAAGCAGCA	AGCCGACATC	ATATTCTATG	1500
	CGTACAATTA	CTTGTGTGAT	GCCAAAGAGC	GCAGAGCACA	CAACATTGAC	CTGAAGGGGA	1560
	CAGTGTGAT	CTTTGACGAA	GCTCACAAAC	TGGAGAAGAT	GTGTGAAGAA	TGGCATCTCT	1620
55	TTGACCTGAC	TCCCCATGAC	CTGGCTTCAG	GACTGGACGT	CATAGACCAG	GTGCTGGAGG	1680
	AGCAGACCAA	GGCAGCGCAG	CAGGGTGAGC	CCCAACCCGA	GTTGAGCGCG	GACTCCCCCA	1740
	CGCCAGGGCT	GAACATGGAG	CTGGAAGACA	TTGCAAGCT	GAAGATGATC	CTGCTGCGCC	1800
	TGGAGGGGGC	CATCGATGCT	GTTGAGCTGC	CTGAGAGCGA	CAGCGGTGTC	ACCAAGCCAG	1860
	GGAGCTACAT	CTTTGAGCTG	TTTGCTGAAG	CCAGATCAC	GTTTCAGACC	AAGGGCTGCA	1920
60	TCCTGGACTC	GCTGGACCAG	ATCATCCAGC	ACCTGGCAGG	ACGTGCTGGA	GTGTTACCCA	1980
	ACACGGCCCG	ACTGCAGAA	CTGGCGGACA	TTATCCAGAT	TGTGTTCAAT	GTGGACCCCT	2040
	CCGAGGGCAG	CCCTGGTTCC	CCAGCAGGGC	TGGGGGCTTT	ACAGTCTTAT	AAGGTGCACA	2100
	TCCATCTCTA	TGCTGGTCA	CGGAGGACGG	CTCAGCGGTC	TGATGCTGG	AGCACCCTG	2160
	CAGCCAGAAA	GCGAGGGAAG	GTGCTGAGCT	ACTGGTGCTT	CAGTCCCGGC	CACAGCATGC	2220
65	ACGAGCTGGT	CCGCGAGGGC	GTCCGCTCCC	TCATCCTTAC	CAGCGGCACG	CTGGCCCCGG	2280
	TGTCTCTCTT	TGCTCTGGAG	ATGCAGATCC	CTTTCCCACT	CTGCCTGGAG	AACCCACACA	2340
	TCATCGACAA	GCACCAGATC	TGGGTGGGGG	TGCTCCCCAG	AGGCCCCGAT	GGAGCCCACT	2400
	TGAGCTCCGC	GTTTGACAGA	CGGTTTTCCG	AGGAGTGCTT	ATCCTCCCTG	GGGAAGGCTC	2460
	TGGGCAACAT	CGCCCGCGTG	GTGCCCTATG	GGCTCTCTAT	CTTCTTCCCT	TCCTATCCTG	2520
70	TCATGGAGAA	GAGCCTGGAG	TTCTGGCGGG	CCCGGACCTT	GGCCAGGAAG	ATGGAGGCGC	2580
	TGAAGCCGCT	GTTTGTGGAG	CCAGGAGCA	AAGGCAGCTT	CTCCGAGACC	ATCAGTGCTT	2640
	ACTATGCAAG	GTTTGGCGCC	CCTGGGTCCA	CGGGCGCCAC	CTTCTGGCG	GTCTGCGGGG	2700
	GCAAGGGCCG	CGAGGGGCTG	GACTTCTCAG	ACACGAATGG	CGGTGGTGTG	ATTGTACCGG	2760
	GCCTCCCGTA	CCCCCACGCG	ATGGACCCCG	GGGTTGTCTT	CAAGATGCAG	TTCTTGGATG	2820
75	AGATGAAGGG	CCAGGGTGGG	GCTGGGGGCC	AGTTCTCTCT	TGGGCAGGAG	TGGTACCGGC	2880
	AGCAGGGCTG	CAGGGCTGTG	AACCAGGCCA	TGGGGCGAGT	GATCCGGCAC	CGCCAGGACT	2940
	ACGGAGCTGT	CTTCTCTGT	GACCAAGGT	TGCTCTTTCG	CGAAGCAAGA	GCCCACTGCG	3000
	CCTCTGGGT	GCGTCCCGAC	GTGAGGCTGT	ATGACAACTT	TGGCATGTCT	ATCCGAGACG	3060
	TGGCCAGTGT	CTTCCGTGTT	GCCGAGCGAA	CTATGCCAGC	GCCGGCCCCC	CGGGCTACAG	3120
80	CACCCAGTGT	GCGTGGAGAA	GATGCTGTCA	GCGAGGCCAA	GTGCGCTGGC	CCCTTCTTCT	3180
	CCACCAGGAA	AGCTAAGAGT	CTGGACCTGC	ATGTCCCCAG	CCTGAAGCAG	AGGTCCTCAG	3240
	GGTCACCAAG	TGCCGGGGAG	CCCGAGAGTA	GCCTGTGTGT	GGAGTATGAG	CAGGAGCCAG	3300
	TTCTGCCCCG	GCAGAGGGCC	AGGGGGCTGC	TGGCCGCGCT	GGAGCACAGC	GAACAGCGGG	3360
	CGGGGAGCCC	TGGCGAGGAG	CAGGCCACCA	GCTGCTCCAC	CCTGTCCCTC	CTGTCTGAGA	3420
	AGAGGCCCGC	AGAAGAACC	CGAGGAGGGA	GGAAGAAGAT	CCGGCTGGTC	AGCCACCCGG	3480

5 AGGAGCCCGT GGCTGGTGCA CAGACGGACA GGGCCAAGCT CTTTCATGGT GCGGTGAAGC 3540
 AGGAGTTGAG CCAAGCCCAAC TTGTCACCT TCACCCAGGC CTTGCAGGAC TACAAGGGTT 3600
 CCGATGACTT CCGCGCCCTG GCGCCTGTG TCGGCCCCCT CTTTGTCTGAG GACCCCAAGA 3660
 AGCACAACCT GTCCAAGGC TTCTACAGT TTGTGGGGCC CCACATAAG CAGCAGTTTG 3720
 AGGAGGTCTG TATCCAGCTG ACAGGACGAG GCTGTGGCTA TCGGCTGAG CACAGCATT 3780
 CCGGAAGGCA GCGGGCAGAG CCGGTCTGTG ACCCACTGG AAGAAGCGCG CCGGATCCCA 3840
 AGCTGACCGT GTCCACGGCT GCAGCCAGC AGCTGGAGCC CCAAGAGCAC CTGAACCAAG 3900
 GCAGGCCCCA CTGTGCGCC AGGCCACCC CAACAGGAGA CCGTGGCAGC CAACCAAGT 3960
 GCGGTCTGG AGTGCCCAAG GCAGGGAAGC AGGGCCAGCA GCGGTGAGC GCCTACTGG 4020
 10 CTGATGCCCG CAGGGCCCTG GGTTCGCGG GCTGTAGCCA ACTCTTGGCA GCGCTGACAG 4080
 CCTATAAGCA AGACGACGAC CTGACAAGG TGCTGGCTGT GTTGGCCGCG CTGACCACTG 4140
 CAAAGCCAGA GGAATTCCTC CTGCTGCACA GGTTCAGCAT GTTTGTGCGT CCACACCACA 4200
 AGCAGCGCTT CTCACAGAGC TGACAGACC TGACGGCGCG GCCCTACCGG GGCATGGAGC 4260
 CACCGGGACC CCAGGAGGAG AGGCTTGCCG TGCTCTGTG GCTTACCCAC AGGGCTCCCG 4320
 15 AACCAAGGCC CTCACGGTCC GAGAAGACCG GGAAGACCCA GAGCAAGATC TCGTCTCTCC 4380
 TTAGACAGAG GCGCAGCAGG ACTGTGGGG GCGGCGGTGA GGATGCAGGT CCCAGCCAGT 4440
 CCTCAGGACC TCCCAACGCG CTGACAGCAT CTGAGTGGGG CCTTAGGAT GTGCCAGACC 4500
 TGCCACACCG CTCCAGGAA GCAGAGCGTC ATGACAGTCT TCTGGCCAGA GCCCAGTGA 4560
 GTGCCACCG AGGCCCCAG CACACCCAAC GTGGCTTGAT CACCTGCCCT TCCAGCTCTG 4620
 20 GTGGGCCAAG AACCCACCCA ACAGAAATAG CCAGCCCATG CCAGCCGGCT TGGCCCGCTG 4680
 CAGGCTCAG GCAGGCGGGG CCTATGGTTG GTCTCTGCGG TGGGACCGGA TCTGGGCGCT 4740
 CCTCTGAGAA GCACTTCAGT ACCTTGGGGT CTGGGGTGGG TTTCTGGAA AGTGCTTCCC 4800
 CAGAACTTCC CTGGCTCTCG GCTGTGAGT GGTGCCACAG GGGCACCCCA GCTGAGCCCC 4860
 25 TCACCGGAA GGAGGAGACC CCGTGGGCA CGTGTCCACT TTTAATCAGG GACAGGGCT 4920
 CTCTAATAAA GCTGCTGGCA GTGCC 4946

Seq ID NO: 37 DNA Sequence
 Nucleic Acid Accession #: NM_015647.2
 Coding sequence: 246..1883

30 1 11 21 31 41 51
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 AGCTCTCCG GCTACTCGG GTACGGTGG GGCCTCTGCA GCAGATGAG GTCTTCACT 60
 CGGTGAAGTG AACCTTGAA GCGCTGTGG GCAGGGCAGC AGGGCTATGG CCACCCCA 120
 35 GGTTCGCTT TGCCGACGCA AGAGCCCAAC TGCCCTCTG GGTGCGTCCC CACGTCAGGG 180
 TGTATGACAA CTTTGGCCAT GTATCCGAG ACGTGGCCCA GTTCTTCCGT GTTGGCGAGC 240
 GAACTATGCC AGCGCGGGC CCGCGGGCTA CAGCACCCAG TGTGCGTGA GAAATGCTG 300
 TCAGCGAGGC CAAGTCGCT GGCCTTCTT TCTCCACAG GAAAGCTAAG AGTCTGGACC 360
 TGATGTCCC CAGCCTGAAG CAGAGTCTT CAGGCTCAC AGCTGCCGGG GACCCGAGA 420
 40 GTAGCTGTG TGTGGAGTAT GAGCAGGAG CAGTTCCTG CCGGCAGAGG CCCAGGGGGC 480
 TGCTGGCGC CCGGAGCAC AGCGAACAG GCGCGGGAG CCGTGGCGAG GAGCAGGCC 540
 ACAGCTGTCT CACCTGTCT CTCTGTCTG AGAAGAGGCC GGCAGAAAG CCGGAGGAG 600
 GGAGGAGAA GATCGGCTG GTACGCCAC CGAGGAGCC GGTGGCTGGT GCACAGACG 660
 ACAGGCCCAA GCTCTTCAT GTGGCGTGA AGCAGGAGT GAGCCAAAGC AACTTTGCCA 720
 45 CCTTACCCA GGCCTGCGC GACTACAAG GTTCCGATG CTTGCGCGCC CTGCGCGCCT 780
 GTCTGCGGC CTTCTTGTG GAGGACCCCA AGAAGCACAA CCGTCTCAA GGCTTCTACC 840
 AGTTTGTGG CCGCCACCAT AAGCAGCAG TTGAGGAGGT CTGTATCCAG CTGACGGGAC 900
 GAGGCTGTG CTATCGGCT GAGCACAGCA TCCCCGAAG GCAGCGGCA CAGCCGCTC 960
 TGGACCCAC TGAAGAAGC GCGCGGATC CCAAGCTGAC CGTGTCCAG GCTGCAGCCC 1020
 50 AGCAGCTGA CCCCCAAGAG CACTGAACC AGGGCAGGCC CCACCTGTG CCCAGGCCAC 1080
 CCCCACAGG AGACCTTGC AGCCAAACAC AGTGGGGTCT TGAAGTGCCC AGAGCAGGGA 1140
 AGCAGGGCCA GCAGCGCGT AGCGCTACC TGGCTGATG CCGCAGGGCC CTGGGCTCG 1200
 CCGGCTGTAG CCAACTCTT GCAGCGCTGA CAGCTTATA GCAAGACGAC GACTCGACA 1260
 AGGTGTGGC TGTGTGGCC GCCCTGACCA CTGCAAAGCC AGAGGACTTC CCCCTGCTG 1320
 55 ACAGGTTAG CATGTTTGT GGTCCACAC ACAAGCAGC CTTCTCACAG ACGTGACAG 1380
 ACCTGACCG CCGGCCCTAC CCGGCGATG AGCCACCGG ACCCCAGGAG GAGAGGCTTG 1440
 CCGTGCTCC TGTGCTTACC CACAGGCTC CCAACACAG CCGCTCACG TCCGAGAAGA 1500
 CCGGGAAGC CCAGAGCAAG ATCTCGTCT TCCTTAGACA GAGGCCAGCA GGAAGTGTG 1560
 GGGCGGGCG TGAGGATGA GGTCCAGCC AGTCTCAGG ACCTCCAC GGGCTGCG 1620
 60 CATCTGAGT GGTGAGCCT CATGGGAGAG ACATCGTGG GCAGCAGGCC ACGGAGCTC 1680
 CCGGCGGGC CCGTCTCAGA GGTGTGTGT GCCAGGGCTG TGGGCGAGAG GACGTGTGT 1740
 CCTTCCAGT CCGTGCCTG GACTTCCAG GCTGCCAAG CTGCTGGCA CCGCACCTTC 1800
 AGGCCTTAG GATGTGCCA CGCTGCCCA CCGCTCCAG GAAGCAGAG GTCATGCG 1860
 TCTTCTGGC AGAGCCCGC TGAGTGCCA CCGAGGCCCC CAGCACACCC AACGTGGCT 1920
 65 GATCACTGC CTGTCCAGT CTGTTGGGCC AAGAACCAC CCAACAGAA AGGCCAGCC 1980
 ATGCCAGCG GCTTGGCGC CTGCAGGCT CAGGCAGGCG GGGCCCATG TTGGTCCCT 2040
 CCGTGGGACC GGATCTGGG CTGCCTCTGA GAAGCCCTG GCTACCTTG GGTCTGGGT 2100
 GGGTTTCTG GAAAGTGCT CCCCAGAACT TCCCTGGCTC CTGGCTGTG AGTGTGCCA 2160
 CAGGGGACC CAGCTGAGC CCCTACCGG GAAGGAGGAG ACCCCCGTGG CACGCTGCT 2220
 70 ACTTTAATC AGGGGACAG GCTCTTAAT AAAGCTGCTG GCAGTGCCCA GGAACAAAA 2280
 AAAAAAA

Seq ID NO: 38 DNA Sequence
 Nucleic Acid Accession #: NM_003823.2
 Coding sequence: 101..1003

75 1 11 21 31 41 51
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 TCCGACGGC GACCGGGGGG AAAGGAGGTG GCATGTCGGT CAGGCACAGC AGGGTCTGT 60
 GTCCGCGCTG AGCGCGCTC TCCCTGCTCC AGCAAGGACC ATGAGGGCGC TGGAGGGSC 120
 80 AGGCCTGTG CTGCTGTGCC TGGTGTGGC GCTGCTGCC CTGCTGCCG TGCCGGCTGT 180
 ACGGAGGTG GCAGAAACAC CCACCTACCC CTGGCGGAGC GCAGAGACAG GGGAGCGGT 240
 GGTGTGCCC CAGTGCCCCC CAGGCACCTT TGTGCAGCG CCGTGCGGCC GAGACAGCC 300
 CACGAGGTG GGCCCGGTG CACCGGCCA CTACACGAG TTCTGGAAT ACCTGGAGC 360
 CTGCGCTAC TGCAACGTC TCTCGGGGA GGTGAGGAG GAGGCAGGG CTTGCCAGC 420
 CACCCACAC CGTGCTGCC GCTGCCGAC CGGCTTCTC GCGCACGCTG GTTCTGCTT 480

5 GGAGCAGCGA TCGTGTCCAC CTGGTGCCGG CGTGATTGCC CCGGGCACCC CCAGCCAGAA 540
 CACGCACTGC CAGCGGTGCC CCCCAGGCAC CTCTCAGCC AGCAGCTCCA GCTCAGAGCA 600
 GTGCCAGCCC CACCGCAACT GCACGGCCCT GGGCTTGGCC CTCAATGTGC CAGGCTCTTC 660
 CTCCCATGAC ACCCTGTGCA CCAGCTGCAC TGGCTTCCCC CTCAGCACCA GGGTACCAGG 720
 AGCTGAGGAG TGTGAGCGTG CCGTCACTGA CTTTGTGGCT TTCCAGGACA TCTCCATCAA 780
 GAGGCTGCAG CCGCTGCTGC AGGCCCTCGA GGGCCCGGAG GGCTGGGGTC CGACACCAAG 840
 GCGCGGCGCG GCGGCTGTGC AGCTGAAGCT GCGTGGGGG CTCACGGAGC TCTTGGGGGC 900
 GCAGGACGGG GCGCTGCTGG TGCGGCTGCT GCAGGCGCTG CCGCTGGCCA GGATGCCCGG 960
 10 GCTGGAGCGG AGCGTCCGTG AGCGCTTCTT CCCTGTGCAC TGATCCTTGC CCCCCTTTAT 1020
 TTATTCTACA TCTTGTGCAC CCCACTTGCA CTGAAAGAGG CTTTTTTTAA AATAGAAGAA 1080
 ATGAGGTTTC TTAAAGCTTA TTTTATAAAA GCTTTTTCAT AAAA 1124

Seq ID NO: 39 DNA Sequence

Nucleic Acid Accession #: NM_032945.1

Coding sequence: 435..1337

15 1 11 21 31 41 51
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 20 CTGACCACTG CAAAGCCAGA GGAATTCCTC CTGCTGCACA GGTTCAGCAT GTTTGTGGGT 60
 CCACACCACA AGCAGCGCTT CTCACAGAGC TGCACAGACC TGACCGGCCG GCCCTACCCG 120
 GGCACTGGAGC CACCGGGACC CCAGAGGAGG AGGCTTGGCG TGCCCTCCTGT GCTTACCCAC 180
 AGGGCTCCCC AACCAGGCCC CTCACGGTCC GAGAAGACCG GGAAGACCCA GAGCAAGATC 240
 TCGTCTCTCC TTAGACAGAG GCCAGCAGGG ACTGTGGGGG CCGGCGGTGA GGATGCAGGT 300
 25 CCGAGCCAGT CCTCAGGACC TCCCCACGGG CCTGCAGCAT CTGAGTGGGG CCTCTAGGAT 360
 GTGCCACACC TGCCACACCG CCTCCAGGAA GCAGAGCGTC ATGCAGGTCT TCTGGCCGGA 420
 GCGCCACAAG GACCATGAGG GCGCTGGAGG GCGCAGGCC CTGCTGCTGT TGCCCTGGTGT 480
 TGGCGCTGCC TGCCCTGCTG CCGGTGCCCG CTGTACGCGG AGTGGCAGAA ACACCCACCT 540
 ACCCTTGGGG GGACGACAGG ACAGGGGAGC GGCTGGTGTG GCGCCAGTGC CCCCCAGGCA 600
 CTTTGTGTGA GCGGCGGTGC GCGCAGACA GCGCCACGCA GTGTGGCCCG TGTCACCCGC 660
 30 GCGCACTACG GCGTCTCTGG AACTACCTGG AGCGCTGCCG CTACTGCAAC GTCTCTGGCG 720
 GGGAGCGTGA GGAGGAGGCA CGGCTTGTCC ACGCCACCCA CAACCGTGCC TGCCGCTGCC 780
 GCACCGCTTT GTTCCGCGAC CTGGTCTTCT GCTTGGAGCA GGCATCGTGT CCACCTGGTG 840
 CCGGCGTGTG TGCCCGGGGC ACCCCAGGCC AGAACACGCA GTGCCAGCCG TGCCCGCCAG 900
 GCACCTTCTC AGCCAGCAGC TCCAGCTCAG AGCAGTGCCA GCGCCACCGC AACTGCACGG 960
 35 CCGTGGGCTT GCGCTCAAT GTGCCAGGCT CTTCCTCCCA TGACACCCCTG TGCAACGACT 1020
 GCACTGGCTT CCCCCTCAGC ACCAGGGTAT CAGGAGCTGA GGAGTGTGAG CGTGGCGTCA 1080
 TCGACTTTGT GGTCTTCCAG GACATCTCCA TCAAGAGGCT GCAGCGGCTG CTGCAGGGCC 1140
 TCGAGGCCCC GGAGGGCTGG GGTCCGACAC CAAGGGCGGG CCGGCGGGCC TTGCAGCTGA 1200
 AGCTGGGTGC GCGGCTCAGG GAGCTCCTGG GGGCGCAGGA CGGGCGGCTG CTGGTGGCGC 1260
 40 TGCTGCAGGC GCTGCGGCTG GCGAGGATGC CCGGGCTGGA GCGGAGCGTC CGTGAGCGCT 1320
 TCCTCCCTGT GCACTGATCC TGGCCCCCTC TTATTATTTC TACATCCTTG GCACCCCACT 1380
 TGCACTGAAA GAGGCTTTT TTTAAATAGA AGAAATGAGG TTTCTTAAAA GCTTATTTTT 1440
 ATAAAGCTTT TCCATAAAA 1459

Seq ID NO: 40 DNA Sequence

Nucleic Acid Accession #: NM_000593

Coding sequence: 165..2591

45 1 11 21 31 41 51
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 50 GGCACGAGGG TGTGCGTGTG GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG 60
 ATCTGATTTT CACGCTTGCT ACCAAAAATAG TCTGGGCAGG CCACCTTTGG AAGTAGGGGT 120
 TATCTAGTGA GCAGGGGGCC GCTTTCGATT TCGCTTTCCC CTAAATGGCT GAGCTTCTCG 180
 CCAGCGCAGG ATCAGCCTGT TCTTGGGACT TTCCGAGAGC CCGGCGCTCG TTCCCTCCCC 240
 CAGCCGCGCAG TAGGGGAGGA CTGGCGGTA CCGGAGCTT CAGGCCCCAC CCGGGCGGGG 300
 55 AGAGTCCAGC ACCCGGCGGG GACCGGAGCG GCGTCCGAGT GCCAATGGCT AGCTCTAGGT 360
 GTCCCGCTCC CCGCGGGTGC CGCTGCCTCC CCGGAGCTTC TCTCGCATGG CTGGGGACAG 420
 TACTGCTACT TCTGCGCCAG TGGGTGCTGC TCCGGACCGC GCTGCCCGGC ATATTCTCCC 480
 TGCTGTGTCC CACCGCGCTG CCACTGCTCC GGGTCTGGGC GGTGGGCGTG AGCCGCTGGG 540
 CCGTGTCTCG GCTGGGGGCC TGCGGGGTCC TCAGGSCAAC GGTGGGCTCC AAGAGCGAAA 600
 60 ACGCAGGTGC CAGGGCTGG CTGGCTGCTT TGAAGCCATT AGCTGCCGCA CTGGGCTTGG 660
 CCTGCGCGGG ACTTGCTTGG TTCCGAGAGC TGATCTCATG GGGAGCCCCC GGGTCCGCGG 720
 ATAGCACCAG GCTACTGCAC TGGGGAAGTC ACCCTACCGC CTTCGTGTGC AGTTATGCAG 780
 CGGCACTGCC CCGCAGCAGC CTGTGGCACA AACTCGGAG CTTCTGGGTG CCGGCGGCTC 840
 AGGGCGGCTC TGGAAACCTT GTGCGTGGCG TTCTAGGCTG CTTGGGCTCG GAGACGCGCC 900
 65 GCCTCTCGCT GTTCTGTGTC CTGTTGGTCC TCTCTCTCTT TGGGAGATG GCCATTCCAT 960
 TCTTTACGGG CCGCTCACT GACTGGATTG TACAAGATGG CTCAGCCGAT ACCTTCACTC 1020
 GAAACTTAAC TCTCATGTCC ATTCTACCA TAGCCAGTGC AGTGCTGGAG TTGCTGGGTG 1080
 ACGGGATCTA TAACAACACC ATGGGCCACG TGCACAGCCA CTTCAGGGA GAGGTGTTTG 1140
 GGGCTGTCTT GCGCCAGGAG ACGGAGTTT TCCAACAGAA CCAGACAGGT AACATCATGT 1200
 70 CTCGGGTAAAC AGAGGACAGC TCCACCTTGA GTGATTCTCT GAGTGAGAA CTGAGCTTAT 1260
 TTCTGTGGTA CTTGTGCGA GGCCTATGTC TCTTGGGGAT CATGCTCTGG GGATCAGTGT 1320
 CCCTCACCAT GGTCACTCTG ATCACCCTGC CTCTGCTTTT CTTCTGCCCC AAGAAGGTGG 1380
 GAAAAATGTA CCAGTTGCTG GAAGTGACAG TCGGGGAATC TCTGGCAAAG TCCAGCCAGG 1440
 TGGCATTGTA GGCTCTGTGG GCGATGCGTA CAGTTGGAAG CTTTGCCAAAC GAGGAGGGCG 1500
 75 AAGCCAGGAA GTTTAGGAAA AAGCTGCAAG AAATAAGAGC ACTCAACCAG AAGGAGGCTG 1560
 TGGCCTATGC AGTCAACTCC TGGACCACTA GTATTTTCAGG TATGCTGCTG AAGTGGGAA 1620
 TCCTCTACAT TGGTGGGCGC CTGGTGACCA GTGGGGCTGT AAGCAGTGGG AACCTTGTCA 1680
 CATTTGTCTT CTACAGATG CAGTTTCAACC AGGCTGTGGA GGTACTGCTC TCCATCTACC 1740
 CCAGAGTACA GAAGGCTGTG GGCTCTCAG AGAAAAATAT TGAGTACCTG GACCGCACCC 1800
 80 CTCGCTGCCC ACCCAGTGGT CTGTTGACTC CTTTACACTT GGAGGGCCTT GTCCAGTTCC 1860
 AAGATGTCTC CTTTGCTTAC CCAAAACCGC CAGATGTCTT AGTGCTACAG GGGCTGACAT 1920
 TCACCCTACG CCGTGGCGAG GTGACGGCGC TGGTGGGACC CAATGGGTCT GGGAGAGGCA 1980
 CAGTGGCTGC CCGTGTGACG AATCTGTACC AGCCCAACCG GGGACAGCTG CTGTTGGATG 2040
 GGAAGCCCTT TCCCAATAT GAGCACCGCT ACCTGCACAG GCAGGTGGCT GCAGTGGGAC 2100
 AAGAGCCACA GGTATTGGA AGAAGTCTTC AAGAAAATAT TGCCTATGGC CTGACCCAGA 2160

5 AGCCAACTAT GGAGGAAATC ACAGCTGCTG CAGTAAAGTC TGGGGCCCAT AGTTTCATCT 2220
 CTGGAATCCC TCAGGGCTAT GACACAGAGG TAGACGAGGC TGGGAGCCAG CTGTCAAGGG 2280
 GTACGGGACA GGCAGTGGCG TTGGCCCGAG CATTGATCCG GAAACCGTGT GTACTTATCC 2340
 TGGATGATGC CACCATGTGC CTGGATGCAA ACAGCCAGTT ACAGGTGGAG CAGCTCCTGT 2400
 ACCGAAAGCCC TGAGCGGTAC TCCCGCTCAG TGCTTCTCAT CACCCAGCAC CTCAGCCTGG 2460
 TGGAGCAGGC TGACCAATCT CTCTTTCTGG AAGGAGGCGC TATCCGGGAG GGGGGAACCC 2520
 ACCAGCAGCT CATGGAGAAA AAGGGGTGCT ACTGGGCCAT GGTGCAGGCT CCTGCAGATG 2580
 CTCCAGAAATG AAAGCCTTCT CAGACCTGCG CACTCCATCT CCTCCCTTT TCTTCTCTCT 2640
 GTGGTGGAGA ACCACAGCTG CAGAGTAGCA GCTGCCCA GAATGAGTTA CTGAAATTT 2700
 10 GCCTTGAGTG TGTTACCTCC TTTCCAAGCT CCTCGTGATA ATGCAGACTT CCTGGAGTAC 2760
 AAACACAGGA TTGTAAATTC CTACTGTAACT GGAGTTTAGA GCCAGGGCTG ATGCTTTGGT 2820
 GTGGCCAGCA CTCTGAAACT GAGAAATGTT CAGAATGTAC GGAAGATGA TCAGCTATTT 2880
 TCAACATAAC TGAAGGCATA TGCTGGCCCA TAAACACCTT GTAGGTTCTT GATATTTATA 2940
 15 ATAAATTTGG TGTTTTGT 2958

Seq ID NO: 41 DNA Sequence
 Nucleic Acid Accession #: NM_002423.2
 Coding sequence: 48..851

20 1 11 21 31 41 51
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 TGCTGTGTGC TGTGTGCTGC CTGCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG 120
 GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
 25 ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAAT 240
 TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
 CCAGATGTGG AGTGCCAGAT GTTGACAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
 CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
 TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCT CTGCATTTC 480
 30 GGAAGTGTG ATGGGGAAT GCTGACATCA TGATTGGCTT TGGCGGAGCA GCTCATGGGG 540
 ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCCTTGGG CCTGGGACAG 600
 GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGCTTAG 660
 GGATTAACCT CCGTATGCT GCAACTCATG AACTTGGCCA TCTTTGGGT ATGGGACATT 720
 CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
 35 AACTTTCCCA GGATGATATT AAAGGCATT AGAACTATA TGGAAAGAGA AGTAATTC 840
 GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCATTCA TTCATTGGAT TGTATATCAT 900
 TGTGTACAAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCAAC 960
 CTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCCTT 1020
 ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080
 40 ATGTTACATA CACAAATAAA TAAATGTTT ATTCATGCTG AAATTTA 1127

Seq ID NO: 42 DNA Sequence
 Nucleic Acid Accession #: NM_018674
 Coding sequence: 390..2009

45 1 11 21 31 41 51
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 CGGAGCACAT GCTGAGCGGA GCGGCTGGGG CTGCGCGGCG TGGCGGAGCA GCGCTGCTC 60
 CCTGCTCAC TCGTCTGCTC GCAGGGACAC ACGCAGGGGC TGACAGCTGT GCTGGTCTG 120
 ATAAGGAAG CCACAAGGAG ACGATCGAGG AGAGAGACAA GCGCAGCAG AGGCAGCAGC 180
 50 GGCAGAGGCA GCACCAGGGC TGCAGGAGTG CTGGGAGTGG GAGTGACTCC CCCACCTCGG 240
 GCGCCACCC TGTCCCTGTC CTCTTCCGCG TGCCTGAG TTTAGAAGAG CAGCCGCTGC 300
 CACCACTGCC ACTCGGAGG GCACCAGGGC TGCTGGCTAG GAGGGGACAG GGCAGGGAGG 360
 CTCTGGCCAG TCCAGCAGCT CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT 420
 TTGCTGAGGA GGATCGGAAA CCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG 480
 55 GGGCTGTGCG CCTTGGAGCA GCGCCCGGAG ACCTGGCCAC CTTTGGCAGC ACCAGCACCC 540
 TGATGGAAT GGGCCGGGCG TGTGGCCAC GCGCCCAAGG ACTGCGCAGA ACCCTGTGGG 600
 CACTGGCCCT ACTCACTCG CTGGCTGCCT TCCTGTACCA GCGCGCTGGC CTGGCCCGGG 660
 GCTACCTGAC CCGGCTCTAC CTGGTGCAA TGGACCCGCG TGCCCAAGC CAGTGGCGG 720
 GCTTCCGGCG TGTCACTCTC TGCAATATCA ACCGCTTCCG GCATTGCGCA CTCAGCGATG 780
 60 CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCCC CAAAGACCGG GATGGGCACC 840
 GTGCGGCTGC CTTGCGCTAC CCAGAGCCTG ACATGGTAGA CATCCTCAAC CGCACTGGCC 900
 ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC TCOCGCCAGCA 960
 ACTTCTCTGT GGTCTATACT CGCTATGGGA AGTGTACAC CTTCAACGCG GACCCGCGGA 1020
 GCTGCTGCC CAGCCGGGCA GGGGGCATGG GCAGTGGCCT GGAGATCATG CTGGACATCC 1080
 AGCAGGAGGA GTACTTGCCC ATCTGGAGGG AGACAAATGA GACGTGCTTT GAGGCAGGTA 1140
 65 TTGGGGTGCA GATCCACAGC CAGGAGGAGC GCGCTACAT CCAACAGCTG GGGTTGCGGG 1200
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 AGCCCTGGGG CAACTGCGCG GCAGAGAGTG AGCTCAGGGA GCTTGAGCTT CAGGGCTACT 1320
 OGGCCTACAG TGTGTCTGCC TGCCGGCTGC GCTGTGAAAA GGAGGCCGTG CTTAGCGCT 1380
 70 GCCACTGCCG GATGGTGAC ATGCCAGGCA ATGAGACCAT CTGCCACCA AATATCTACA 1440
 TCGAGTGTGC AGACCACACA CTGGACTCCC TGGGTGGGGG CCTGAGGGGC CCGTCTTCT 1500
 GCGCCACCCC CTGCAACCTG ACACGCTATG GGAAGAGAT CTCCATGGTC AGGATCCCCA 1560
 ACAGGGGCTC AGCCCGGTAC CTGGGAGGA AGTACAACCG CAACGAGACC TACATACGGG 1620
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 GAGCAGCCTA TGGCTGTGCA GCGCTGTGAG GAGACCTCGG GGGACAGATG GGCCTGTTCA 1740
 75 TTGGGGCCAG CATCTCACAG TTGCTGGAGA TCCTCGACTA CATCTATGAG GTGTCTGGG 1800
 ATCGACTGAA CGGGGTATGG AGGCGTCCCA AGACCCCTCC CGGCACTTCC ACTGGGGGCA 1860
 TCTCCACTTT GGGGCTTCAG GAGCTGAAGG AACAGAGTCC CTGCGGAGC CTGGGCGGAG 1920
 CGAGGGGTGG GGGGGTTCAG AGTCTGCTCC CCAATCACCA CCACCCCGAC GGTCCCCCAG 1980
 80 GAGGTCTCTT TGAAGATTTT GCTTGTAGG ACGGTGCTGT GACTGAAAGG ACCCAGGAGT 2040
 CTGGGACCCC CTCTGGGATC CCCAGCACAT TCTCTGCTC CTGGGAGAGG CCTGGGGGCG 2100
 GTGCTCACTG GGAGGGCCAG GACTCAGTTC CTGCTCTCAT CCTCCCTGCG CTGATGTCA 2160
 GCTGCTTTTG ACAAGGTCC TTCTTGTTCA CACCCCTTAT CCCCAGGCTG GTGCCCCGGG 2220
 AGGGCTGGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGAGGG 2280
 GGAGGATAGA GCCCATCCCA GCGGGGAGG GGGAGCCCTC GTACATTTG TAAATATTTA 2340

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GGGAAAGCCG GGTGGGGGA GGGGATACAG ATGTAGAAGG TGGGTAGGGC TACAGGGGTG 2400
 GGTGATTTAG GGACAGCCAG GGTCCCAGCC CCAATGTCAG CAGGATAGGG AGAGCCCCAG 2460
 GACTCAGGAG TGCTGGGCTG GTCCCTACTC CTGCCCTCT CCAGGCCACG CTCCCCTCTT 2520
 GGCAAGGGGA GAGGATGGCC CAGCAGGCTT GGCCAGCTC CCAGTTCCCC CTGCACCAGC 2580
 CCCACCCCTA GAGTCCCTTC TATAGGGAGG GGGCAGGAGA CCTTCCAGAC TTCGGCTGAG 2640
 CTGTGAGGGT GGGAAAGGAG CCTTCTCAGT CCTCTCTCCC TCCAGTCTGA TTTTATAAAG 2700
 TGCTGACGAG 2710

Seq ID NO: 43 DNA Sequence
 Nucleic Acid Accession #: AK091016
 Coding sequence: 201..2291

1 11 21 31 41 51
 GATCTCAGCT CCTTTTCAGC TAGTGGGTGG AACCCAGGA GGGAAACTC AGGGAAGCCC 60
 AGGAGGAAAGT GAAAATACCC CATGGAGTGA AGCTTGTGTG CTACCTGGGT TCGGGGCCAG 120
 TGATCCAGCT CTGGGGGGC ATCAGCCACG GCCAGGCAGG GGGGAGCTG CCACCAAGAC 180
 TGGAGGTTCT AGAGGACTTG ATGGAGGTCA GCTCACCCTC ACCTGCCAG AGGCTCAGAA 240
 GGAAGAAAG GCCATGGTG CAGGGCCCTG CTGGGTGCCA GGTTTTCCAG CCTTCTCCTT 300
 CAGGAGGCAC AGCAGGGGAC CCTGGTGGCC TCTCTGACCC CTCTACCT CCAAGAAGCG 360
 GTTCCCTGGC CCTTGGGAGC CCCAGCTCGG ACCCTGCATG TTCCAGAGT GGGCCAAATGG 420
 AGGCTGAAGA GGATTTCTTT CCGGAGCAGC CAGAGGACTC AGCTCAGCTC CAACAGGAGA 480
 AGCCATCCCT GTATATTGCG GTGGGGGCA CTGTTGTCCG TTCCATGCAG GAGGTACTAT 540
 GACTCGCCT TCGGAGCTC CCAGACCCAG TGCTGAGTGA GGAGGTGGTG GAGGGCATTG 600
 CTGCTGGCAT TGAGGCAGCC CTCTGGGACC TGACACAAGG CACCAATGGC CGGTACAAGA 660
 CCAAGTATCG CAGCTGCTG TTCAACCTGC GGGACCCAG GAACCTGGAC TTGTTTCTCA 720
 AAGTGGTTCA TGGAGATGTC ACCCCTACG ACCTGGTGGG GATGAGCTCG ATGCAGCTGG 780
 CCCCCAGGA GCTGGCCCGG TGGCGGGACC AGGAGGAGAA AAGGGGCTTG AATATCATTT 840
 AGCAGCAACA GAAGGAGCCG TGCAGACTTC CAGCTCCCAA AATGACCCAC AAGGGCAGAG 900
 TGGAGATTCA GCGGGACATG GACCAGACAC TGACCTGGGA GGATCTGGTG GGACCGCAGA 960
 TGTTTCATGA CTGCAGCCCA CAGGCCCTGC CCATCGCATC AGAGGACACC ACGGGCAGC 1020
 ATGACCACCA CTCTTAGAC CCAACTGACC ACATCTGCAA GGACTGGAG CCCTCGAATG 1080
 AGCTGTCTAG CTCTTCGAA GCGGCCAAGA GCTGCGGGGA CAATATCTTC CAGAAAGCCC 1140
 TAAGCCAAAC TCCTATGCCCT GCTCCAGAGA TGCCCAAAAC CAGGAGTTG TCTCCACGG 1200
 AACCACAGGA CAGGGTCCCT CCATCTGGGC TCATGTGCC TGCTGCACCC ACAAGGCC 1260
 TGCCCTGCCT GCCACCTCGG GAAGGTGTTT TGGACATGTT CTCCATCAAG CGGTTCGGGG 1320
 CCAGGGCCCA GCTGGTCTG GGACACAGCT TCGGCTTGT CCAGGCTCTG CCCACCGTGA 1380
 TCCGCTCGGC AGGCTGCATC CCTCCAACA TTGTCTGGGA CCTTCTGGCC AGCATCTGCC 1440
 CAGCCAAAGC CAAGGAGCTC TCGGTGTCA GACTGTGCC ACATGGGGCC CGGGACACCC 1500
 AGAACTCCCG CCTGCTCTAC TCATACCTCA ATGATAGGCA GCGCCACGGG CTGGCTCTG 1560
 TGGAGCACAT GGGGATGGTC CTGCTGCCCC TGCTGCGCTT CCAGCCCCTG CCCACGAGG 1620
 TGCGCCCTTT GGGGGGCCA GGTCTGGAGG TCACTCACTC AAGTCTGTG CTGGCTGTGC 1680
 TGCTCCCCAA GGAAGGGCTT CCAGACACAG CAGGGTCCAG CCCCTGGTG GGGAAAGTTT 1740
 AAAAGATGGT CTCTTCAAC AGTAAGGTGG AGAAGAGATA CTATCAGCCA GATGACAGGA 1800
 GGCCGAATGT GCCCTGAAG GGCACCCCTC CCCCAGGAGG TGCTGGCAG CAGAGCCAGG 1860
 GCAGGGGAG TATAGCTCCA AGGGGAATCT CTGCTTGCCA GAGGGCCCCC AGAGCCAGGG 1920
 GGAGGCTCTG GCCAGAGCCT GAAAACTGGC AGCATCCTGG GCGAGGGCAG TGGCCCCAG 1980
 AGCCAGGCTT GCGCCAGTCC CAGCATCCTT ATTCAGTAGC ACCAGCTGCT CATGGCTTTG 2040
 CCGTGGCCA GCATTCAC AGGACTCCT GTCCCCACCA AGCCCTGCTC CGGCACCTCG 2100
 AATCCCTGGC GACCATGAGT CACCAGCTCC AAGCCTTACT GTGCCCCAG ACCAAGAGCT 2160
 CCATCCCCCG CCCTCTGAG CGTTTGTCTA GCGCCCTTGC AGCTCCAGAG CCCCTGGCC 2220
 CAGCCCGTGA CTCTCTTTG GGGCTACAG ATGAAGCTGG CTCTGAGTGT CCTTCCCTA 2280
 GAAAGGCTG ACCTCCTTA CCCACAGAA CAGGGGTTTT GATGCCCTCA CTAGTGTGA 2340
 AGCCTGTTCC AGAGAGAGGT GGGACTGCAA GGAGAGGATG GTCAGCCCTA CCCACCTGCC 2400
 CTGTTTGAAC TTCTGTTTG ACAATGTTTG CTGTGATTT TTTGTTCAAT AAAGAATTG 2460
 GT 2462

Seq ID NO: 44 DNA Sequence
 Nucleic Acid Accession #: NM_005291
 Coding sequence: 75..1178

1 11 21 31 41 51
 CCGACACCA CGGGCGGAGA TCACCTGCTG CCCCAGAC CCCTGTCCCT TCCTCCCGGA 60
 CCAGCAGCTA GAGGATGTCC AAAACGAGTT GGTGGGCTGG ATCCAGAAAG CCCCCAAGAG 120
 AGATGCTGAA ACTCTCAGGC TCTGACTCCA GCCAAAGCAT GAATGGCCTT GAAGTGGCTC 180
 CCCCAGTCT GATCACCAAC TTCTCCCTGG CCACGGCAGA GCAATGTGGC CAGGAGACGC 240
 CACTGGAGAA CATGCTGTTC GCCTCCTTCT ACCTTCTGGA TTTTATCCTG GCTTTAGTTG 300
 GCAATACCTT GGCTCTGTGG CTTTTCATCC GAGACCAAA GTCCGGGACC CCGGCCAACG 360
 TGTTCCTGAT GCATCTGGCC GTGGCCGACT TGTGTTGGT GCTGGTCTG CCCACCCGCC 420
 TGGTCTACCA CTCTCTGGG AACCACTGGC CATTTGGGGA AATCGCATGC GGTCTCACCG 480
 GCTTCTCTT CTACCTCAAC ATGTACGCCA GCATCTACTT CCTCACCTGC ATCAGGCGCG 540
 ACCGTTTCTT GGCCATTGTG CACCCGGTCA AGTCCCTCAA GCTCCGAGG CCCCTCTAG 600
 CACACCTGGC CTGTGCCCTC CTGTGGGTGG TGGTGGCTGT GGCCATGGCC CCGTCTCTGG 660
 TGAGCCACCA GACCGTGAG ACCAACCACA CGGTGGTCTG CCGCAGCTG TACCGGGAGA 720
 AGGCCCTCCA CCATGCCCTG GTGTCCCTGG CAGTGGCCTT CACCTTCCCG TTCTACCA 780
 CGGTCACTG CTACCTGCTG ATCATCCGA GCCTCGGCA GGGCCTGGT GTGGAGAGC 840
 GCCTCAAGAC CAAGGCAGTG GGCATGATCG CCATAGTGTG GGCCATCTTC CTGGTCTGCT 900
 TCGTGCCCTA CCACGTCAAC CGCTCCGTCT ACGTGTGCA CTACCCGAGC CATGGGGCTT 960
 CCTGGCCAC CCAGCGCATC CTGGCCCTGG CAAACCGCAT CACCTCTGCT CTCACCGCC 1020
 TCAACGGGGC ACTCGAGCCC ATCATGTATT TCTGTGTGG TGAGAAGTTC CGCCAGCTCC 1080
 TGTGCACTT GCTCTGTGG AAAAGGCTCA AGGGCCCGCC CCCCAGCTTC GAAGGGAAAA 1140
 CCAACGAGAG CTCCTGAGT GCCAAGTCAG AGCTGTGAGC GGGGGGCGCC GTCCAGGCCG 1200
 AGCGCAGAT GTTTAGGACT CAGCAGACCC AGCAAGAGGC ATCTGCCCTT TCCCCAGCCA 1260
 CCTCCCCAGC AAGCAACCTG AAATCTCAGC AGATGCCAC CATTTCTCTA GATCGCCTAG 1320
 TCTCAACCA TAAAGAGAA GAACCTGACAA AGGGATCCA TCGGCCACCC CTCTGCAGGG 1380

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GCTTGTGATG GCTACAATGG CTCCTAGACA CTCAACGACT TCATCTGTGG CAGGGAGAGA 1440
GGAGGGCCGA AGAACAAACC CTGAACAAATG GAGGCCTTTC TTTCCCGCTA GGCTCCCAGC 1500
CTGCTTCCCG CTACAGAAATC GCTCATCGGC GAGGCTCAGC AGAAAGACCC TGAAGGCAGG 1560
CTGCAAAATGA CCGAAGAGAG GGACCTGGGA GTCTGTGTGG GGACGGGGAG GGAGTCTCAA 1620
TACTCCTTTG CAGCGCAAGG TACTCTGAGT CCCCTCTGTA GTGCCTCTGC CAGACACACA 1680
CTGCCTGAGT TGAAGAGACA CAGGCCACAC ATTTTCAGGCT GGTTGCCAGC GGAGCTCAGC 1740
ACTCACGGCC TGCGGGGACT CAGCACAGCT CTGGATTCTG GATCTCTCCT GCTGTAACCC 1800
CACGCACAAG CCTGCAACCC CCAGAGCTCT TTGACAGGCT CCCAGGCCCT CCAGTCTCTG 1860
ACAAGCATGT GCAGTCAAGG GAGCTCAGCT CAGGCCAGGG CTGGGCTGTG CACCTGCCTC 1920
CCACTGACCC AGACCCACTT CCTCCAGAGA GGCCTCTCTC CGCCTGAGCT ATTTCCCTTG 1980
CTAGTGTGCA GATATTTCCC TAAACATGTC TTTTGTGTAT TTGTTGTAC GGACCATAAA 2040
TATAACTGTA GCTTTAAGAC TAAAAAATAA 2070

Seq ID NO: 45 DNA Sequence
Nucleic Acid Accession #: NM_018643
Coding sequence: 48..752

1 11 21 31 41 51
| | | | |
CTACTACTAC TAAATTCCGC GCCGCTCGAC GCTGTGTGAC AGGAAGGATG AGGAAGACCA 60
GGCTCTGGGG GCTGCTGTGG ATGCTCTTTG TCTCAGAACT CCGAGCTGCA ACTAAATTAA 120
CTGAGGAAAA GTATGAACCTG AAAGAGGGGC AGACCTTGGA TGTGAATGT GACTACAGCC 180
TAGAGAAGTT TGCCAGCAGC CAGAAAGCTT GGCAGATAAT AAGGGAACGA GAGATGCCCA 240
AGACCCCTGGC ATGCACAGAG AGGCCCTTCAA AGAATTCCTA TCCAGTCCAA GTGGGGAGGA 300
TCATACTAGA AGACTACCAT GATCATGGTT TACTGCGCT CCGAATGGTC AACCTTCAAG 360
TGGAAAGATTG TGGACTGTAT CAGTGTGTGA TCTACCAGCC TCCCAAGGAG CCTCACATGC 420
TGTTGATGCG CATCCGCTTG GTGGTGACCA AGGGTTTTTC AGGGACCCCT GGCTCCAATG 480
AGAATTCTAT CACAGAATGTG TATAAGATTG CTCTTACCAC CACTAAGGCC TTGTGCCCATC 540
TCTATACAGC CCCCAGAACT GTGACCCAAAG CTCCACCCAA GTCAACTGCC GATGTCTCCA 600
CTCTGACTC TGAATCAAC CTTACAAATG TGACAGATAT CATCAGGTT CCGGTGTTC 660
ACATTGTAT TCTCTGGCT GGTGGATTCC TGAGTAAGAG CCTGGTCTTC TCTGTCTCTG 720
TTGCTGTGAC GCTGAGGTCA TTTGTACCTT AGGCCACGA ACCACAGAGA ATGTCTCTG 780
ACTTCCAGCC ACATCCATCT GGCAGTTGTG CCAAGGGAGG AGGGAGGAGG TAAAAGGCAG 840
GGAGTTAATA ACATGAATTA AATCTGTAAT CACCAGCTAT TTCT 884

Seq ID NO: 46 DNA Sequence
Nucleic Acid Accession #: NM_003467
Coding sequence: 1..1059

1 11 21 31 41 51
| | | | |
ATGAGGGGGA TCAGTATATA CACTTCAGAT AACTACACCG AGGAAATGGG CTCAGGGGAT 60
TATGACTCCA TGAAGGAACC CTGTTTCCGT GAAGAAAATG CTAATTTCAA TAAATCTTTC 120
CTGCCACCA TCTACTCCAT CATCTTCTTA ACTGGCATTG TGGGCAATGG ATGGTTCATC 180
CTGGTCTAGG GTTACAGAA GAAACTGAGA AGCATGACGG ACAAGTACAG GCTGCACCTG 240
TCAGTGGCCG ACCTCCTCTT TGTATCAGC CTTCCTTCTT GGGCAGTTGA TGCCGTGGCA 300
AACTGGTACT TTGGGAACCT CTTATGCAAG GCAGTCCATG TCATCTACAC AGTCAACCTC 360
TACAGCAGTG TCCCTCATCT GGCCTTCATC AGTCTGGACC GCTACCTGGC CATGTGCCAC 420
GCCACCAACA GTCAGAGGCC AAGGAAGCTG TTGGCTGAAA AGGTGGTCTA TGTGGCGTCT 480
TGGATCCCTG CCCTCCTGCT GACTATTCCC GACTTCATCT TTGCCAACGT CAGTGAGGCA 540
GATGACAGAT ATATCTGTGA CCGCTTCTAC CCCAATGACT TGTGGGTGGT TGTGTTCCAG 600
TTTCAGCACA TCATGGTTGG CCTTATCCTG CTGGTATTG TCATCTGTCT CTGCTATTGC 660
ATTATCATCT CCAAGCTGTG ACATCTCAAG GGCACACAGA AGCGCAAGGC CCTCAAGACC 720
ACAGTCTGTG TCATCTGCTG TTTCTTCGCC TGTGGCTGCT CTTACTACAT TGGGATCAGC 780
ATGACTCTCT TCATCTCTCT GGAATCATC AAGCAAGGGT GTGAGTTTGA GAACACTGTG 840
CACAAGTGGT TTTCCATCAC CGAGGCCCTA GCTTCTTCTC ACTGTTGTCT GAACCCCATC 900
CTCTATGCTT TCTCTGGAGC CAAATTTAAA ACCTCTGCCC AGCACGCACT CACTCTGTG 960
AGCAGAGGGT CCAGCTCAA GATCCTCTCC AAAGGAAAGC GAGGTGGACA TTCATCTGTT 1020
TCCACTGAGT CTGAGTCTTC AAGTTTTTAC TCCAGCTAA 1059

Seq ID NO: 47 DNA Sequence
Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGGAGG CTGTCCAAGG 60
AGTAGGCTCA GTAGCACGAA CTGCAAAATC TTGAGAAAGG AAAAGTTTCA CCTGTGCTGT 120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA 180
ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAA TGGTGTAAAT AATAGCACCC 240
ACCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
CTGTTCTCTG TAAGCTCTGT GAAAGAAGTC TATGGATTAT ACTCAACCTA CACTCCAGTT 360
AAAGGAACAT CTACACAGAG AGGAAATGAA TAACATGAAG TGAAGTCTTC ATCTCCATTG 420
CCACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAATAATCAG TTTATTTTCC 480
CCTGGTGCAA AGAACAGTCG TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG 540
GTCCTCCGGA AAAGGGAGCT GAAGCCCTCT TTGTAATTTT GCATTAGCG TGCTCTCTG 600
GCAGCAGGGA AACCTCATCA GAGAAGTCAG CCAAGGAAAG TCTTTAAATG GAAATGTGTC 660
AAACGAGGAG CAATATGATT AAAAAGTTGC TGACGGGCAT GAAATGCTTT GATGTGAAGA 720
CGGAAACTC CAAGCAGGAA GGATTTTAACT ATTTTGAATC TGATTGACTC TGTGTTTCT 780
CAGCAGATT ATTCATGGG CTAAAATAAA TGCAGAAATG GTACTTTCAG ACCACAGCTG 840
CAGAGGGGAT CGTGGTGAAT TTCAATGAAA ATCCATTGTA ATCTTGAGGT TCAGATCTTA 900
AAAAAGCAAA GGACATGAGA GAAGTAATAT TGTGCTTGA AATTTTATTG CTTATATCTA 960
AAAGAACTC CTATTTTTTA GAGAAATGTT GAATCTTTGC AACGTGGTAG ACGTCCCAC 1020
AAAACCTTCT CCTGAAATAG GAGATAAATG TTGGAAGAG GCAATGTATT GAGTATGCTG 1080
ATAGAGGTGG AGTTTCAGAG CAGGCAAGCA TACATAAGAG TCAGGATGTT TTTCAGTATT 1140
ATCTTTACAA ATGAGTTTCT TACAGTGGTC AATGACAAAC CAATTTTATT CAAAGCTTGC 1200
TTCAATAGGC AATGGTTTGA TGCCAAATATG TTAGCTATTT ACTTTGACCA CCGTATGCAT 1260
TAAAAGAAAG AAAAATTAAG AATACTCAAG CAGAACTCC AACTTAGATA GCACCTTCCA 1320

CAAAAAGTAA TGGAGGGATA GACTGAAATT AAATGGGATC AGGTATGTGA TGAGATCTCA 1380
 GAAGTGTGTTG CACAATAATG CAGATACTCA TTTTAAACAG AGTCATAAGG ATTGGAACTA 1440
 ATAAAAATAA TAGAATAAAA TACCGATCAA GAATGTGTCC TCCTGCGTAT CTGGGTTTTG 1500
 AATTCTGGCT CCACAGAACT TGTGAGATAT ATGACATTAA AC 1542

Seq ID NO: 48 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..1131

1 11 21 31 41 51
 | | | | |
 10 ATGCATCTCT AAGTGGTCAT CTTAAGCCTC ATCCTACATC TGGCAGATTG TGTAGCTGGT 60
 TCTGTAAAGG TTGGTGGAGA GGCAGGTCCA TCTGTACAC TACCCTGCCA CTACAGTGGG 120
 GCTGTACAT CAATGTGCTG GAATAGAGGC TCATGTTCTC TATTTCATCG CCAAAATGGC 180
 15 ATTGTCTGGA CCAATGGAAC CCACGTCAAC TATCGGAAGG ACACACGCTA TAAGCTATTG 240
 GGGGACCTTT CAAGAAGGGA TGTCTCTTTG ACCATAGAAA ATACAGCTGT GTCTGACAGT 300
 GGGCTATATT GTTGGCGTGT TGAGCACCGT GGGTGGTTCA ATGACATGAA AATCACGCTA 360
 TCATTGGAGA TTGTGCCACC CAAGGTCAAG ACTACTCCAA TTGTCAACAC TGTTCACACC 420
 GTCACGACTG TTCGAACGAG CACCACTGTT CCAACGACAA CGACTGTTCC AACGACAACT 480
 20 GTTCCAACAA CAATGAGCAT TCCAACGACA ACGACTGTTT CGACGACAAAT GACTGTTTCA 540
 ACGACAAAGA GGGTTCACAC GACAACGAGC ATTCACAAAC CAACAAGTGT TCCAGTGACA 600
 ACAACGGTCT CTACCTTTGT TCCTCCAATG CCTTTGCCCA GGCAGAACCA TGAAACGAGTA 660
 GCCACTTTCAC CATCTTCACC TCAGCCAGCA GAAACCCACC CTACGACACT GCAGGGAGCA 720
 ATAAGGAGAG AACCCACCAG CTCACCATG TACTCTTACA CAACAGATGG GAATGACACC 780
 25 GTGACAGAGT CTTGAGATGG CCTTGGAAAT AACAAATCAA CTCACCTGTT CCTAGAACAT 840
 AGTCTACTGA CGGCAATATC CACTAAAGGA ATCTATGCTG GAGTCTGTAT TTCTGTCTTG 900
 GTGCTTCTTG CTCTTTTGGG TGTATCATTT GCCAAAAAGT ATTTCTTCAA AAAGGAGGTT 960
 CAACAACATA GTGTTTCATT TAGCAGCCTT CAAATTAAG CTTTGCAAAA TGCAGTTGAA 1020
 AAGGAAGTCC AAGCAGAAGA CAATATCTAC ATTGAGAATA GTCTTTATGC CACGGACTAA 1080

Seq ID NO: 49 DNA Sequence
 Nucleic Acid Accession #: NM_004932.2
 Coding sequence: 327..2699

1 11 21 31 41 51
 | | | | |
 35 ACTTCATTCA CTTGCAAAATC AGTGTGTGCC CACAAGAGCC AGCTCTCCCG AGCCCGTAAC 60
 CTTGCGATCC CAAGAGCTGC AGTTTCAGCC GCGACAGCAA GAACGGCAGA GCCGGCGACC 120
 GCGGCGGCGG CGGCGGCGGA GGCAGGAGCA GCCTGGGGGG GTGCGAGGGT CTCGCGGGGC 180
 GCAGGAAGGC GAGCAGAGAT ATCCTCTGAG AGCCAAGCAA AGAACATTAA GGAAGGAAGG 240
 40 AGGAATGAGG CTGGATACGG TGCAAGTAAA AAGGCACCTC CAAGAGTGGG GCACTCACTA 300
 GGCACAGACT CGACGGTGCC ATCAGCATGA GAACCTTACC CTACTTCTTG CTGCTCTTTT 360
 GGGTGGGCCA GCCCTACCCA ACTCTCTCAA CTCACATATC AAAGAGGACT AGTGGTTTCC 420
 CAGCAAAAGAA AAGGGCCCTG GAGCTCTCTG GAAACAGCAA AAATGAGCTG AACCGTTCAA 480
 AAAGGAGCTG GATGTGGAAT CAGTTCTTTC TCCTGGAGGA ATACACAGGA TCCGATTATC 540
 45 AGTATGTGGG CAAGTTACAT TCAGACCAGG ATAGAGGAGA TGGATCACTT AAATATATCC 600
 TTTCAAGAGA TGGAGCAGGA GATCTCTTCA TTATTAATGA AAACACAGGC GACATACAGG 660
 CCACCAAGAG GCTGGACAGG GAAGAAAAAC CCGTTTACAT CCTTCAGCT CAAGCTATAA 720
 ACAGAAAGAC AGGGAGACCC GTGGAGCCCG AGTCTGAATT CATCATCAAG ATCCATGACA 780
 TCAATGACAA TGAACCAATA TTCACCAAGG AGGTTTACAC AGCCACTGTC CCTGAAATGT 840
 50 CTGATGTGGG TACATTGTGT GTCCAAAGTC CTGCGACGGA TGCAGATGAT CCAACATATG 900
 GGAACAGTGC TAAAGTTGTC TACAGTATTC TACAGGAGCA GCCCTATTTT TCAGTTGAAT 960
 CAGAAACAGG TATTATCAAG ACAGCTTTGC TCAACATGGA TCGAGAAAAC AGGGAGCAGT 1020
 ACCAAGTGTG GATTCAAGCC AAGGATATGG GCGGCCAGAT GGGAGGATTA TCTGGGACCA 1080
 CCACCGTGAA CATCACACTG ACTGATGTCA ACGACAACCC TCCCGATTTC CCCACAGTA 1140
 55 CATACCACTT TAAACTCTCT GAATCTTCTC CACCGGGGAC ACCAATTGGC AGAATCAAAG 1200
 CCAGCGACCG TGATGTGGGA GAAAAAGCTG AAATTAGGTA CAGCATCACA GACGGTGAGG 1260
 GGCTGGATAT GTTGTATGTC ATCACGACC AGGAAACCCA GGAAGGGATT ATAAGTGTCA 1320
 AAAAGCTCTT GGACTTTGAA AAGAAGAAAG TGTATACCTT TAAAGTGGAA GCCTCCAATC 1380
 CTTATGTTGA GCCACGATTT CTCTACTTGG GGCCTTTCAA AGATTGAGC ACGGTTAGAA 1440
 60 TTGTGGTGA GATGTAGAT GAGCCACCTG TCTTCAGCAA ACTGGCCTAC ATCTTACAAA 1500
 TAAGAGAAGA TGCTCAGATA AACACCACAA TAGGCTCCGT CACAGCCCAA GATCCAGATG 1560
 CTGCCAGGAA TCCTGTCAAG TACTCTGTAG ATOGACACAC AGATATGGAC AGAATATTCA 1620
 ACATTGATTC TGGAAATGGT TCGATTTTCA CATCGAAACT TCTTGACCGA GAAACACTGC 1680
 TATGGCACAA CATTACAGTG ATAGCAACAG AGATCAATAA TCCAAAGCAA AGTAGTCGAG 1740
 65 TACCTCTATA TATTAAAGTT CTAGATGTCA ATGACAACGC CCCAGAAATT GCTGAGTTCT 1800
 ATGAAACTTT TGTCTGTGAA AAAGCAAAGG CAGATCAGTT GATTGAGACC CTGCATGCTG 1860
 TTGACAAGGA TGACCTTAT AGTGGACACC AATTTTGGTT TTCCTTGGCC CTGGAAGCAG 1920
 CCAGTGGCTC AAATTTTACC ATTCAAGACA ACAAGACAA CACGGCGGGA ATCTTAACTC 1980
 GGAATAATGG CTATAATAGA CACGAGATGA GCACCTATCT CTTGCTGTG GTCATTTTCA 2040
 70 ACAACGACTA CCCAGTTCAA AGCAGCACTG GGACAGTGAC TGTCCGGGTC TGTGCATGTG 2100
 ACCACCAAGG GAACATGCAA TCCTGCCATG CGGAGGCGCT CATCCACCCC ACGGGACTGA 2160
 GCACGGGGGC TCTGTTTGGC ATCCTTCTGT GCATGTGTAT CCTACTAGTG ACAGTGGTGC 2220
 TGTGTCAGC TCTGAGGCGG CAGCGAAAAA AAGAGCCTTT GATCATTTC AAAGAGGACA 2280
 TCAGAGATAA CATTGTCACT TACAACGACG AAGGTGGTGG AGAGGAGGAC ACCCAGGCTT 2340
 75 TTGATATCGG CACCTGAGG AATCTGAAG CCATAGAGGA CAACAAATTA CGAAGGGACA 2400
 TTGTGCCGGA AGCCCTTTTC CTACCCGAC GGAATCCAAAC AGCTCGGAC AACACCGATG 2460
 TCAGAGATTT CATTAACCAA AGGTAAAGG AAAATGACAC GGACCCCACT GCCCGGCCAT 2520
 AGCACTCTTT GGCCACTTAC GCCTATGAAG GCACTGGCTC CGTGGGAGAT TCCCTGAGCT 2580
 CGCTGGAGTC AGTGACCAAG GATGCAGATC AAGACTATGA TTACTTATG GACTGGGGAC 2640
 80 CTCGATTCAA AAAGCTTGCA GATATGTATG GAGGAGTGGG CAGTGACAAA GACTCCTAAT 2700
 CTGTTGCCCT TTTTATTTTC CAATACGACA CTGAAATATG TGAAGTGGCT ATTTCTTTAT 2760
 ATTTATCCAC TACTCCGTA AGGCTTCTCT GTTCTACCCG TTCCAAAAGC CAATGGCTGC 2820
 AGTCCGTGTG GATCCAATGT TAGAGACTTT TTTCTAGTAC ACTTTTATGA GCTTCCAAGG 2880
 GGCATAATTT TATTTTATAG TGCATCCAGT TAACCAAGTC AGCCCAACAG GCAGGTGCCG 2940
 GAGGGGAGGA CAGGGAACAG TATTTCCACT TGTCTCAGG GCAGCGTGCC CGCTTCCGCT 3000

5 GTCCGTGGT TTTACTACAC TCCATGTCAG GTCAGCCAAC TGCCCTAACT GTACATTTC 3060
 CAGGCTAATG GGATAAGGA CTGTGCTTTA AAGATAAAAA TATCATCATA GTAAAAGAAA 3120
 TGAGGGCATA TCGGCTCACA AAGAGATAAA CTACATAGGG GTGTTTATTT GTGTCACAAA 3180
 GAATTTAAAA TAACACTTGC CCAATGCTATT TGTCTTCAA GAACTTTCTC TGCCATCAAC 3240
 TACTATTCAA AACCTCAAAT CCACCCATAT GTTAAAAATC TCATTACTCT TAAGGAATAG 3300
 AAGCAAATTA AACGGTAACA TCCAAAAGCA ACCACAACC TAGTAGACT TCATTCTTC 3360
 CACTAACTCA TAGTTTGTTA TATCCTAGAC TAGACATGCG AAAGTTTGCC TTTGTACCAT 3420
 ATAAAGGGGG AGGGAATAG CTAATAATGT TAACCAAGGA AATATATTTT ACCATACATT 3480
 TAAAGTTTTG GCCACCATAT GTATCACGGG TCACCTGAAA TTCTTTCAGC TATCAGTAGG 3540
 10 CTAATGTCAA AATTGTTTAA AAATCTTGA AAGAATTTTC CTGAGACAAA TTTTAACTTC 3600
 TTGTCTATAG TTGTCAATAT TATCTACTA TACTGTACAT GAAAGTAGCA GTGTGAAGTA 3660
 CAATAATTCAT TATCTTCTAT ATCTTCTTA CAGGACTAAG TTGAATTAGT AAAGTTAGAT 3720
 TAAATAAACA TTAATCTCA CTCTAGGAGT TCAGTGGAGA GGTTAGAGCC AGCCACACTT 3780
 GAACCTAATA CCCTGCCCTT GACATCTGGA AACCTCTACA TATTTATATA ACGTGATACA 3840
 15 TTTGGATAAA CAACATTGAG ATTATGATGA AAACCTACAT ATTCCATGTT TGGGAAGACC 3900
 TTGGAAGAGG AAAATGAT TCCCTTAAAC AAAAGTGTTC AAGATTGTAA TTAATATGAT 3960
 AGTTGATTTT CAAAAGCAT AATTTTTTTT CATTGTTTTT AACTTTGCTT TCATGACCAT 4020
 CCTGCCATCC TTGACTTTGA ACTAATGATA AAGTAATGAT CTCAAACAT GACAGAAAAG 4080
 TAAATGTAAA TCCATCCAA CTATTATTTC TCTAATTATG CAATTAGCCT CATAGTTATT 4140
 20 ATCCAGAGGA CCCAATGAA CTGAATTAAT CCTTCTGGCA GATTCAAAAT GTTTATTTC 4200
 CACGCTGTTT TAATGGCACT TATCATTAGA ATCTTACCTT GTGAGTCAT CAGAAATTC 4260
 AGCGTACTAT AATGAAAACA TCCCTGTTTT GAAAACCTAA AAGACAGGCT CTGTATATAT 4320
 ATATATCTAA GAATATGCTG ACTTCACTTA TTAGTCTTAG GGATTTATTT TCAATTAATA 4380
 TTAATTTTCT ACATAAATTT TTAGTGTGAT TTCCATTGGG GGATATTGTC ATATCAGCAC 4440
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Seq ID NO: 50 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
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 Nucleic Acid Accession #: Eos sequence
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	GCCCGCTCCA	CGCTGCTCAG	GACCATCCGC	AGTGTATTAA	ACCCGACCCC	TACGCATCTG	1080
	ATCCGGGAAA	TCATATTAGT	GGATGACTTC	AGCAATGACC	CTGATGACTG	TAAACAGCTC	1140
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	GAGGTGAACA	GGGACTGGCT	CCAGCCTCTG	TTGCACAGGG	TCAAAGAGGA	CTACACCGCG	1320
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	GTCTCTAAGG	CCGTTAAGTT	CCAGTCTCTG	CCAGTCATT	CCTGATTGGT	ATCTGGAGAC	2580
	AGAAACCTAA	TGGGAAGTGT	TTATTGTCTC	TTTCTCTACA	AAGGAAGCAG	TCTCTGGAGG	2640
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Coding sequence: 641..2299

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 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 400..1959

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 Seq ID NO: 54 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1241..2377

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Seq ID NO: 55 DNA Sequence

Nucleic Acid Accession #: NM_001218

Coding sequence: 1..1080

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Seq ID NO: 56 DNA Sequence

Nucleic Acid Accession #: BC000278

Coding sequence: 113..1144

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	GTGAGAAGGC CTCGCTGTCC TGCTGTCTCT CATTGAGATG GGCTCCTTCA ATCCGTCTTA 660
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10	GGGATTCAAC ATTAAGAGC TGCTTCCGGA GAGGACCGCT GAATATTACC GCTACCGGGG 780
	GTCCCTGACC ACACCCCTT GCAACCCAC TGTGCTCTGG ACAGTTTTC GAAACCCCGT 840
	GCAAAATTCC CAGGAGCAGC TGCTGGCTTT GGAGACAGCC CTGTAAGTCA CACATATGGA 900
	CGACCTTCC CCCAGAGAAA TGATCAACAA CTTCGGCAG GTCCAGAAAT TCGATGAGAG 960
	GCTGGTATAC ACCTCTCTCT CCCAAGGCAT CATCTCTCA CTGGCCCTGG CTGGCATTCT 1020
15	TGGCATCTGT ATTTGGTGG TGGTGTCCAT TTGGCTTTTC AGAAGGAAGA GTATCAAAAA 1080
	AGGTGATAAC AAGGGAGTCA TTTACAAGCC AGCCACCAAG ATGGAGACTG AGGCCCAAGC 1140
	TTGAGGTCCC CGAGGCTCCC GGGCACATCC AGGAAGGACC TTGCTTTGGA CCCTACACAC 1200
	TTCCGCTCTC TGGACACTTG CGACACCTCA AGGTGTTCTC TGTAGCTCAA TCTGCAACAA 1260
20	TGCCAGGCTC CAGGCTCTCT CTGCTGGGTG CCTCCTTGCC TTGGGACCAT GGCCACCCCA 1320
	GAGCCATCCG ATCGATGGAT GGGATGCACT CTCAGACCAA GCAGCAGGAA TTCAAAGCTG 1380
	CTTGCTGTAA CTGTGTGAGA TTGTGAAGTG GTCTGAATTC TGGAAATACA AACCAAGCCA 1440
	TGCTGGTGGG CCATTAATGG TTGGAAAAA CTTTCATCCG GGGCTTTGCC AGAGCGTGCT 1500
	TTCAAGTGTC CTGGAAGTCT TGCTGCTTCT CCAAGCTTTC AGACAAGAAT GTGCACTCTC 1560
25	TGCTTAGGTT TTGCTGGGA AACTCAACTT CTTTCTCTG GAGACGGGGC ATCTCCCTCT 1620
	GATTTCTTTC TGCTATGACA AAACCTTTAA TCTGCACCTT ACAACTCGGG GACAAATGGG 1680
	GACAGGAAGG ATCAAGTTGT AAAAAAATA AAAAAAATA 1718

30	Seq ID NO: 57 DNA Sequence
	Nucleic Acid Accession #: NM_006632.1
	Coding sequence: 377..1582
	1 11 21 31 41 51
	ACGCGTCCGC CCACGCGTCC GCCACGCGT CCGTCCGGGG CCAGAGCGCA GGTGTACCTG 60
	GCGGCGGTGC TGGAGCACCT GACCGCGAG ATCCTGGAGC TGGCTGGCAA CCGGCCCGGC 120
35	GACAAGAGA CCCGATCAT CCTGCGCCAC CTGTAGCTGG CCATTTCGCA CCGCGAGGAG 180
	CTTAACAAGC TGCTGGGGCA AGTCACCATC GCGCAGGGCG GTGTCCTGCC CAACATTTCAG 240
	GGCGTGTCTT TGCCTCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTTCA 300
	CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
40	CAAGAAGCCA CAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
	ATGTTCTGCT CGCTATGAA TAGCCCTCGT CTATCATTTT TCCAATTTCA CAACGATAGC 480
	ACAAAAATGC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACA GCCCTCAATC 540
	CCAGCTCAAT GATTCTCTG AGGTGCTGCC TGTGACTCA TTTGTTGGCC TAAGTAAAGC 600
	CCCAAGAGAT CTTCCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
	GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGAGCATT GCTTTATCAG GAATGTTACT 720
45	GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCCCTG GGTGGCCCTT 780
	TGCTCTCTAT ATCTTTGGAG GTGTGGCTG TGTCTGTGC CTTCCTGGT TGTGTGTGAT 840
	TTATGATGAC CCCTTTCTCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC 900
	CTCCTTGAAA CAACAGGTGG GGTCTTCTAA GCAGCCTCTT CCCATCAAAG CTATGCTCAG 960
50	ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGTT TAGTTAGCAC 1020
	AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
	TGGACTCTTA TCTGCCCTTC CTTTATTGTT TGCTGGGGTC ATAGGCATGG TGGGAGGCTA 1140
	TCTGGCAGAT TTCCTCTTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC 1200
	AATTTTAGGA AGTCTCCCTT CTTCAGCACT CATTGTGTCT CTGCCCTACC TCAATTCCGG 1260
55	CTATATACA GCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTCACTG 1320
	AGGGATTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
	ATCAAGAGGA TTTTCGAGCA TAGCACCTGT CATTGTACCC ACTGTACGG GATTTCCTCT 1440
	TAGTCAGGAC CCGTAGTTTG GGTGGAGGAA TGTCTTCTTC TTGCTGTTTG CCGTTAACTC 1500
	GTTAGGACTA CTCTCTTACC TCATATTGG AGAAGCAGAT GTCCAAGAAT GGGCTAAAGA 1560
	GAGAAAATCT ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG 1620
60	TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAAAGATT TTTTTCCTCT 1680
	GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTTT TTTGAGAGAA 1740
	ATGTAAGATG AATAAAAAAT CAAATAAAAT GATAACTAAG AAAAAAATA AAAAA 1795

65	Seq ID NO: 58 DNA Sequence
	Nucleic Acid Accession #: NM_003058.1
	Coding sequence: 145..1812
	1 11 21 31 41 51
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70	GGGTTTGTGC TGAGCTGGCT GCAGCGGCTC TCAGCCTCGC TCCGGGCAAG TCGGGCAGCC 120
	TCGGGCGCTC CTGCTGCGAG GATCATGCC ACCACCGTGG ACGATGTCTT GGAGCATGGA 180
	GGGGAGTTTC ACTTTTCTCA GAAGCAAAATG TTTTCTCTCT TGGCTCTGCT CTGGCTACC 240
	TTCCGCGCCA TCTACGTGGG CATGCTCTTC CTGGGCTTCA CCCTGACCA CCGCTGCCGG 300
75	AGCCCCGAG TGGCCGAGCT GAGTCTGCGC TGGCGCTGGA GTCTGCGAGA GGAACCTGAAC 360
	TACACGCTGC CGGCGCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
	GAGGTGGACT GGAACAGAG CACCTTTGAC TGCGTGGACC CCCTGGCCAG CCGTGCACAC 480
	AACAGAGCC CCCTGCCACT GGGGCCCTGC GGGGTGACGA GACGCTGGC 540
	TGCTCATCG TCACCGAGTT TAACCTGGTA TGTGCCAATC CCTGATGTT GGACCTATTC 600
80	CAGTCATCAG TGAATGTAGG ATCTTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
	AGGTTTGGCC TGAAGCTCTG CCTCTTAATC ACAGTCTCTA TAAATGCTGC AGCTGGAGTT 720
	CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTGCTTAAT CCAAGGACTG 780
	GTACGAGAA CAGTGGGGAT TTTTACCAA GTTCCTATA CAGTTGGGCT CCTGGTGTCT 840
	TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTCCTATA CAGTTGGGCT CCTGGTGTCT 900
	GCTGGGGTGG CTTACGCACT TCCTCACTGG AGGTGGTTGC AGTTACAGT TGCTCTGCC 960

	AACTTCTTCT	TCTTGTCTA	TTACTGGTGC	ATACCTGAGT	CTCCCAGGTG	GCTGATCTCC	1020
	CAGAATAAGA	ATGCTGAAGC	CATGAGAATC	ATTAAGCACA	TCGCAAGAA	AAATGGAAAA	1080
	TCTCTACCCG	CCTCCCTTCA	GCGCCTGAGA	CTTGAAGAGG	AAACTGGCAA	GAAATTGAAC	1140
5	CCTTCATTTT	TTGACTTGGT	CAGAACTCCT	CAGATAAGGA	AACATACTAT	GATATTGATG	1200
	TACAACCTGGT	TCACGAGCTC	TGTGCTCTAC	CAGGGCCTCA	TCATGCACAT	GGGCCTTGCA	1260
	GGTGACAATA	TCTACCTGGA	TTTCTTCTAC	TCTGCCCTGG	TTGAATTCCT	AGCTGCCTTC	1320
	ATGATCATCC	TCACCATCGA	CGCATCGGA	GCGCGTTACC	CTTGGGCTGC	ATCAAAATATG	1380
	GTTCGAGGGG	CAGCCTGTCT	GCGCTCAGTT	TTTATACCTG	GTGATCTACA	ATGGCTAAAA	1440
10	ATTATTATCT	CATGCTGGGG	AAGAATGGGG	ATCACAATGG	CCTATGAGAT	AGTCTGCCTG	1500
	GTCAATGCTG	AGCTGTACCC	CACATTCAAT	AGGAATCTTG	GCGTCCACAT	CTGTTCCTCA	1560
	ATGTGTGACA	TTGGTGGCAT	CATCACGCCA	TTCTGGTCT	ACCGGCTCAC	TAAACATCTGG	1620
	CTTGAGCTCC	CGCTGATGGT	TTTCGGCGTA	CTTGGCTTGG	TTGCTGGAGG	TCTGGTGCTG	1680
	TTGCTTCCAG	AACTAAAGG	GAAAGCTTGG	CCTGAGACCA	TCGAGGAAGC	CGAAAATATG	1740
	CAAGACCAA	GAAAAATATA	AGAAAAGATG	ATTTACCTCC	AAGTTCAGAA	ACTAGACATT	1800
15	CCATTGAATC	AAGAGAGAG	ACCGTTGCTG	CTGTGATGAC	CTAGCTTTGA	TGGCAGCAAG	1860
	ACCAAAAGTA	GAAATCCCTG	CATCATCTAC	AAAGCCCAT	CAACTCAACC	AAACTTACCC	1920
	CTGAGCCCTA	TCAACCTAGG	TCTACAGCCA	GTGGAGTCTA	TTGTACACTG	TGAAAAATA	1980
	CCCATGGGAC	CAGATCTGTC	CAAATCTTTC	CAGCTCACIT	TAITCTCAGC	ATTCTAGGA	2040
20	CATTGGACAT	TGGTTTTCTG	GAGGGTTTTT	TTTCCGATCT	TTGTATTTT	TTAAATTTGA	2100
	TTCTTTTCTT	TGCAATGCTA	GCAACCAGAA	TACATAGGGG	AACTGTGGGC	TAGGCAANA	2160
	AAATAGAAAA	AGTGTAAAA	ACAGTAAAGT	TGGGAGAGGA	GCATCTATTT	TCTTAAAGAA	2220
	ATAAACACCC	NAAAACAAAA	AAAAAATAAA	AAAAAATA			2257
25	Seq ID NO: 59 DNA Sequence						
	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 227..2311						
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30	GTGAGGGGCG	TGTTGGCCCC	GCACAGATTG	AGCCGAGTTG	TGCCCCGCT	GGGAGAAGTG	60
	ACCCCTCTGC	GCCTGATCAG	AACACTGAGG	CTCAGAGAAG	TTAACTACTC	CAAAAGTCTA	120
	TAGCCAGTAT	TTTCTGGAGC	TGTAATTCAA	ATCAGATGTG	TTCAATACTT	TCTACTACCC	180
	CATTGCTGTC	TTTATGAAAA	GAAATTTTCT	TTCAATATAG	GTGACTATGC	AGCCTGCAAT	240
	TCAAGTATGG	TTTGAGGAAG	ATCTGCCCTC	AAGTCTCTCG	AGTCTCTGTA	CTCCAGACCA	300
35	CGGACCAAGG	TTGGCTAATG	TTTGTGAGTA	CGATGAGTGG	ATAGCTGTGA	GGCATGAAGC	360
	CACTTTGTGG	CCCATGCAAG	AAGATCTGTC	AATCTGGTTA	TCTGGTTTAT	TAGGTATTAA	420
	AGTTAAGGCA	GAAAAATTAT	TGGAAAGACT	TGATAATGGA	GTACTATTAT	GTCAACTGAT	480
	TGATGTTCTT	CAAAACATGG	TGAAAACATG	CAACTCTGAA	GAATCAGGGA	ATTTTCCAAT	540
	GAGAAAAAGT	CCCTGTAAAG	AAGATGCTGC	ATCAGGTTCA	TTCTTTGCTC	GGGACAATAC	600
40	CGCAAACTTC	CTTCACTGGT	GTAGGGACAT	TGGGGTTGAT	GAAACTTACC	TCTTTGAATC	660
	TGAAGGTTTA	GTTTTGACCA	AAGATCCAAG	ACAGGTGTAT	CTTTGTCTTC	TTGAAATTGG	720
	TGCAATTGTG	TCAAGATACG	GGGTTGAGCC	ACCAGTGTTA	GTAAAACTTG	AGAAAGAAAT	780
	TGAGTTAGAA	GAGACTTTGC	TTAATACTTC	TGGGCTGAA	GATTCATCA	GCATTCAAA	840
	ATCATGCTGT	CGGCATGAAG	AGCTACATGA	AGCTGTTAAA	CATATTGCTG	AGGACCTTCC	900
45	TTGTAGTTGT	TCTCATCGAT	TTTCTATTGA	GTATTATATC	GAAGGACGGT	ACCGACTAGG	960
	GGATAAATA	CTCTTTATAA	GAATGCTTCA	TGAAAAACAT	GTGATGGTTC	CGGTTGGTGG	1020
	AGGCTGGGAT	ACTCTTCAAG	GATTTTGTCT	TAAATATGAC	CCCTGTGCAA	TATTACAGTT	1080
	TGCCACATTA	GAACAAAAAA	TTTTAGCATT	TCAAAAAGGA	GTITCTAATG	AAAGTGATCC	1140
	TGATTTCGCT	GCCAGAACAC	CTCAGCTTCC	TGAAATGAAT	CCTTTGTGAG	CAGTTAACT	1200
50	GTTCAGAAAA	CAAAATTCAA	AACCCAGCGT	GCCAGTTAGT	ATTCCAAAAA	GCAAGAAAAA	1260
	ACAGGGAGCT	CCACAGGCTG	CATTGGTGCC	AGCATCTTCA	CTGAAAGGAG	GTAACTGGG	1320
	CTCTATTTGT	GTCCGTTCTA	AATTGCCAAA	TTCTCCAGCA	GCATCTTCTC	ATCCCAAGCT	1380
	CAAGTCTTCA	AAAGGCATAA	CGAAGAAACC	GCAGGCTCTC	TCAAACAATG	CATCATCTTC	1440
	ACTTGTCTCA	TTAAATCCAG	TAGGTAAAAA	CACCTTCTCA	CCAGCTTTAC	CAAGAACTGC	1500
55	ACCTTGTATG	TCTGAGTCAC	CGAGAAAAATG	TATTTTATCC	CCCAATACCC	CCAGGGCCAA	1560
	GGTTATTCCA	GCCAGAAATT	CAGCAGATCT	GCCCGAGTCC	ACACTTTTGC	CAATAAAGTG	1620
	TTCAGGAAAA	ACTCAACCTA	AGTATTGAAA	ACATAATCAT	ATTTCTTCCA	GAGATAATGC	1680
	AGTATCTCAC	TTAGCTGCAC	ATTCAAATTC	ATCCTCAAAA	TGTCCCAAGC	TGCCTAAAGC	1740
	AAATATACCT	GTAAGACCTA	AACCTTCTTT	CCAGTCTCTT	GCAAAAATGA	CAAAAACCAAG	1800
60	TTCCAAAACC	ATAGCCACGG	GTCTAGGAAC	ACAGTCTCAA	CCATCCGATG	GAGCCCCACA	1860
	AGCAAGGCCA	GTCCAGCAGC	AGAACTTAA	ATCGGCTTGT	AATTTAAATC	AGCCAGTTTC	1920
	TGTGTCTTCA	GTTCCTCTGT	TAAAAGCCAC	ACAGAAATCA	AAAGATAAGA	ATATAGTTTC	1980
	AGCTACCAAA	AAGCAGCCTC	AGAATAAAAG	TGCATTTCAG	AAGACAGSAC	CCAGCTCCTT	2040
	GAAGTCTCCT	GGCCGTACCC	CACGTGCCAT	CGTGAGCCTA	CCCCAGTCTT	CTACCAAAAC	2100
65	ACAAACTGCA	CCGAAGTCAG	CACAGACTGT	CGCTAAGAGC	CAGCATTTCA	CTAAAGGGCC	2160
	TCCAGAAAGT	GGCAAAACCC	CAGCTTCAAT	CAGGAAACCA	CCCTCATCTG	TAAAGGATGC	2220
	AGATAGTGGG	GATAAAAAAC	CTACTGCAAA	GAAAAAGGAA	GATGATGACC	ATTATTTTGT	2280
	CATGACTGGA	AGTAAGAAAC	CTAGAAAAATA	AATACATACT	CATTATAAAA	AAAGAGAAAA	2340
	GGAGAATAGA	ATGTGTTAGC	TTACATCTTT	AAAAGTTTCT	CCTATTTTGT	TCTGTCTAAA	2400
70	TAGGTGCAGA	CACATAAGGAT	AGTGAGGATG	GAGGCTGGGA	TGAGGAAAGG	GTTTATCAGA	2460
	ATTCACATAT	CTGAATTAC	TGGAAAGAGC	CCTTCTGAAG	CAACAGTTTG	TAAATCACT	2520
	GCAAGGTTTT	TATTAATAAT	AGACATGTAT	ATGATTTTCA	GTCTATAGCA	TCTTTGTTAA	2580
	CATCTGCCCT	TTGCAGGAAA	TGTAAGAGTT	ATTTAACACT	ACAAGAAATT	TAACAATAGT	2640
	TGCTCTATT	TTGAATATGT	ATTAATAATG	GAGTTTCAAT	ACCTGTCTAT	ATCAACGGTG	2700
75	GTGCTCTTAC	TATTAGTTAA	TTGCATTTTG	GTAAAAAATA	AAAAAGCAAC	AGTTTGGCAC	2760
	TTGTCTTACA	AAAGGCACCT	AATTTAATTT	TCTGATCAGG	ATTGCTGTAT	CCAACAGTGC	2820
	TAAGTCATGG	CTGCTGCTGA	CTAGCTTGGC	ATTATTTCTG	GTTAGGTAGA	ATTCTTATTA	2880
	TTTATTTTTT	TAAGCTTTTC	AAATTGGAAG	GAACGTATTG	TTTATGTGGG	CTTATATTTA	2940
	CATTGGTAAT	ATTTTGTGAC	CAATATTTTT	GGTTAAAAAA	AATCCAACAA	ATTAACCTAC	3000
80	TGAAATATAA	ACAAATTTTG	TAAACAATTT	TTTATATTAT	CTATAAAAC	GTAGACACCT	3060
	TATGTTTTCAC	ATGTTGTGCA	ATGTGACAGG	GGAAGCTGAT	TTAGTAGCTT	TAGCATATT	3120
	AAAAATAATT	TTTTATAATG	TAATTTCCCTG	TGAGTGCAGA	CCTGACATTT	TACATTAATA	3180
	TAAATGTAAA	CATCAGAATT	ATGTTTAAAC	AACTTTAAAA	TAAAGATGAT	GTTAAAAATA	3240
	TTTATAGATT	ATGCTATGGA	AAAATTTCTAT	CATGAAATTA	TTTTTCTCTA	GATAGCACAA	3300
	TACCAATTTT	AATTAATTTT	TTCCAATTAG	GTTACTTTTC	TTAATAAAG	TTATGCTGCC	3360

	TTCAAGTTTTC	CAATGGCAAG	TAGACAGGAT	ATGTTCAAGG	TTTTCTGCAC	TGTAGGCACA	3420
	GTCTCTCAAG	CATATCTCTGA	TCATGTAATG	ACTGCATAAA	CTCCATCAAC	CTAAGGTGAT	3480
	ACCTGTAAAT	AATTTATTTT	TAAAGGATGG	TGACTTTAAA	AATTATTAAT	GAACCTTGAG	3540
	AAGTTTAAAG	AGTGGCTTTA	AAACTTCACA	GTATTGCCAA	TTATCTTAGG	TTATTCAGTA	3600
5	TTCAAGTTTG	TGTTTCTCTG	TTTTAAACTA	AAATGTGTTT	TCTGAAGAAA	AAAATAATAG	3660
	TTTACACAAA	TGTACAATCA	TAGAATAAGC	ATTTTAAGCT	GGCGACTAGT	GTTCTATAGA	3720
	TTACAAAGCA	AGAAAACCTT	CTATGAAGAT	AAATGACCTT	TTGCCTGAAG	AGTACAGATA	3780
	AAATCAAAGA	TGTGTGCAAG	CTAGTTTTTG	GAAGAAGTGA	TGCTTCTCTT	CTTTAAAGAG	3840
	ACAGTCACCA	AATACTTGTT	TTAACTCGAC	TATTGACTTG	GGCATTGAGA	GAGATGATAT	3900
10	ATACATCTTT	GGAAAGTGAA	GTCAATGTTT	AAGAGGTGAT	AGAAGCTTTA	CTTTTATAGT	3960
	ATCAGAAATA	TTTAGTGCAT	CTTTTCAGAC	AGGAAGAATT	TTATCATCAA	GTATTCCTTT	4020
	ATAAAACCAA	GTAAACACTT	TTTATCAGTA	ACTTTTAGAA	CTTAAAGAAA	AGCAAAAAGT	4080
	AAATGGAATT	GTAGGCAATT	TATGAATCCT	AGTAGATTTT	ACAATATGTA	ATTTATGTTG	4140
	TTTACAGTAT	ATAAACACTA	AGTTTGTGTT	TAAATGTGAT	CAGGAATAAA	AGTATCCCAC	4200
15	AGGCATCTGA	CACAAATTC	AGAATTAGCC	AAAGAATTGT	TTATTTGAGG	CCAGGCAATC	4260
	CCAGCATTTT	GGGAAGCCAA	GTGGGCGAGA	TCACGAAGTC	AGGAGTTTGA	AATCAGCCTG	4320
	ACCAACATGG	TGAAACCTCT	TCTCTACTAA	AAATACAAAA	TTAGCCGGGC	ATGGTGGCAC	4380
	ATGCCATATA	TCTCAGCTAC	TCAGGAGGCT	GAGGCAGGAG	GATCGCTTGA	ACCCGGGAGG	4440
	CAGAGGTGTC	AGTGAGCCAA	GATTGCGCCA	CTGCACTCCA	GCCTGGGCAA	CAGAGTGAGA	4500
20	CTCTGTCTCA	AAAAAAGAAA	AAAAAAGAAA	AAAAAAGAAA	AGGTTTATTT	GAATAATTGG	4560
	AAGTCAGTTT	ATACATTACT	ATTTTTCAGC	AGTAGGGAAT	TTCTCCAATT	ACATTTCATG	4620
	TGAATGAATT	TTTATTTATA	TATAGCTTAC	CCTTCCAAAA	TAAAGTGTGT	TTTTTAATGT	4680
	TGTTTTGTGT	TGTTTTGTGT	TTTTCTTTT	TTGAGACGGA	GTTTCACTCT	TGTTGCCAG	4740
	ACTGGAGTGC	AGTGGCACA	TCTCAGCTCA	TTGCAACCTC	TGCTTCTGG	GTTCAAGTGA	4800
25	TTCTGCTGCC	TCAGCTCCT	GAGTGGTTGG	GATTACAGGC	ATCCACCACC	AGGCCAGCT	4860
	AATTTTTTTT	TATTTTCAGT	AGAGATGGGG	GTTTCACTAT	GTGCGCCAGG	CTGATCTCAA	4920
	ACTCCTGACC	TCAGGTGATC	CACCTGCCTC	AGCCTCCCAA	AGCGCTGGGA	TTACAGGCAT	4980
	GAGCCATCAC	ACCCAGCGAA	AAGTTTGTGT	TGAATAAACA	ATATCCGAAA	GACAATTAGT	5040
	TTCTTCAGAT	GTATTTTGAA	ATTCTCCTAA	AGAGCTAGTG	TTTCTATTCA	TTTTCACAAT	5100
30	TTAAAAACAG	CTCTTAACAT	TGCTGAAGTT	GGGAGAAGCT	TCCATCTCTT	CTTAATAACA	5160
	GTGCAAGATT	TTGTAATTC	TTTTTTGTGT	TTAATGTTTA	ATAAAACGAG	TATTAAGCTT	5220
	AAATTACTGA	AGTACCTGGG	AGAAAGTAATG	ATGTGTAATT	TCAAAAAAAT	GGAAAAATGCT	5280
	TTTATTTTAT	TTTCTATAAT	TTGTTAACAT	GATATGTAAA	ATTAAGCTTC	GGAGCACAAT	5340
	GAAATGCCGA	TTATTTTAC	CTTGTTTGGG	CTTAAAGTAG	GTATTTAAGG	TTTATGTGTT	5400
35	CAAAATGCCCT	TGGTAAATTG	GATGACCTCT	AACCTTACTG	TCCATATGGA	GTTTGTCAAT	5460
	CTTTATGATG	AAGAGAACTT	AAGGAAAAAT	TACTGTTTTT	CTTCAGTCTT	TTTATATCTA	5520
	TCTGATTTAA	AATCTGTTAC	TTTATTAAAA	GGCTTCAACA	ACAGGTTGTT	AGGATGTAGT	5580
	CTTACATCCA	GGTTACATA	ATAACCCCAT	TTGAATCCAA	ATTGTGTAT	ATTTTCTTAT	5640
40	GCCAGCAGTA	TTGTATCCA	ATTTTAACTT	AGGTTTGTGT	TCTTGAG		5687

Seq ID NO: 60 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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45							
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	AAACAAAGT	TAAATTTTAT	ACATCATAGA	ATTACTATTT	AGAAACAAAT	AGGACATGTT	120
	AGAAAGTAAG	AAAAATAAAA	CACTTTGTG	AAGTTATATA	CCTATTGGGA	TTTTTTTAAA	180
	AGCATTACCC	AATAGGCTAT	AGAACGATGC	CAACACATAA	TGCCAGGTTG	CAAGGCATGG	240
	AGAATGGGAG	AATGTGACAT	GACTGTCTAA	TGGGTATAAA	GCTCCCTTTT	GAAGTGAAAA	300
50	AATTACTTTG	GATCTAGATA	GTAGTGGTAC	TGGCAAAATG	GCTAAACGCC	AATGAATAAT	360
	GCACATTAAA	TGGTTTAATT	GTATAATTTT	GTGGTGTAAG	ATTCCTATAT	CAATTATTCT	420
	TTAAATAAAC	AAGTGCTGCA	CCAGATTGGA	CCAAGAGACC	ATAGTTTGTG	AGCCCTTGTT	480
	TTATGCTACA	AATTTAATTC	CCATATGCTT	GAAATAGTAA	ATGCTGTGAT	TTAATTCATT	540
	TACATTAGAA	ACATGGGATG	TTTTGAAACT	ATAATATGTT	ATGCAATTAT	ATGAACACTA	600
55	AAATTATTAC	TGTGGAATTT	TTTTATTGTT	AGTAACGGGA	GTATGCAATT	TTATTTTGCT	660
	GTACACA						667

Seq ID NO: 61 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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60							
	GACCTAAGAA	CTTATCAAG	AACTCAGCAG	TATGAGAATA	GATCAATACA	TAGAGGGTTT	60
	CCTTTAAGTC	TTGTAGAAAC	TCATTACTCT	CCAGTCTCTT	TTTCCACTTA	TAGTAGAGAG	120
	AATCAGACTT	CGCGATATCC	AGTTAACTAT	CAATACCTTT	AAAAAATGTG	AACAAGCAGT	180
65	CCATCTGAAT	AATTATACCA	AATGTCAAGG	CTTTTAAAG	TGCTTAACTT	TAAAGTCTCT	240
	TTGCAGTTGT	TCAGACCTAG	ATTCTCAGTT	CAGTTAGCAC	AGAGAGAGAC	AAGGAAAAAA	300
	TGAGGAACAC	TTTTCTCAG	CATAAATATT	CACTGGTTTT	TGAATACTA	TTGATTCTCT	360
	GGATAAGAAA	ATAGGTCAAC	TTTATAGCTT	TTTGTCTCGA	AATTGATTTG	CCGCCACAGA	420
	CAGTGGCTTG	GTGCTATATA	TCCAGCCTA	CATGGGAGGC	TGAGSTGGGA	GATCGCTTGA	480
70	GCCCAAAAAG	TCAGAGGTGC	AGTGAGCTGT	GATTGTGCCA	CTGTATCCCA	ACCTCAT	537

Seq ID NO: 62 DNA Sequence

Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
75							
	TTTTTTTTT	TTTTAATTTT	AATAAGTTAA	ATTTTAAATA	ATTGATTTAT	TTTACTCCA	60
	AAGGATACAA	CATGCAAAAT	GTCTACCCAC	TCCAGCTACC	ATCAGTTTCA	CATTTATAAC	120
	TACTATCAAT	AATGTTTTCA	TGTAAGACAG	CCATCACCTA	AAGGAATACT	TTTAAACAG	180
	GTTGTACAAT	AAAACAGGTT	GGACCAATAT	AAAAGAAATA	TAAATAAAGG	TGTTTTATTT	240
80	AAATGTAAT	ACACAGATAC	TTCCATTAAA	TCTAAACAAA	CTTTAAAAAG	AGGAGCAAAAT	300
	AATGAGTAAT	GCCATAGAAC	ATTAGAAGAA	CACAGTTAAC	GAATGGAAAC	TTGTAAACAG	360
	ATACACACAC	ACGCATGCAT	ATATATATGT	ATCATATATA	TCACTAAAAA	GACATTTTCT	420
	TAGAGCATAT	TGAATTGTGA	ATAATTATTT	GAAAGTACAT	GTGGTGGGAC	ATAAATCAAG	480
	ACTCAGTAAA	TTTGAAAAGA	TTCAATATCA	TAAAGAATAT	ATGATCCAGC	CTTAGTAGAA	540

GTAAGGGAAA TTTAAAAAAT GTAACATAAA TATCTTTAAT TTTGGAAATT AAGAAAATAC 600
 ACTTCAAAAA AATTTAAAGT CTTGCTCAG CTTCCCCAGT AGCTGGGATT ACAAGCATGC 660
 ACCACCATGT CCAAGCAATT TTGTAATTAT AGTAGAGACA GG 702

5

Seq ID NO: 63 DNA Sequence

Nucleic Acid Accession #: AK025967

	1	11	21	31	41	51	
10	ACAACAGGAA	CACATATAGC	TGGAATGCAG	ATGGGATCTG	TGCTACTTAC	GCTAGCCATG	60
	GGATGATTAG	AACAAGATAA	GAGACATGAG	GAAGACTTCT	TCAAGGAGGT	GCTCAAGCCA	120
	TGTTTTGGAA	AAGAGAACTC	AAGGTCTGGC	AGGGAGAAAG	GAGCAAGGTC	CTCTTCTCCC	180
	TGAAGGCTGT	CACAGTTCTT	GTGCAGAGAG	AGAGGGCACT	GCAGCACCCA	GGCGCTGACT	240
	GCCTTTTGT	AGTCTCATTT	GCAGGCCCCC	AGCTGGAGAA	CCCAGGAGGA	AGAGGAAAAA	300
15	AGTTTTTTCC	TCCTCTACAC	TCCCATGCA	TGACTAAAGA	GTAGGAGGAG	TCAGCAAGGC	360
	AGACATATAT	AGTACCCAGG	AGGTGGACAA	ACAACCTGCT	TGGTGGAAAC	TCTGTCTTTT	420
	CTGGACTTAT	CCTGGTGGCA	CTGAGACTGT	GCAGATTTAG	ATCTACAATC	CACCTGGAAT	480
	TGATTTTTGT	ATATGGAGTG	AGGTCCCAAC	CTTACAGGGA	AAGCATCACC	CGAAAGTGAG	540
	AATGCCTAGA	GGCAGGAATC	ATGGAGGCTT	CCTTAAACCG	CTGTCTGCAA	CAGCAGGTGC	600
20	TAGAGATGAC	ACTGCAGAGT	AGAGAACAAA	GGAATCTTAG	TAATTGTTC	ATCCAAATCTC	660
	CACACTTTAA	AGATGAAGAA	ACTGGTATTG	AGAAAAATAC	ACAGCTTATC	CAAGGTTGCA	720
	CTGCTGGTGT	GTAGCTGAGA	TGAATTTAGA	ACCCACATCT	GATGACTACA	CCATATTGCT	780
	CCCAGTTTTT	CTGTCTGTTT	CACATGTAAT	AGTCTGACTC	TTCACTTCTC	CTTTGAGTAT	840
	ATAGACTTTT	AACATTTTGT	TATGTCAAGA	TGGACTTTTC	CTCATAACCA	GGCCCTCGCT	900
25	TTTCTCTCTC	CTTCATACCT	TGCAGGATCT	TTAACAAGAT	TTAAAAGGAG	TTTTTTTGT	960
	TGTTTTGATG	TATCTAATAA	AAGTCAAGGG	AGGGAGAGGG	CCAGTATAAG	CAAGAGTACA	1020
	GTTTCTAGT	TGTAGATGTC	GCTAGTCTGA	GGAATCAGAA	ACACACAAAG	GTTTGGAGAA	1080
	CTGGTACATG	CTCCAGGTG	GGAAGCCAGG	ACTCTTGGTA	GGATCTTGAG	GACAAGGCCA	1140
	AGGACAATAA	GAGAGCGAGG	GGATCCTAGA	GGTGGAAATCA	AGGAAGAGAA	ACTAGAGAGA	1200
30	GAAAAAGGAA	CTGGCTATCC	ATCCATGATG	GATCCTGTGT	GGACTGATGG	GTGGCTTGGC	1260
	ATCATCTCTT	AGTAGACTTC	ATGTGGTTGA	ATAATTGGCC	AATGGAAGGA	ATTTCITTTT	1320
	TGGTAACAGA	CTCTGTGTGT	ACAGTTATGG	GTCTTAATTT	ATAATAAAG	GTTACATTGA	1380
	AAATTGAAAA	AAAAAAA					1398

35

Seq ID NO: 64 DNA Sequence

Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
40	GGCAGGAGGA	GAGAAACTCC	ATCTCAAAAA	CAAAACAACA	CAAAACAACA	AAAGAGAGAG	60
	AATCAAAAGT	TGTTCCCTGT	CTCTCTCTCT	CCACATGTGA	GCACACAAAG	AGGTCAAGTG	120
	AACACACAAT	GAGAAGGAGG	CTGCCCTGCA	GTTAAGAGAA	GAGGCCCTCAG	CATGAAACCT	180
	GCCTTACTGG	CACCTTGGTC	TTGAACCTCC	CAGCCTCTAA	AACCTGTGAG	AATAAGTTTC	240
	TGTTGTTTCA	GCCACCCAGT	CTATGGTATT	CTGTATGGCA	GCCAGAAATTA	AGACACCAGT	300
	GAAGCAAGAT	AATCAGTAAC	TGGATACTTA	ACTGTGTGGT	ATAAAACATA	GGGGCTTTAG	360
45	TAGAGAAGAA	AATTGGACTT	TGTTGGGGAC	ATCCTTACTA	CTTCTGCTCA	TGTATCATGC	420
	TTTAGCTTGT	TTCTGTCTTT	GGAGGAGGCT	GCAATTTTTT	AAAATACCCC	CAAAAGTACA	480
	AAGACTAATG	TTATAGCCCC	TGTGTTCTCA	TTATCCAGGC	TTAATAAATG	TTGGCCATTT	540
	TCCACTTTTG	TTTCATATAT	AAGTTTCTAC	AAAATGACAA	CACCTTAGAT	AAAGCTGAAG	600
	TTCATGTTTC	ATTCTGCATC	CCTTCCCCCA	AGGGCTTCTT	TTGCTCAATA	TGGGACTCAT	660
50	GAGAGTCATC	GGTGTGTGTG	GAGGCAGCTG	TTTGTGTATT	TTCTGGACCA	AATAATGTTT	720
	CACCGTGTGA	CTGGACATAC	CTTAGTCTAT	CCATTCTACC	ACTGATGAGC	ATGTAAGCTG	780
	TTACTATTTT	TAACATTAAC	AAATATCTTT	GCTAACACAT	TTTTGTGCAT	GTCTTTTGGT	840
	GACCAAAATG	ACTCATTTCT	CTCAGGTATG	TATCTCAGAG	TGAAACTGTT	TTATCAGAGT	900
	GTATGCTTTA	TATTTAGTGC	TTTCCAATTC	CTGATTAAGA	AATCTTTGCC	TGCTCCTAAG	960
55	GATGTAAAG	TATTTCTTTA	TGGCCTGGCT	CAGTGGCTCA	TGCTGTAAAT	CCAGCAATT	1020
	TGGGAGGCCA	AGGTGGGAGG	ATTGCTTGAG	GCCAGGAGTT	CAAGACCAGC	CTGGGCAACA	1080
	TACTGAGACC	CTCATCTCTA	CAAAAAAATA	AAATTTGTTT	AATTAGCTGA	GCTTGGTGGT	1140
	ATGCACCTAT	AGTCTAGCTC	ACTCAGGAGG	CTGAGGCAGG	AGGATCGCTT	GAGCCACGGA	1200
	ATTGAGAGAT	GCAGTAAGCT	ATGATCATGC	CAGTGTATTA	CAGCCTGGGT	GATAGGGTGA	1260
60	GACCCGTGCT	CTAAAGAGAT	ACATCTATTA	AAAATAATAT	TATTTTATTT	TATTTTATTT	1320
	TATTTTATTA	TTATACTTTA	AGTTTATGGG	TACATGTGCA	CATTTGTGAG	GTTAGTTACA	1380
	TATGTATACA	TGTGCCATGC	TGGTGCATCG	CACCCACTAA	CTCGTCATCT	AGCATTAGGT	1440
	ATATCTCCCA	GTGCTATCCC	TCCCCCTCCC	CCCGACCCCA	CAACAGTCCC	CAGAGTGTGA	1500
65	TGTTCCCTTT	CCTGTGTCCA	TGTGATCTCA	TTGTTCAATT	CCCACCTATG	AGTGAGAATA	1560
	TGCGGTGTTT	GGTTTTTTGT	TCTTGCAGTA	GTTTACTGAG	AATGATGATT	TCCAATTACA	1620
	TCCATGTCCC	TACAAAGGAC	ATGAACCTAT	CATTTTTTAT	GGCTGCATAG	TAAAAATACA	1680
	TTTTAAAAAA	TAATAAATTA	TTCTCTTATG	TTATTGTCTA	GAATCTTCAT	TATTTTACCT	1740
	TTTCAATTTA	GATCTACAAT	CCACCTGGAA	TTGATTTTTG	TATATGGAGT	GAGGTCCAC	1800
	ACTTACAGGG	AAAGCATCAT	CCGAAAGTGA	GAATGCCTAG	AGGCAGGAAT	CATGGAGGCT	1860
70	TCCTTAACCG	TCTGTCTGCA	ACAGCAGGTG	CTAGAGATGA	CATGTCAGAG	TAGAGAACAA	1920
	AGGAATCTTA	GTAATTTGTT	AATCCAATCT	CCACACTTTA	AAGATGAAGA	AACGTGTATT	1980
	GAGAAAAATA	CACAGCTTAT	CCAAGGTTGC	ACTGCTGGTT	GGTAGCTGAG	ATGAATTTAG	2040
	AACCCACATC	TGATGACTAC	ACCATATTGC	TCCAGTTT	CCTGTCTGTT	CCACATGTAA	2100
	AAGTCTGACT	CTTCATCTCT	CCTTTAGTGA	TATAGACTTT	TAACATTTT	GTATGTCAAG	2160
75	ATGGACTTTT	CCTCATACCC	AGCCCCTGCC	TTTTCTCTCT	CCTTCATACC	TTGAGGATC	2220
	TTTAAACAGAA	TTTAAAGGGA	GTTTTTGT	TTGTTTTGAT	GTATCTAATA	AAAGTCAAGG	2280
	GAGGGAGAGG	GCCAGTATAA	GCAAGAGTAC	AGTTTCTTAG	TTTGTAGATG	CGGTAGTCTG	2340
	AGGAATCTTA	AACACACAAA	GGTTTGGAGA	ACTGGTACAT	GCTCCAGGT	GGGAAGCCAG	2400
	GACTCTTGGT	AGGATCTTGA	GGACAAGGCA	AAGGACAAAT	AGAGAGCGAG	GGGATCCTAG	2460
80	AGGTGGAATC	AAGGAAGAGA	AACATAGAGAG	AGAAAAAGGA	ACTGGCTATC	CATCCATGAT	2520
	GGATCCTGTG	TGGACTGATG	GGTGGCTTGG	CATCATCCTT	TAGTAGACTT	CATGTGGTTG	2580
	AATAATTTGC	CAATGGAAGG	AATTTCTTTT	TTGGTAACAG	ACTCTGTGTG	TACAGTTATG	2640
	GGTCTTAATT	TATAATAAAA	GGTTACATTG	AAAAATTGAA	AAAAAAAATA	AAAAAAAATA	2700
	GCATTATAAG	TGTACTTCTA	GCCTTACTTC	GTCCGGGTAA	TTGATCTCTG	CTCTGTCTGG	2760
	CTG						2763

Seq ID NO: 65 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1863

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	CCCAATGCCG	TGGGCCCCGAA	GGAGGTGGAG	CTCATCCTTG	TCAAGGAGCA	GAACGGAGTG	120
10	CAGCTCACCA	GCTCCACCCT	CACCAACCCT	CGGCAGAGCC	CCGTGGAGGC	CCAGGATCGG	180
	GAGACCTGGG	GCAAGAAGAT	CGACTTTCTC	CTGTCCTGCA	TTGGCTTTGC	TGTGGACCTG	240
	GCCAACTGCT	GGCGGTTCCC	CTACCTGTGC	TACAAAAATG	GTGGCGGTGC	CTTCTGGTTC	300
	CCCTACCTGC	TCTTCTGGT	CATTGCTGGG	ATGCCACTTT	TCTACATGGA	GCTGGCCCTC	360
	GGCCAGTTCA	ACAGGGAAGG	GGCCGCTGGT	GTCTGGAAGA	TCTGCCCAT	ACTGAAAGGT	420
15	GTGGGCTTCA	CGGTATCCT	CATCTCACTG	TATGTGCGCT	TCTTCTACAA	CGTCATCATC	480
	GCCTGGGCGC	TGCATATCT	CTTCTCTCTC	TTACCCAGG	AGCTCCCTG	GATCCACTGC	540
	AACAACTCCT	GGAAACAGCC	CAACTGTCTG	GATGCCATC	CTGGTGACTC	CAGTGGAGAC	600
	AGCTCGGGCC	TCAACGACAC	TTTGGGACC	ACACCTGCTG	CCGAGTACTT	TGAACGTGGC	660
	GTGCTGCACC	TCCACCAGAG	CCATGGCATC	GACGACCTGG	GGCCTCCGCG	GTGGCAGCTC	720
	ACAGCCTGCC	TGGTGTGGT	CATCGTCTG	CTCTACTTCA	GCCTCTGGAA	GGGCGTGAAG	780
20	ACCTCAGGGA	AGGTGGTATG	GATCAGAGCC	ACCATGCCAT	ACGTGGTCTT	CACTGCCCTG	840
	CTCCTGCGTG	GGGTCACTCT	CCCTGGAGCC	ATAGACGGCA	TCAGAGCATA	CCTGAGCGTT	900
	GACTTCTACT	GGCTCTGCGA	GGCGTCTGTT	TGGATTGACG	CGGCCACCCA	GGTGTGCTTC	960
	TCCCTGGGCG	TGGGTTCTGG	GGTGTCTGATC	GCCTTCTCCA	GCTCAACAA	GTTCAACAA	1020
25	AACTGTCTAC	GGGAGCGGAT	TGTCAACACC	TCCATCAACT	CCCTGACGAG	CTTCTCTCTC	1080
	GGCTTCTGTC	TCTTCTCTCT	CCTGGGGTAC	ATGGCAGAGA	AGCACAGTGT	GCCCATCGGG	1140
	GACGTGGGCA	AGGACGGGCC	AGGGCTGATC	TTTATCATCT	ACCCGGAAGC	CATCGCCATC	1200
	CTCCCTCTGT	CCTCAGCGTG	GGCCGTGGTC	TTCTTATCA	TGCTGTCTAC	CCTGGGTATC	1260
	GACAGCGCCA	TGGTGGTAT	GGAGTCAGTG	ATCACCGGGC	TCATCGATGA	GTTCCAGCTG	1320
30	CTGCACAGAC	ACCGTGAGCT	CTTCACGCTC	TTTATCGTCC	TGGCGACCTT	CCTCTGTCTC	1380
	CTGTTCTGCG	TCACCAACGG	TGGCATCTAC	GTCTTACGCG	TCCTGGACCA	TTTTGCAGCC	1440
	GGCAGCTCCA	TCTCTTTTGG	AGTGCTCATC	GAAGCCATCG	GAGTGGCCTG	GTTCTATGGT	1500
	GTTGGGCAGT	TCAGGAGCGA	CATCCAGCAG	ATGACCGGGC	AGCGGCCAG	CCTGTACTGG	1560
	CGGCTGTGCT	GGAAGCTGGT	CAGCCCTGCT	TTTCTCTGT	TCGTGTCTGT	GGTCAGCATT	1620
35	GTGACCTTCA	GACCCGCCCA	CTACGGAGCC	TACATCTTCC	CCGACTGGGC	CAACGCGCTG	1680
	GGCTGGGTCA	TCGCCACATC	CTCCATGGCC	ATGGTGCCCA	TCTATGCGGC	CTACAAGTTC	1740
	TGCAGCCTGC	CTGGGTCTCT	TCGAGAGAAA	CTGGCCTACG	CCATTGCACC	CGAGAAGGAC	1800
	CGTGAGCTGG	TGGACAGAGG	GGAGGTGGCG	CAGTTCACGC	TCGCGCACTG	GCTCAAGGTG	1860
	TAG						1863

Seq ID NO: 66 DNA Sequence
Nucleic Acid Accession #: NM_022073.1
Coding sequence: 327..1046

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	GAGTCTGGCC	GCAGTCGCGG	CAGTGGTGGC	TTCCCATCCC	CAAAAGGCGC	CCTCCGACTC	60
	CTTGGCGCGC	ACTGTGCGCC	GGGCCAGTCC	GGAAACGGGT	CGTGGAGCTC	CGCACCACTC	120
	CGCGTGGTTC	CCGAAGGCAG	ATCCCTTCTC	CCGAGAGTTG	CGAGAAACTT	TCCCTTGTCC	180
	CCGACGCTGC	AGCGGCTCGG	GTACCGTGGC	AGCCGCAAGT	TTCTGAACCC	CGGCGCACGC	240
	TCGCCGCGCC	TCGGCTTCCG	GCTCGTGTAG	ATCGTTCCCT	CTCTGGTTGC	ACGCTGGGGA	300
50	TCGCCGACCT	CGATTCTGCG	GGCGAGATGC	CCCTGGGACA	CATCATGAGG	CTGGACCTGG	360
	AGAAAATGCG	CCTGGAGTAC	ATCGTGCCCT	GTCTGCACGA	GGTGGGCTTC	TGCTACCTGG	420
	ACAACTTCTC	GGCGAGGTG	GTGGGCGACT	GCGTCTGGGA	GCGGCTCAAG	CAGCTGCACT	480
	GCACCGGGGC	CCTGCGGGAC	GGCCAGCTGG	CGGGGCGCGG	CGCCGCGCTC	TCCAAGCGAC	540
55	ACCTGCGGGG	CGACAGATGC	ACGTGGATCG	GGGGCAACGA	GGAGGGCTGC	GAGGCCATCA	600
	GCTTCTCTCT	GTCCCTCATC	GACAGGCTGG	TCCTCTACTG	CGGGAGCCCG	CTGGGCAAA	660
	ACTACGTCAA	GGAGAGGTCT	AAGGCAATGG	TGGCTTGCTA	TCCGGGAAAT	GGAACAGGTT	720
	ATGTTGCGCA	CGTGGACAA	CCCAACGGTG	ATGGTCTGCT	CATCACCTGC	ATCTACTATC	780
	TGAACAAGAA	TGGGATGCC	AAGCTACATG	GTGGGATCCT	GCGGATATTT	CCAGAGGGGA	840
60	AATCATTAT	AGCAGATGTG	GAGCCCATTT	TTGACAGACT	CCTGTTCTTC	TGGTCAGATC	900
	GTAGGAACCC	ACACGAAGTG	CAGCCCTCTT	ACGCAACCCG	ATATGCTATG	ACTGTCTGGT	960
	ACTTTGATGC	TGAAGAAAGG	GCAGAAGCCA	AAAAGAAATT	CAGGAATTTA	ACTAGGAAAA	1020
	CTGAATCTGC	CCTCACTGAA	GACTGACCGT	GCTCTGAAAT	CTGCTGGCCT	TGTTCAATTT	1080
	AGTAACGGTT	CCTGAATTTCT	CTTAAATTTCT	TTGAGATCCA	AAGATGGCCT	CTTCAGTGAC	1140
65	AACAATCTCC	CTGCTACTTC	TTGCATCTCT	CACATCCCTG	TCTTGTGTGT	GGTACTTCAT	1200
	GTTTTCTTGC	CAAGACTGTG	TTGATCTTCA	GATACTCTCT	TTGCCAGATG	AAGTTATTTG	1260
	CTAACTCCAG	AAATTTCTGC	AGACATCTTA	CTCGGCCAGC	GGTTTACCTG	ATAGATTCCG	1320
	TAATACTATC	AAGAGAAGAG	CCTAGGAGCA	CAGCGAGGGA	ATGAACCTTA	CTTGCACTTT	1380
	ATGTATACTT	CCTGATTTGA	AAGGAGGAGG	TTTGAAGAAG	AAAAAATGGA	GCTGGTAGAT	1440
70	GCCACAGAGA	GGCATCACGG	AAGCCTTAAC	AGCAGGAAC	AGAGAAATTT	GTGTCATCTG	1500
	AACAATTTCC	AGATGTTCTT	AATCCAGGGC	TGTTGGGGTT	TCTGGAGAA	TATCACAACC	1560
	TAATGACATT	AATACCTCTA	GAAAGGGCTG	CTGTATAGT	GAACAATTTA	TAAGTGTCCC	1620
	ATGGGGCAGA	CACCTCTTTT	TTCCAGTCC	TGCAACCTGG	ATTTTCTGCC	TCAGCTCCAT	1680
	TTTGCTGAAA	ATAATGACTT	TCTGAATAAA	GATGGCAACA	CAATTTTTC	TCCATTTTCA	1740
75	GTTCTTACCT	GGGAACCTAA	TTCCCCAGAA	GCTAAAAAAC	TAGACATTAG	TTGTTTGGT	1800
	TGCTTGTGTA	CAATGGAAAT	TAAATTTAAA	TGAAAGGAAA	AATATATCCC	TGGTAGTTTT	1860
	GTGTTAAACA	CTGATAACTG	TGGAAGAGGC	TAGGTCTACT	GATATACAAT	AAACATGTGT	1920
	GCATCTTGAA	CAATTTGAGA	GGGGAGGTGG	AGTTGGAAAT	GTGGGTGTTT	CTGTTTTTTT	1980
80	TTTTTTTCTT	TTTTTTTTTT	AGTTTTCTCT	TTTAAAGAGC	TCACCCCTTA	ACACAAAAAA	2040
	AGCAGGGTGA	TGTATTTTAA	AAAAGGAAGT	GGAAATAAAA	AAATCTCAAA	GCTATTTGAG	2100
	TTCTGTCTG	TCCCTAGCAG	TCTTTCTTCA	GCTCACTTGG	CTCTCTAGAT	CCAATGTGGT	2160
	TGGCAGTATG	ACCAGAAATCA	TGGAACCTGC	TAGAATCTGT	GAAGCTTCTA	CTCCTGCACT	2220
	AAGCACAGAT	CGCACTGCCT	CAATAACTTG	GTATTGAGCA	CGTATTTTGC	AAAAGTACT	2280
	TTTCTAGTT	TTTCTAGTTA	CTTTTCTGTT	TTAAAAATCC	CTTTAAATTC	TTGCTTGAAG	2340
	ATCCCATGAA	CATTAAAGAG	CCAGAAATAT	TTTCTTTTGT	TATGTACGGA	TATATATATA	2400

5 TATATAGTCT TCCAAGATAG AAGTTTACTT TTTCTCTTTC TGGTTTTGGA AAATTTCCAG 2460
 ATAAGACATG TCACCATTAA TTCTCAACGA CTGCTCTATT TTGTTGTACG GTAATAGTTA 2520
 TCACCTTCTA AATTACTATG TAATTACTCT ACTTATTATG TTTATTGTCT TGTATCCTTT 2580
 CTCTGGAGTG TAAGCACAAT GAAGACAGGA ATTTTGTATA TTTTAAACCA ATGCAACATA 2640
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Seq ID NO: 67 DNA Sequence
 Nucleic Acid Accession #: NM_139314.1
 Coding sequence: 196..1416

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 15 ATAAAAACCG TCCTCGGGCG CGGCGGGGAG AAGCCGAGCT GAGCGGATCC TCACACGACT 60
 GTGATCCGAT TCTTTCCAGC GGCTTCTGCA ACCAAGCGGG TCTTACCCCC GGTCTCTCCG 120
 GTCTCCAGTC CTGCGACCTG GAACCCCAAC GTCCCGGAGA GTCCCGGAAT CCCCGCTCCC 180
 AGGCTACCTA AGAGGATGAG CGGTGCTCCG ACGGCCGGGG CAGCCCTGAT GCTCTGCGCC 240
 GCCACCGCCG TGCTACTGAG CGCTCAGGGC GGACCCGTGC AGTCCAAGTC GCCCGCTTT 300
 20 GCGTCTGGG ACGAGATGAA TGTCTTGGCG CACGGACTCC TGCAGCTCGG CCAGGGGCTG 360
 CGCGAACACG CGGAGCGCAC CCGCAGTCAG CTGAGCGCGC TGGAGCGGGC CTTGAGCGCG 420
 TCGGGTCCG CCTGTGAGG AACCGAGGGG TCCACCGACC TCCCGTTAGC CCTGAGAGC 480
 CGGGTGGACC CTGAGGTCTT TCACAGCCTG CAGACACAAC TCAAGGCTCA GAACAGCAGG 540
 ATCCAGCAAC TCTTCCACAA GGTGGCCGAG CAGCAGCGGC ACCTGGAGAA GCAGCACCTG 600
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 25 GTGCCAAGC CTGCCCCGAG AAGAGGCTG CCGGAGATGG CCCAGCCAGT TGACCCGGCT 720
 CACAATGTCA GCCCGCTGCA CCGGCTGCCG AGGGATTGCC AGGAGCTGTT CCAGGTTGGG 780
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 GACTTCAACC GGCCTGGGA AGCCTACAAG GCGGGGTTTG GGGATCCCCA CGCGAGTTT 960
 30 TGGCTGGGTC TGGAGAAGGT GCATAGCATC ACGGGGAGCC GCAACAGCCG CTTGGCCGTG 1020
 CAGCTGGGGC ACTGGGATGG CAACGCCGAG TTGCTGCAGT TCTCCGTGCA CTTGGGTGGC 1080
 GAGGACACGG CCTATAGCCT GCAGCTCACT GCACCGGTGG CCGGCCAGCT GGGCCGCCAC 1140
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 35 CGCAGGGACA AGAATGCGC CAAGAGCCTC TCTGGAGGCT GGTGGTTTGG CACTGCAGC 1260
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 GCCACGAAA GACGGTGACT CTTGGCTCTG CCGAGGATG TGGCGTTTCC CTGCTGGGC 1500
 40 AAGGCCCCCT TTCTGAGTGC AGGGGGGCTG CATGCGTTGC CTCCTGAGT CGAGGCTGCA 1560
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 CTCAGTCACA TTGACTGACG GGGACAGGG CTTGTGTGGG TCGAGAGCGC CCTCATGGTG 1740
 45 CTGGTCTGT TGTGTGTAGG TCCCTGGG ACACAAGCAG GGGCCAATGG TATCTGGCG 1800
 GAGCTCACAG AGTTCTTGA ATAAAGCAA CCTCAGAAC CTTAAAAA AAAAAAAAAA 1860
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1920
 AAAAAAAAAA 1967

Seq ID NO: 68 DNA Sequence
 Nucleic Acid Accession #: NM_016109.2
 Coding sequence: 196..1416

50 1 11 21 31 41 51
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 55 ATAAAAACCG TCCTCGGGCG CGGCGGGGAG AAGCCGAGCT GAGCGGATCC TCACACGACT 60
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 GTCTCCAGTC CTGCGACCTG GAACCCCAAC GTCCCGGAGA GTCCCGGAAT CCCCGCTCCC 180
 AGGCTACCTA AGAGGATGAG CGGTGCTCCG ACGGCCGGGG CAGCCCTGAT GCTCTGCGCC 240
 GCCACCGCCG TGCTACTGAG CGCTCAGGGC GGACCCGTGC AGTCCAAGTC GCCCGCTTT 300
 60 GCGTCTGGG ACGAGATGAA TGTCTTGGCG CACGGACTCC TGCAGCTCGG CCAGGGGCTG 360
 CGCGAACACG CGGAGCGCAC CCGCAGTCAG CTGAGCGCGC TGGAGCGGGC CTTGAGCGCG 420
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 GACTTCAACC GGCCTGGGA AGCCTACAAG GCGGGGTTTG GGGATCCCCA CGCGAGTTT 960
 70 TGGCTGGGTC TGGAGAAGGT GCATAGCATC ACGGGGAGCC GCAACAGCCG CTTGGCCGTG 1020
 CAGCTGGGGC ACTGGATGG CAAAGCCGAG TTGCTGCAGT TCTCCGTGCA CTTGGGTGGC 1080
 GAGGACACGG CCTATAGCCT GCAGCTCACT GCACCGGTGG CCGGCCAGCT GGGCCGCCAC 1140
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 75 CATTCCAACC TCAACGGCCA GTACTTCCG TCCATCCAC AGCAGCGGCA GAAGCTTAAG 1320
 AAGGGAATCT TCTGGAAGAC CTGGCGGGGC CGTACTACC CGCTGCAGGC CACCACCATG 1380
 TTGATCCAGC CCAATGGCAGC AGAGGCAGCC TCCTAGCGTC CTGGCTGGGC CTGGTCCCAG 1440
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 GAGCTCACAG AGTTCTTGA ATAAAGCAA CCTCAGAAC CTTAAAAA 1843

	1	11	21	31	41	51	
5	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCCTGTCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCTCTGTCCAT	CCGCCAGAGT	TGCCCCGAGT	CAGGAGGAGT	180
10	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGCGGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCAACCCAG	AGGAGGAGGAT	CCACCCTGAG	AGGAGGATCT	ACCTGGGAGG	300
	GAGGATCTAC	CTGGAGGAGA	GGATCTTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAAGGAGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTACCT	GAGGCTCCTG	GAGATCGCTCA	AGAAACCCAG	420
	AATAATGCCC	ACAGGGGACA	AGAAAGGGAT	GACCAGAGCT	ATTGGCGCTA	TGGAGGCGAC	480
15	CGCCCTTGGC	CCCCGGGTGC	CCCAGCCTGC	GCGGGCGCGT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCCAGC	TCCGCGCCTT	CTGCGCCGGC	CTGCGCCCCC	TGGAACCTCT	GGGCTTCCAG	600
	CTCCCGCGCC	TCCGAGAACT	GCGCCTTGGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTCT	660
	CCTCCTGGGG	TAGAGATGGC	TCGTGGGTCCC	GCGGGGGAGT	ACCGGGCTCT	CGAGCTGCAT	720
	CTGCACTGGG	GGGCTCGAGG	CTGCTCGGGC	TOGGAGACA	CTGTGGAGAG	CCACCGTTTC	780
20	CTCGCCGAGA	TCCACTTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCCTG	840
	GGGGCGCCGG	GAGCGCTGGC	CGTGTGTGGC	GCCTTTTGGT	AGGAGGGGCC	CGAAGAAACG	900
	AGTGCCTATG	AGCAATTGCT	GTCCTCGTTG	GAGAAATGCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGGTCOCAG	GACTGGACAT	ATCTGCACCT	CTGCCCTCTG	ACTTCAGCGC	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCCGCCCTG	CTGCCGGGTG	TCATCTGGAC	TGTGTTTAACT	1080
25	CAGACAGTGA	TGCTAGATGC	TAAGCAGCTC	CACACCTCTC	CTGACACCACT	GTGGGGACCT	1140
	GGTGACTCTC	TGCTACAGCT	GAACTTCCGA	GGCAGCGACG	CTTTGAATGT	GGCGAGTATT	1200
	GAGGCTCTCT	CCCTGCTCGG	AGATGGACAG	AGTCTCTGGG	CTGTGAGGCC	AGTCCAGCTG	1260
	AAITCTCTGG	TGGCTGCTGG	TGACATCTTA	GCCTCGGTTT	TGCGCTCTCT	TTTTCGCTGC	1320
	ACGAGCGTGC	GCTTCTCTTG	GCAGATAGAG	AGGCGAGACA	GAGGGGAGAC	CAAGAGGGGT	1380
30	TTAGACTACC	CGCCAGCAGA	GGTAGCCGAG	ACTGAGCCTC	AGAGGCTGGA	TCTTGGAGAA	1440
	TGTGAGAAGC	CAGGACGAGG	CATCTGAGGG	GGAGCGCGTA	ACTGTCCTGT	CTCGCTCAAT	1500
	ATTGCCACTC	CTTTTAAGTG	CAAGAATAAT	TTTAAATAAT	AATAATTATA	AT	1552

	1	11	21	31	41	51	
	CTTCTCTCTC	CATTCACTGC	ACGCGTTACT	TGGGCTAAAA	GGAGGTGAGC	GGCACTCTGC	60
40	CTTTCACAG	CAAGCATGGA	GCAACAGGAT	CAGACCATGA	AGGAAGGGAG	GCTGACCGCT	120
	GTGCTGCGCC	TGGCAACCTC	GATAGCTGCC	TTTGGGTCAAT	CCTTCCGAGT	TGGGTACAAC	180
	GTGGCTGCTG	TCAACTCCCC	AGCACTGCTC	ATGCAACAAT	TTTACAATGA	GACTTACTAT	240
	GTGAGGACCG	GTGAATTTCG	GGAAAGTCTC	CCCTTGAGCT	TGCTGTGGTC	TGTAACCGTG	300
	TCCATTGTTT	CATTTGAGAG	GATTATCGGA	TCCTCTCGTG	TGCGCCCTTG	GGTGAATAAA	360
45	TTTGGCAGAA	AAGGGGCGCT	GCTGTTCAC	AACATATTTT	CTATCGCTCT	TGCGATCTTA	420
	TTGGGATGCA	CAGAGTTCGC	CACATCATT	GAGCTTATCA	TATTTCCAG	ACTTTTGGTG	480
	GGAAATATGT	CAGAGTGATC	TTTCAACAGT	GTCCCCATGT	ACTTAGGGGA	GCTGGCCCCCT	540
	AAAAACCTCG	GGGGGGCTCT	CGGGGCTGGT	CCCCGACTCT	TCATCACTGT	TGGCATCTCT	600
	GTGGCCGACA	TCTTTGGTCT	TGCGAAATCT	CTGTCAAACT	TAGATGGGTG	CGCGATCTGT	660
50	CTGGGGCTGA	CGGGGGTCCC	CGCGGGCTGT	CAGCTCCTTC	TGCTGCCCTT	CTTCCCCGAG	720
	AGCCCCAGGT	ACCTGTCTGAT	TCAGAAAGAA	GAGGAAAGCG	CGCCCAAGAA	AGCCCTACAG	780
	ACGCTGCGCG	GCTGGGACTC	TGTGGGACAG	GAGGTGGCGG	AGATCGCGCA	GAGGAGTAGG	840
	CGCAGAAAG	CGCGGGGCTT	CATCTCCGTG	CTGAAGCTGT	TCGGGATGCG	CTCGCTCGCC	900
	TGGCACTGTC	TGCTCATCAT	GCTGCTCATG	GCGGGCCAGT	AGCTGTGGGG	CGTCAACGCT	960
55	ATCTACTACT	ACGCGGACCA	GATCTACCTG	AGCGCCGGCG	TGCCGGAGGA	GCACGCTGAG	1020
	TACGTGAGCG	CGCGCAGCCG	GGCGGTGAAC	TGTGCTCATG	CCTTCTGGCG	CGTGTTCGTG	1080
	GTGAGCTCTC	TGGGTGCGAG	GCTGCTCTGT	CTGCTGGGCT	TCTCCATCTG	CTCTATAGCC	1140
	TGCTGCTGTC	TCACTGCGAG	TCCTGGCACTG	CAGGACAACG	TGTCTTGATG	GCTCATACCT	1200
	AGCATCGTCT	GTGTCTATCT	TACGTGCTA	TGCTGCTCCC	TCGGGGCCAG	TCCCATACCC	1260
60	GGCGTGCTCA	TCACGTAGAT	CTTCTCTGAG	TCCTCTCGGC	CATCTGCGTT	CATGTGGGGG	1320
	GGCAGTGTGC	ACTGGCTCTC	CAACTCTCAC	GGCGGCTTGA	TCTTCCGCTT	CTCCACAGAG	1380
	GGCCTCGGCG	CGTACAGCTT	ATTGTTCTTC	TGCTGGATCT	GCTCTCTCAC	CACCATCTAC	1440
	ATCTTCTTGA	TTGTCCCGGA	GACCAAGGCC	AAGACGTTGA	TAGAGATCAA	CCGAGATTTC	1500
	ACCAAGATGA	ATAAGGTGTC	TGAAGTGTAC	CCGGAAAAAG	AGGAACCTGA	AGGATTTCCA	1560
65	CCTGTCTACT	CGGAAGAGTC	ACTCTGAGA	GGAGAGCCAG	GGAGCTGTGT	TGCCAGGGGC	1620
	TTTCCCACTT	GGCTTATTTT	TGCTGACTTT	AGCTGTCTCT	GAATATCCAG	AAATAAAAAA	1680
	ACTCTGATGT	GGAAATGCAGT	CCTCATCTCC	AGCTCCCCCA	CCCGAGTGGG	AAATGTGCAA	1740
	AGGGCTGCTC	TGCTGTTCTT	GAACTGGGG	TGTCCTCTCT	CATGTTGGCC	TGTCACACGA	1800
	CCCGAGTCAA	TTAAACAGCT	GGTCTCTCAC	TTTGTGTTGT	CAGCCTTCGT	TGCTGCTCTG	1860
70	GTAAAGTGGC	TCCACCTTGA	TGGGTCAATG	TTTGTGTGGC	TCTGTGTAAC	ATGAACAACAA	1920
	CAGTTACTAT	AGTGTGTAGA	TGGAAGGAAT	CAAAATTTGC	CAGAGAAACT	AACTCGGTGG	1980
	CCCCAACAGG	TCTTCCGGGG	CCATGGGCAT	TTGTTTAGAG	CCAAATTTAT	CTCTTATCCA	2040
	GATCCTTTTC	CAGAAATACC	TGCTAGGAA	GGTGTGATGT	CAGAAACAAT	GACATCCAGA	2100
	AAGCTGAGGA	ACAGGTTCTT	TGGGAGACAC	TGAGTCAAGAA	TTCTTATCC	AAATATTTT	2160
	GTTAGTGGAA	AATGGAATGT	CTTCTGTGTA	TGTCAATAAA	TBAACCTGAT	CACTTTTC	2220

80	1	11	21	31	41	51	
	GGCTGGTCCC	CTGACAGGTT	GAAGCAAGTA	GACGCCCCAGG	AGCCCCCGGA	GGGGGCTGCA	60
	GTTTCCTTCC	TTCCTTCTCG	GCAGCGCTCC	GGCCCCCAT	CGCCCTCCT	CGCTAGCGG	120
	ATGATGATCG	CGCGGCAGTA	CCGAGGAGG	GTTCCGGCTG	CTCGGTGCG	CTGACGCCCT	180
	AGGGGTGCT	CCTCGGGGCT	CGTTTGGTCC	CTATGGTTCG	GGGCTTGGT	ATCTGCGCTG	240

5 TGGTGTGCAT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT 300
 GGGACGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
 GGCAGGGGGG CCAGCACTG GCGCGCTCCT TCCTGCATGG ACCAGAGCTG GACAAAGGGG 420
 AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGACG CTGGCCATCT 480
 GCTCTCCAC GAGCGCTCC AGGCACACC CCACCACCT GCCGCTGGGA ATCTGCTCTC 540
 CCGCTCCCG TAGCATCAGC CTGCTGCGTC TCAGCTTCCA CCAAGTTGT ACCATTGCCT 600
 CCCAGCGCCT GAGCGCCCTG GCCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
 TTTTGCCTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
 10 CACTGTCTGT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
 AGTGATACACA CAGGGCCAC CCGGGTGTG GGTGGGAGTG TGGTGGGGG TAGTGGTGGC 840
 AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTCTT ATTAATAA 888

Seq ID NO: 72 DNA Sequence

Nucleic Acid Accession #: NM_018092.2

Coding sequence: 13..618

15 1 11 21 31 41 51
 | | | | |
 AGCAGGTTTC GAATGCTCTT TACTTCCTTT GTGGAGCAAA AGAAAAAGC AGGAGTATTT 60
 20 GAACAAATCA CTAAGACTCA TGAACAATT ATTGGCATT CTTAGGGAT TGTCTTGGTC 120
 CTCTCATTAT TTCTATTTT AGTACAAGTG AAACAGCCTC GAAAAAGGT CATGGCTTGC 180
 AAAACCGCTT TTAATAAAAC CCGGTTCCAA GAAGTGTGTG ATCCTCTCA TTATGAACTG 240
 TTTTCACTAA GGGACAAGA GATTCTGCA GACCTGGCAG ACTGTGCGA AGAATTGGAC 300
 AACTACCAGA GGATGGGCG CTCTCCACC GCCTCCCGCT GCATCCACGA CCACCACTGT 360
 25 GGGTGGCAGG CTCCAGCGT CAAACAAAGC AGGACCAACC TCAGTTCAT GGAGCTTCT 420
 CTCCGAATG ACTTTGCACA ACCACAGCCA ATGAAAACAT TTAATAGCAC CTTCAAGAAA 480
 AGTAGTTACA CTTTCAACA GGGACATGAG TGCCCTGAGC AGGCCCTGGA AGACCGAGTA 540
 ATGGAGGAGA TTCCCTGTGA AATTATATGC AGGGGCGGAG AAGATTCTGC ACAAGCATCC 600
 ATATCCATTG ACTTCTAAT TTCTGTAAT GGTGATGTGA ATTCTTAGGG TGTGTAGTA 660
 CGCAGCTCC AGGGCACCAT ACTGTTTCCA GCAGCCCAACC CTTTCTCCC ATCACAATA 720
 30 CGAAGACCTT GATTTACCGT TAACCTATTG TATGGTGATG TTTTATTCT CTCAGGCAGT 780
 CTATATATGT TAAACCAAT AAGGAACCTA CTCTATTGAG TGGAAACAAT AATCATCTCT 840
 ATTGCTTGGT GTCAATTATA GGAAGCACTG CCAGTTAAAG AGCATTAGAA GAGGTGGTTG 900
 GATGGAGCCA GGCTCAGGCT GCCTCTCGT TTTAGCAACA AGAAGACTGC TCTTGACTGA 960
 35 TAACAGCTCT GTCAATATTT TGATGCCACA ATAACTTGA TTTTCTTTA CATTCCTTT 1020
 ATTTTCTCTT TCTCTAAAT TAAITGTTT TATAAGCCTA TCGTTTACC ATTTCATTT 1080
 CTTACATAAG TACAAGTGGT TAATGTACCA CATACTCAG TATAGGCATT TGTCTTGAG 1140
 TGTGTCAAAA TACAGTAGT TACTGTGCCA ATTAAGACCC AGTTGTATTT CACCCATCTG 1200
 TTTCTCTTG GCTAATCTCT GTACTCTGC CTTTAAATTA CTGGGCCCTT ATTCCTTAT 1260
 40 TTCTGTGAGA AATAATAGAT GATATGATT ATTACCTTTC AATTATATTT TTCTCAGTTA 1320
 TACTAGAAAA TTTCAATAT CTGGGATATA TGTACCATTG TCAGCTATGA CTAATAATTT 1380
 GAAAAAGATA AAAATTTCTA GCAAGCCTTT GAAGTTTACC AAGTATAGTC ACATTCAGTG 1440
 ACAGCCCAT CATTCCAGTA AAGAATCATT TCATTCACCT TGGGAGAGGC CTATAATTAC 1500
 45 ATTATTTGCA AATGTTTCTC TTGCTAGAT TGTACATAG CTCCCTCTCT GTTGGTTTGT 1560
 CTTACAGCAT ATGTAAACCA AGGTTAGATG CCAGTTAAAA TTCTTTAGAA ATTGGATGAG 1620
 CCTTGAGATT GCTTCTTAAC TGGGACATGA CATTTTCTA GCTCTTATCA AGAATAACAA 1680
 CTTCCACTTT TTTTAAACT GCACTTTGA CTTTCTTAT GGTATAAAAA CAATAATTTA 1740
 TAAACATAAA AGCTCATTGT GTTTTTTGA CTTTGTATAT TATTTGATAC TGTACAACT 1800
 50 TTATTAATC AAGATGAAAG ACCTACAGGA CAGATTCCCT TCAGTGTTC CAATCAGTGGC 1860
 TTTGTATGCA AATATGCTGT GTTGGACCTG GACGCTATAA CTTATTGTAA AGACCTTGA 1920
 AATGTGGACA TAAGCTCTT CTTTCTTTT GTTACTGTAT TTAGTTTGTG ATAAATTTT 1980
 CACTGTGTGA TATTTATGCT CTAATCACT ACACAAATCC CATATTAATA TATACATTGT 2040
 ACCTGACCTT TTAATCATGT TATTTATGCC ACCAAGGTTG TGGATCTTAA GGTATGTATG 2100
 GAAAGGAAT CATTATCAAA ATTGTAAGTA ATACAGACAT GCCATTTAAA AGAGGTAAAT 2160
 55 TCTGTGTTTC TATATTGTT TAGTAAATTC TCAATGAAAT AAGTTGAAGT TTCCTGGAT 2220
 TTTCAATACT TTTAAATATT ACATATATGT GTTTCTCAG ATTAGTGAAG ATTGTGACCT 2280
 TAAATTTAAT ACACATATAC TGCCCTCAG 2308

Seq ID NO: 73 DNA Sequence

Nucleic Acid Accession #: Eos sequence

60 1 11 21 31 41 51
 | | | | |
 GCTGAATGTT TTTTCACTT TCCTGAGAGA TGCAATGTT CATTCACTCA TCTCATTATA 60
 CAACACAGTA CATAAATGTA GCTTCAGAGC GTATTAAGTG CTTTATACA CAAGTGCTGG 120
 65 CTGTGTGGAC CAGGTGGTAG CTCAATTAGG CCCCAAATTC ATTAAGGGCA GGGTCTGACT 180
 CTTAGGCTTC TTAATATTTG GTTGGTGCA TGGTCAAGAG CTGGACCCAC ATGTTGCATA 240
 GCAGCAGGGC TGATATGTTT AAAGACGCTG GGCTTTTCT GCTCTGGGGC CCTTCCCGG 300
 GGGTTCCGGT GAGTCCCTCC CCAGGTGGGT CTGCCCCAC CCGTGTGGGC GGGATTAGCT 360
 CCCAGGGCT GGCAGGGCCC CACCTGGGGG AGGCTTGAGG GCAGGGCCCC AAGCTGAGA 420
 70 TTCAGGCTTG GGGGAACAGA GCAGGAAAGA GACCCGCTAC CGAAAGTGAG CGGGCAGGC 480
 ACCTAGTCAC ATGGGTAATG GGCAGGGGTC GGTCACTGGC TTTGGCTCCA GGGCCAGAGC 540
 AGTCTGACTT AGTGTGAGC TCCAAGCATG GAACACTGGA GTTGGTTTAT TTTGACCAGC 600
 AAGCCTCTAA ATGGGTGCCCT TGATTACCCA CCGCAAGGAG AGGGCAGTTG CCTTTTATG 660
 ACATGTTAAT TCCAGCCAGG TGAGTCACCA GGTAGCTCTC ATCCTCTGTC CAGGCTCCCC 720
 75 TGCCGTGCGG TTTGGCATTG TCAGATAATG TGATCATTCA TTGAAGTGAC ATTTGAGTTC 780
 CAAACAGTTT TTCTCTTTA ACCATTTTAC CTTGAGGAGT GATTCTCCTT TGTTTGGCAT 840
 TGTGAGGAAA TGTGATGATC CATTCAATG ACTTTTGAGT TCCAAATAGT GTTTCTACTT 900
 TAACCTCCTA AATGAAAAA AAAAAAAAAA AAA 933

Seq ID NO: 74 DNA Sequence

Nucleic Acid Accession #: Eos sequence

80 1 11 21 31 41 51
 | | | | |
 TTTTCTTTT TCAATTAGGA AGTTAAAGTA GAAACACTAT TTGGAACCTA AAAGTCATT 60
 GAATGGATCA TCACATTTCC TGACAATGCC AAACAAAGGA GAATCACTCC TGAGGTGAA 120

5
 10
 15
 20
 25
 30
 35
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 45
 50
 55
 60
 65
 70
 75
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ATGGTTAAAG GAGAAAACTG GTTTGGAAC CAAATGTCAC TTCAATGAAT GATCACATTA 180
 TCTGACAATG CCAAAACGAC AGGCAGGGGA GCCTGGCAGG AGGATGAGAG CTACCTGGTG 240
 ACTCACCTGG CTGGAATTA CAATGTCTAA AAAGGCAACT GCCTCTCTCT TCGGGTGGGT 300
 AATCAAGGCA CCATTTTAGA GGCTTGCTGG TCAAAATGAA CCAACTCCAG TGTTCCATGC 360
 TTGAGCTCA AACTAAGTC AGACTGCTCT GGCCCTGGAG CCAAGGCCAG TGACCGACCC 420
 CTGCCCATTA CCCATGTGAC TAGGTGCTCT CCCGCTCAC TTTGGGTACC GGGTCTCTTT 480
 CTTGCTCTGT TCCCCCAAGC CTGAATCTCA GCCTTGGGGC CTTGCCCTCA AGCCTCCCCC 540
 AGGTGGGGCC TGGCCAGCCT C 561

Seq ID NO: 75 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..459

1 11 21 31 41 51
 15 ATCATTGCGC CCACGATTAA TAATGCCAGC ATGACTTCCC CAATTGACAA TGCTGGACTT 60
 GCAGCAGATG ACTTCAAAT GAATGCATCC TTGCAGACAC AGATCTCCAC GGATGCTGAA 120
 CGAGTTAGCT CGGCCAAGAG TGAGATAATG GAGCTGAAAC AAGTCTCTCA GTCCCTCCAG 180
 CATGAATGCG AGTCTGTCTT GGCCATGCAA AGCTCCCCAG AAGGAACCCCT GGCTGACACA 240
 GAAGCTGGCT ACGTGGCTCA CCGTGCAGAA ATTAAGATGT ATATCAGCAT CCTGGAGGAG 300
 20 CAGATCTGCC AGATCCGGGG CGAGACTGAA TACCAGAACA CAGAGTATGC ACAACTGCGAG 360
 GACATCAAGA CAGCCCTGGA GGTGGAGATC GAGACCTACC ACCGCTGTCT CGGTGGAGAG 420
 GGAGGTTCTG AGGCCAGAGA AGCTGAATCT AAAGGATGAT TCTCTGTGGA CTCCAAGGA 480
 ATAACCAACA CAGCTCAATC GAGGGGAAGA GTGCTTTTT AAAATTTCAC TAAAGCAGA 540
 GGAACCGGC TGGTGAACGA TAATGACCAA CTAAATTCAT CTCACACTG TTTCTGATGT 600
 25 AAAATTCAAG AGTAAGATGC AGGCAGCTGA GTCTGTCCC CAGGATGTAA ATGATGACAC 660
 CTAACAAAGG CGTGCTGAAG CACTGCAACA AACTTGGCGC CACAGAGCTG CAGTACTCTC 720
 TGTAACTCCT TCTCAGATTG TTTTGTCTTA TTGGTTCGGT TTTGTCTTTA AATTGCAAAA 780
 TGTGTTTTCC TTCTTAATCA TTCTGTGTG ATAACTTTT TGCTGTGTC AAATCAA 837

Seq ID NO: 76 DNA Sequence
 Nucleic Acid Accession #: NM_003265.2
 Coding sequence: 102..2816

1 11 21 31 41 51
 35 CACTTTGCGC AGTGGCTGCT ATTTGCCACA CACTTCCCTG ATGAAATGTC TGGATTGGA 60
 CTAAGAAAAA AAGGAAGGC TAGCAGTCAT CCAACAGAAT CATGAGACAG ACTTTGCCCT 120
 GTATCTACTT TTGGGGGGGC CTTTGGCCCT TTGGGATGCT GTGTGCTATC TCCACCACCA 180
 AGTGCATGCT TAGCCATGAA GTTGCTGACT GCAGCCACCT GAAGTTGACT CAGGTACCCG 240
 40 ATGATCTACC CACAACATA ACAGTGTGTA ACCTTACCCA TAATCAACTC AGAAGATTAC 300
 CAGCCGCCAA CTTCAACAAG TATAGCCAGC TAATAGCTT GGATGTAGGA TTTAACACCA 360
 TCTCAAACT GGAGCCAGAA TTGTGCCAGA AACTTCCCAT GTTAAAGATT TTGAACCTCC 420
 AGCAAAATGA GCTATCTCAA CTTTCTGATA AAACCTTTGC CTTCTGCAGC AATTGACTG 480
 AACTCCATCT CATGTCCAAC TCAATCCAGA AAATTAAGAA TAATCCCTTT GTCAAGCAGA 540
 45 AGAATTTAAT CACATTAGAT CTGTCTCATA ATGGCTTGTC ATCTACAAA TTAGGAATCT 600
 AGGTTCAGCT GGAAATCTCT CAAGAGCTTC TATTATCAAA CAATAAAATT CAAGCGCTAA 660
 AAAGTGAAGA ACTGGATATC TTTGCCAATT CATCTTTAAA AAAATTAGAG TTGTCATCGA 720
 ATCAAAATTA AGAGTTTCTT CCAGGGTGTG TTCACGCAAT TGAAGATTA TTTGGCCTCT 780
 TTCTGAACAA TGTCAGCTG GGTCCAGCC TTACAGAGAA GCTATGTTG GAATTAGCAA 840
 50 ACACAAGCAT TCGGAATCTG TCTCTGAGTA ACAGCCAGCT GTCCACCACC AGCAATACAA 900
 CTTTCTTGGG ACTAAGATGG ACAAACTCA CTATGCTCGA TCTTCTCTAC AACAACTTAA 960
 ATGTGGTGGG TAAAGATCTC TTTGCTTGGC TTCCACAAC AGAATATTTC TTCCTAGAGT 1020
 ATAAATATAT ACAGCATTTG TTTTCTCACT CTTTGCACGG GCTTTTCAAT GTGAGGTACC 1080
 TGAATTTGAA ACGGTCTTTT ACTAAACAAA GTATTTCCCT TGCCCTCACTC CCAAGATTG 1140
 55 ATGATTTTTT TTTTCACTG CTAATAATGTT TGGAGCACCT TAACATGGAA GATAATGATA 1200
 TTCCAGCGAT AAAAAGCAAT ATGTTACAGC GATTGATAAA CCGAAAATAC TTAAGTCTAT 1260
 CCAACTCTCT TACAAGTTTG CGAACTTTGA CAAATGAAC ATTTGTATCA CTTGCTCATT 1320
 CTCCCTTACA CATACTCAAC CTAACCAAGA ATAAATCTC AAAATATAG AGTGATGCTT 1380
 TCTCTGGTT GGGCCACCTA GAAGTACTTG ACCTGGGCTT TAATGAATTT GGGCAAGAAC 1440
 60 TCACAGGCCA GGAATGAGAG GGTCTAGAAA ATATTTTCGA AATCTATCTT TCCTACAACA 1500
 AGTACCTGCA GCTGACTAGG AACTCCTTTG CTTGGTCCC AAGCCTTCAA CGACTGATGC 1560
 TCCGAAGGGT GGCCTTAAA AATGTGGATA GCTCTCCTTC ACCATTCCAG CCTCTCTGTA 1620
 ACTTGACCAT TCTGGATCTA AGCAACAACA ACATAGCCAA CATAATGAT GACATGTTGG 1680
 AGGGTCTTGA GAACTAGAA ATTCTCGATT TGCAGCATA CACTTAGCA CGGCTCTGGA 1740
 65 AACACGCAAA CCTGTGTGT CCCATTTATT TCCTAAAGGG TCTGTCTCAC CTCCACATCC 1800
 TTAACCTTGA GTCCAAACGG TTTGACGAGA TCCAGTTGA GGTCTTCAAG GATTATTATT 1860
 AACTAAGAT CATCGATTGA GGATTGAATA ATTTAAACAC ACTTCCAGCA TCTGTCTTTA 1920
 ATAAATCAGG GTCTCTAAAG TCATTGAACC TTCAGAAGAA TCTCATAACA TCGTTGAGA 1980
 AGAAGGTTTT CGGCCAGCT TTCAGGAACC TGACTGAGTT AGATATGCGC TTTAATCCCT 2040
 70 TTGATTGCAC GTGTGAAAGT ATTGCCTGGT TTGTTAATTG GATTAAAGAG ACCCATACCA 2100
 ACATCCCTGA GCTGTCAAGC CACTACCTTT GCAACACTCC ACCTCACTAT CATGGGTTCC 2160
 CAGTGAGACT TTTTGATACA TCATCTTGCA AAGACAGTGC CCCCTTTGAA CTCTTTTTC 2220
 TGATCAATAC CAGTATCTCT TTGATTTTTC TCTTTATTGT ACTTCTCATC CACTTTGAGG 2280
 GCTGGAGGAT ATCTTTTTAT TGGAAATGTT CAGTACATCG AGTTCCTGGT TTCAAGAAA 2340
 75 TAGACAGACA GACGAACAG TTTGAATATG CAGCATATAT AATCATGCC TATAAGATA 2400
 AGGATTGGGT CTGGAACAT TTCTCTTCAA TGGAAAAGGA AGACCAATCT CTCAAATTTT 2460
 GTCTGGAAGA AAGGACTTT GAGGCGGGTG TTTTGAAC TGAAGCAATT GTTAACAGCA 2520
 TCAAAAGAG CAGAAAATTT ATTTTGTGTA TAACACACCA TCTATTAATA GACCATTAT 2580
 80 GCAAAAGATT CAAGGTACAT CATGCAGTTC AACAAAGCTA TGAACAAAT CTGATTCCA 2640
 TTATATTGGT TTTCTTTGAG GAGATTCCAG ATTATAAAT GAACCATGCA CTCTGTTTC 2700
 GAAGAGGAAT GTTTAAATCT CACTGCATCT TGAACCTGGC AGTTCAGAAA GAACGGATAG 2760
 GTGCCTTTTC TCAATAATTG CAAGTAGCAC TTGGATCCAA AAACCTGTGA CATTAATTT 2820
 ATTTAAATAT TCAATTAGCA AAGGAGAAAC TTTCTCAATT TAAAGAGTTC TATGGCAAT 2880
 TTAAGTTTTT CATAAAGGTG TTATAATTG TTTATTCATA TTTGTAATG ATTATATTCT 2940
 ATCACAATTA CATCTCTTCT AGGAAAATGT GTCTCCTTAT TTCAGGCTA TTTTGGACAA 3000

TTGACTTAAT TTTACCCAAA ATAAACATA TAAGCACGTA AAAAAAAAAA AAAAAAA 3057

Seq ID NO: 77 DNA Sequence

Nucleic Acid Accession #: Eos sequence

5	1	11	21	31	41	51	
	ATCAAGGAGG	ACAGATTTTA	TATGCTTAAG	ACTGGAGGGA	GAGAGACCAG	TTAGAAAGAC	60
	TCTGGCTATA	ATCCAAGCAA	GCCATACTAT	GGGCTGGTTT	GGTGGAGGTA	GAGGAATGTC	120
10	CAGATTGGAG	AAACAGGAAG	TTAAAAATGG	GCAGGGCTTG	CTGACTGTTT	GAAACTAGGG	180
	GGTGTGAAGG	GAGGCAGCAC	TCTAGGATAA	ACACCAGACT	TGCCGATTGT	TTGGGAATAT	240
	CCAATTCTGC	TGTAGAAGAC	AGGAAAAACA	TAAACTCAAA	AGAAAGTGTG	CACATAGATA	300
	ACTAAATTAG	TCATCTGTAG	ATAGTACAAC	ATATTCTGTG	GTACAGAGAT	CAAAAGGGAC	360
	AGAAAGACCA	AGGAGGCACT	AAATATTAC	GGTACCCCTA	ATACGTGAGA	CATGAGGCAC	420
15	TCAGGATGCA	GGAGGTTTCA	ATTTGACAGG	ATGGATGCAC	ACTGCATGAC	CCACAGTTCA	480
	GCTGGTGTGA	TCATTCCACC	CAACTGCCCC	CCTCTCCCGT	GTGTTGACCC	ACCCAGCAC	540
	CTGCCTCCTG	CTTCTCAGAA	TGTGTTTAC	ATTTATTATA	TAAACGATGT	TATTTAGCA	600
	TTTA						604

Seq ID NO: 78 DNA Sequence

Nucleic Acid Accession #: Eos sequence

20	1	11	21	31	41	51	
	TTTTTTTTTT	TTTTTTTITA	AATGCTCAAA	TAACATCGTT	TATTAATAAA	ATGTAAACAA	60
	CATTCTGAGA	AGCAGGAGGC	AGGTGCTGGG	GTGGGTCAAC	ACACGGGAGA	GGGGCAAGT	120
25	TGGGTGGAAT	GATCGATCAC	ACCAGCTGAA	CTGTGGGTCA	TGCAGTGTGC	ATCCATCTCTG	180
	TCAAATTCGA	ACCTCTCTGA	TCCTGAGTGC	CTCATGTCTC	ACGTATTTAG	GGTACCGTGA	240
	ATATTAGTGC	CCTCTCTGGT	CTTCTGTGCC	CTTTGTATCT	CTGTACACAC	GAATACGTTG	300
	TACTATCTAC	AGATGACTAA	TTAGTTATC	TGTGTGAAC	ACTTCTTTTG	AGTTTATTGT	360
30	TTTCTGTCT	TCTACAGCAG	AATTGGATAT	TCCCAAAACA	TCTGCAAGTC	TGGTGTTTAT	420
	CCTAGAGTGC	TGCCCTCCCT	CACACCCCT	AGTTTCAAA	AGTCAGCAAG	CCCTGCCCAT	480
	TTTTAACTTC	CTGGTTTCTC	AATCTGGACA	TTCTCTTACC	TCCCAAAACA	CAGCCCATAG	540
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Seq ID NO: 79 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 315..1416

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	TAAACTTTCA	GACCCAGAGAT	CTATTCTCTA	GCTTATTTTA	AGCTCAACTT	AAAGGAAGA	180
	ACTGTTCTCT	GATTCTTTTC	GCCTCAATA	CACCTAATGA	TTTAACTCCA	CCCTCCTTCA	240
45	AAAGAAACAG	CATTTCCTAC	TTTTATACCT	TCTATATGAT	TGATTTGAC	AGCTCATCTG	300
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	ACTGTCCCTT	TCCTGGGTCA	CTATGCTGCC	GCCTCAGTGG	ACTTTGGAAA	TACAATGTGT	660
	CAACTCTTGA	CAGCGCTCTA	TTTTATAGGC	TTCTTCTCTG	GAATCTTCTT	CATCATCTCT	720
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	GGGCTGGTCC	TGCCGCTGCT	TGTCAATGGT	ATCTGCTACT	CGGGAATCCT	AAAAATCTTG	1020
	CTTCGGTGTG	GAAATGAGAA	GAAGAGGCAC	AGGGCTGTGA	GGCTTATCTT	CACCATCATG	1080
	ATTGTTTATT	TTCTCTTCTG	GGCTCCCTAC	AACATTGTCC	TTCTCTTGAA	CACCTTCCAG	1140
60	GAATCTTTTG	GCCTGAATAA	TTGCAGTAGC	TCTAACAGGT	TGGACCAAGC	TATGCAAGTG	1200
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	TCCACTGGGG	AGCAGGAAAT	ATCTGTGGGC	TTGTGACACG	GACTCAAGTG	GGCTGGTGAC	1440
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	TTGGCATCTG	TTTAAAGTAG	ATTAGATCTT	TTAAGCCCAT	CAATTATAGA	AAGCCAAATC	1620
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	GTCTTGCTAT	GGGGAGAAAA	GACATGAATA	TGATTAGTAA	AGAAATGACA	CTTTTCATGT	1920
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	CTTGACGGCA	TGCTCCCTC	TAAGTCATGA	GCTGAGCAGG	GAGATCCTGG	TTGGTGTTCG	2220
	AGAAAGTTTA	CTCTGTGGCC	AAAGGAGGGT	CAGGAAGGAT	GAGCATTTAG	GGCAAGGAGA	2280
	CCACCAACAG	CTCTCAGTGC	AGGGTGAGGA	TGGCTCTGTC	TAAGCTCAAG	GCCTGAGGAT	2340
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	TGACTTCATA	GATTTCCTTC	CCATCCACGC	TGAAATACTG	AGGGGTCTCC	AGGAGGAGAC	2700

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Seq ID NO: 80 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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 GCTGTATTAA CCAAGGCTAG AAGAATTTT AGCCCTCCGA AAGTTAAAGC GAGGGAAGAG 300
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Seq ID NO: 81 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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	GAAACACATC	CATGGCATGT	CCTCAGGGCA	TTTGTGCATG	GGATTAAGCA	AATGTTTCCCT	2580
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	CCACGGGGAC	AGTCTCTTGT	GGTCTGTGTC	TCCCCCTTCA	GCCCCCTGTG	GGGCAGTTAG	2940
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	AGCGTGGACC	TGTGTGAACA	GATGGCGGCA	GACCTGCACG	TGGAGACACA	GACATGCAGG	3240
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	TGTTCTGGTG	ACACATGGGA	GGCAGAACC	AGAGACTGGG	CCCAGGAGCC	CTTCTGCTGA	3420
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Seq ID NO: 82 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..651

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	GCTCAGCTCA	TAGTGGAGCC	AGGGCCCCCT	GGCCCCCCTG	GCCCCCAGG	CCGATGGGGC	300
	CTCCAGGGAA	TCCAGGGTCC	CAAGGGCTTG	GATGGAGCAA	ACGGAGAGAA	GGGTGGGTGG	360
	GGTGAGAGAG	GCCCCAGCGG	CTGGCTGGG	CAAGTTGGCC	CACCGGGCCT	TATTTGGGCTG	420
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Seq ID NO: 83 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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Seq ID NO: 84 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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GGAGGTGGGT TCTGTGAGCT GAAGCCATT CCATCATTC AACAGCCAGT TACAATTTTC 5340
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Seq ID NO: 95 DNA Sequence

Nucleic Acid Accession #: NM_134421.1

Coding sequence: 527..1108

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CCACCTTCCC CGGTCCGGGT TTGCTTCTCT TTAATAAGAG GACAGCTCTC CCCTTGGGGG 180
CTGTGGTGAC AGGTGAAATG AGAAGCAGCT GAAGCAGACT CTTGGTCCAA AGCCCCGAC 240
ACAGGGCATG GTCTAGTGGC CCACTCAGGA CGCGGAAACA CTCCCTGGAG GTTCTGACCC 300
ACTCCCTCTC AGCCTCGGCC TGGTCTCTGG GTTGGCTGTT CCAGCTCCAA AGAGAAGGAG 360
GAACCTTTTC CTCTTGACAG CCTTCCCAC CAGCTCCATT CCTTAGCTGG GGTGAGACCT 420
GGGGTCTCTA CTGCACTGG CCTCTGGCAG CGTTCTCAGG CTAGCCCTCC CTGCTGAAAA 480
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CGAGCACGTC TTCGCACTT TCGACACCAA CGGCGACGGC ACCATCGACT TCCGGGAGTT 780
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CAGGCTTGTC GTGCCGTTTA AGCTTTGCTT GCAAGAGTGG ATGCCCGCA ATCGTTCTCT 1200
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CGGCTCACG GGGAGCTCAG AGGTCCATGC CGAGGAGACC AGGCAGGACC TCCCGAGGCT 1440
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Seq ID NO: 96 DNA Sequence

Nucleic Acid Accession #: NM_002149.2

Coding sequence: 375..956

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	CGGGCGCAG	GAGGCCGCG	CTGCTAGTCA	CTCCTCCCGG	CCTCGGCGCG	CTTGTCCCGG	180
5	GCAGCGCCCC	GGGCGCGCTG	CAGCGCGCGC	CGGCGCCGAA	CTTGGGCTCG	GGAAAGCGGC	240
	GGACGCGGTC	CTGCGCGCGA	GCAGGGGCAT	GGTCTAGTGG	CCCAGTCAGG	ACGCGGAAAC	300
	ACTCCCTGGA	GGTTCTGACC	CACTCCCTCT	CAGCCTCCGC	CTGGTCTCTG	GTGTAGTCCG	360
	CGCCGCGAGC	CGCCATGGGC	AAACAGAACCA	GCAAGCTGCG	GCCCGAGGTG	CTGCAGGACC	420
	TGCGGGAGAA	CACGGAGTTC	ACCGACCACG	AGCTGCAGGA	GTGGTACAAG	GGCTTCCTCA	480
10	AGGACTGCCC	CACCGGCCAC	CTGACCGTGG	ACGAGTTCAA	GAAGATCTAC	GCCAACTTCT	540
	TCCCCTAGCG	CGAGCGCTTC	AAGTTCCGCG	AGCACTCTTT	CCGCACTTTC	GACACCAACG	600
	GGAGCGGCAC	CATCGACTTC	CGGGAGTTCA	TCATTGCGCT	GAGCGTGACC	TGCGGGGCA	660
	AGCTGGAGCA	GAAGCTCAAG	TGGGCCTTCA	GCATGTACGA	CCTGGACGGC	AACGGCTACA	720
	TCAGCGCAG	CGAGATGCTG	GAGATCGTGC	AGGCCATCTA	CAAGATGGTG	TCGTCTGTGA	780
15	TGAAGATGCC	GGAGGATGAG	TCCACCCCGG	AGAAGCGCAC	AGACAAGATC	TTCAGGCAGA	840
	TGGACACCAA	CAATGACGGC	AAACTGTCTT	TGGAAGAATT	CATCAGAGGT	GCCAAGAGCG	900
	ACCCCTCAT	CGTCCGCTTG	CTGCAGTGG	ACCCGAGCAG	TGCCAGTCAG	TTCTGAGCGA	960
	GGGCGCCCTG	GACAGTTGCA	GAGAAACACA	GGCTTGTCTG	GCCGTTTAA	CTTTGCTTGC	1020
	AAGAGTGAT	CGCCGCAAT	CGTTCTGTCT	CTCCGCGGCC	CGGGCCTGG	GGCATGCGTT	1080
20	GCACCTGCCC	GGCCCGGTGG	CTGCGCTTCC	CTCCTCCACC	TGACCAACGC	GACATTCTCT	1140
	CCCTCACGCC	TGGCCGGTGC	CCTTCCAGGG	CAACTCCAG	GGATGTGGTG	ACATGCAGGG	1200
	TTCAAGTGT	CTTGTGTCCA	GGCACTTCCC	GGCTCACGGG	GAGCTCAGAG	GTCCATGCCG	1260
	AGGAGACGAC	CGAGGACCTC	CCGAGGCTGC	GCCCGCGCG	GCCCATGCGT	TTTGTGATCC	1320
	CAAGTGACTC	TGTGGGAAGG	GTGGGGACGA	GGCGTCGGGA	GGGTATACAG	GGAGCCCTCT	1380
25	CCGTGCATGG	CTGCCCCCCC	GTTCAATTTT	TCCACCACAG	CCGCTTGAC	GTATAGATAC	1440
	TGTGTGCTCC	TTTCTTTTAA	TATATAAATT	ATGTATGGTG	AAGTGGAGTG	TATTGTGTAG	1500
	GTCCCGTATT	TAATGCCTCT	GACTGCCTTT	GAAGCGCAGC	CCTCTGTGGC	CCGAGCCCTC	1560
	CTGAGCCTGG	CTGTGTGTGT	GTATTATATG	TCTCTTTGTC	TGCCTGTTTC	TAAGGAAATG	1620
	CATGTGTGCT	CTGCCCGTGG	ATGATCTCTC	CATCCGTGTT	GTGAGCACAG	GCATTTGTGT	1680
30	CTGGTCTGTC	CTCCCTGTTG	ATTGGTCTGG	CATTTCGGGT	ATTAAATGA	TAAATAAAT	1740
	GGCATTTTCT	GAAAAAATAA	AAAAAATAA				1769

Seq ID NO: 97 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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	AACTGCTCT	TTAAACAAAA	TTATGAAAGG	TTAAAAAGAG	TCTATAAAAA	CTTACCTTAT	120
	GGTCAACAT	GAAAAATTGG	ATAAATATGT	CTACAAGGTT	TTATTAAAAAT	TAAGTTTAAAC	180
40	ATTAATAACA	CACATAATATA	AAGGTAAAAT	TGAGCTTATC	TGGTATAAAA	GTACATACAGG	240
	AAGCATTAGT	AAATATAAAA	TAGCGTTTAG	CTTTCTTTTG	TCTAAAAAAT	AATAAAAAAT	300
	GGTGCTAAAG	GAAGCATTCA	TTTTACTAGA	GGATCATAAA	AGTTAAAGAC	TTAAAAACAA	360
	CTTTGCAAT	TAAGACAGCA	TACCAAGATG	CAATGCCTG	GTTGAAATGG	ATCAATATTT	420
	CCATCTGCAG	GTTAAACAAA	AGCAATTAGC	ATGCTTGTGC	ACATGGCAGG	CCAGAGACCC	480
45	TGATTGTCCC	CCTTCCACTA	AGGTGGTCTT	CCAGTGCACC	AGGCATGGGG	TGCATGGTAG	540
	CTCTTTTCCA	GGATTCTACA	GCCTGGAGTA	ATAAGTCATG	CCAAGCTCTC	TCTGCTATAT	600
	CCTGAAGTCC	CTGCGGGTCA	GCCCCGAGG	GCCATCCAGC	TTCGCTCTCC	CAACACTAAG	660
	TTCACTTCTT	GTCTCTCATG	GCAGGGAGGA	GACTTAGCAT	TCCTTGGAGA	CCTGAAGGGA	720
	TGCACTGAGC	TTAAGAAATT	TCAAGAGCTT	ATCAATCAGT	CAGCCCTTGT	TCATCCCGGA	780
50	GCGGATGTGT	GGTGGTATTG	TGGTGCACCT	TTATTGGGCA	CTCTGCCGAA	TAACATAGAT	840
	GGCACTTGTG	CTTTAGCCTA	TTTGGCTATC	CCTTTACCC	TGGCATTTC	TCAACAGAG	900
	GAAGGAAAAA	AAAAATAATA	AGACATCGTA	AAGCGAGAGA	AGCCCTTAT	GGGTCTTCA	960
	ACTCTCACAT	CTATTAGAT	GCAATCGAAG	CCCCGCAAGG	AACACCATAG	CAATTTAAAG	1020
55	TCCGAAATCA	AATAGCTACA	GGATTTAAGT	CAATATTTTG	GTAGATGAGA	GTCAATAAAA	1080
	ATGTAGATTA	GATAAACTGC	ATCTATTACA	CCCAACAGCA	ATGAGCTTTT	CATGAGTTGA	1140
	AAAAAGAGAA	AACTCATGTC	GGCCCCAGCC	CTGAGGCTAC	CTGACCTGAC	AAAACTCTTT	1200
	ACACTCTATG	TGTGAGAAAG	AGAAAAAATG	GCAGTTGGAG	TTTTAACCCA	GACTGTAGGG	1260
	CCCTGGGCAA	GGCCAGTGGC	CTATCTCTCA	AAACAACTAG	ACGGGGTTTC	CAAGGGCTGG	1320
	CCCCCATGAC	CAAGGGCCCT	GGCAGCAATA	GCCCTGTTAG	CACAAGAAGC	AGATAAGCTA	1380
60	ACTCTTAGGC	AAAACTTAAA	CATAAAGTCC	CCCATGCTG	TGGTAACTTT	AATAAATACC	1440
	AAAGGACATC	ATTAGCTAAT	GAATGCTAGA	CTGACTGACT	AGATACCAAA	GCTTGCTCTG	1500
	TGAAAAATCC	TGCATAACCG	TGAAAGTTTG	CAACACCTTA	AACCCAGCCA	CCTTACTCCT	1560
	GGTATCAGAG	AGCCCAAGTG	AACATAACTG	TGTAGAGTTA	TTGGACTCAG	TTTATTCTAG	1620
	TGGGTCCAAC	TCCAAGACCA	TCCTTAAACA	TCAGTAGACT	GGGAGCTGTA	CGTGGATGGG	1680
65	AGCACTGTCG	CCAACCCCTG	CAAAGTGATT	CTGAAGAAGA	CGACAAGCGC	TGCTCCAGTC	1740
	ACACCCGGAA	GCTGACTGGT	CCAATCATGG	CCGAGCATGA	GGAACTCAT	CGCGGACTC	1800
	ATTTTCCTTA	AAATTTGGAC	TTGCACAGTA	AGGACTTCAA	CTGACCTTCC	TCAGACTGAG	1860
	GACTGTTCCC	AGGATATACA	TCAAGTCACT	GAGGTAGGGA	AAAAAGGTTG	CTACAGTCTT	1920
	ATTATTTTAT	AGTTATTATG	AATGCCCTAG	AACTCCAAAA	GGAACTTGT	TGTACAATAA	1980
70	CACCTAGTAC	AAAGTATGTA	ATCCAGGAAG	TGACCCAGCT	GAAGCGTGT	ATGACTCACT	2040
	GTAAGCTCTC	CATGATTAAG	GACTGATCCT	TTTCTAAGTG	ACAGAAGTAG	AGTAATAGCT	2100
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Seq ID NO: 98 DNA Sequence

Nucleic Acid Accession #: NM_003946.2

Coding sequence: 98..724

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	GTACAGAGCT	ATCGACCGCG	AGCGGAAACG	CCTGGTCCAG	ACGCTGCAGG	CGGACTCGGG	180
	ACTGCTGTTG	GACGCGCTGC	TGGCGCGGGG	CGTGCTCACC	GGGCCAGAGT	ACGAGGCATT	240
	GGATGCAGCTG	CCTGATGCCG	AGCGCAGGGT	GCGCCGCTTA	CTGCTGTCTG	TGCAGGGCAA	300
	GGGCGAGGCC	GCCTGCCAGG	AGCTGCTACG	CTGTGCCAG	OGTACCGCGG	GCGCGCGGA	360

CCCCCTTGG GACTGGCAGC ACGTGGGTCC GGGCTACCGG GACCGCAGCT ATGACCCCTCC 420
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 GACCCCGGAG GAGCCAGAGC CAGAGCTGGA AGCTGAGGCC TCTAAGAGG CTGAACCGGA 600
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 GCCAGAACCG GACCCAGAGC CCGAGCCCGA CTTCGAGGAA AGGACGAGT CCGAAGATTC 720
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 GCTGGAGCTG AATCGGATGC CACCAAGGCT CGGTCCAGCC CAGTACCGCT GGAAGTGAAT 840
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 AGCTGAACAT GGAGCAAGGG GAGGTGACT TCTCTCCACA TAGGGAGGGC TTAGAGCTCA 1200
 CAGCCTTGGG AAGTGAGACT AGAAGAGGGG AGCAGAAAGG GACCTTGAGT AGACAAAGGC 1260
 CACACACATC ATTGTCAAT TGTCTTAAAT TGTCTGGCTT CTCTCTGGAC TGGGAGCTCA 1320
 GTGAGGATTC TGACCAAGTA CTTACACAAA AGGCGCTCTA TACATATTAT AATATATTGC 1380
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20 Seq ID NO: 99 DNA Sequence
 Nucleic Acid Accession #: NM_004207.1
 Coding sequence: 63..1460

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 GGGGCTGGGC CGTGTCTTTC GGCTGTTTCG TCATCACTGG CTCTCCTAC GCCTTCCCCA 180
 AGGCCGTGAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA 240
 CAGCCTGGAT CTCTCCATC CTGCTGGCCA TGCTCTACGG GACAGGTCCG CTCTGCAGTG 300
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 TCATCAAGGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT 480
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 TGTGTGCCCT GAGCCCGCTG GGGCAGCTGC TGCAGGACCG CTACGGCTGG CGGGGGGGCT 600
 35 TCCTCATCCT GGGCGGCGTG CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC 660
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 40 ACACCAAGGC CGCCTTCTCT CTACCATCC TGGGCTTCAT TGACATCTTC GCGCGGCCCG 900
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 TCGAGGTGCT CATGGCCATC GTGGGCACCC ACAAGTCTC CAGTGGCATT GGCTGGTGC 1140
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 45 CGACCCAGCT CTACATGTAC GTGTTATCC TGCGGGGGGC CGAGGTGCTC ACCTCTCTCC 1260
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 CCGCGGAAC AAGTGTCTGA GTGGCTGGGC GGGGCGGGCA GGCACAGGGA GGAGGTACAG 1500
 50 AAGCGGCAAA CGCTTGCTAT TTATTTTACA AACTGGACTG GCTCAGGCAG GGCCACGGCT 1560
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 55 CCGCAGACAG GCTGGCAGGG CAGGTGCTGC TGGGGCCCT CTCCAGCCCG TCCTACCCCTG 1860
 GGCTCACATG GGGCCTGTGC CCACCCCTCT TGAGTGTCTT GGGGACAGCT CTTTCCACCC 1920
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 TT 1982

60 Seq ID NO: 100 DNA Sequence
 Nucleic Acid Accession #: NM_018325.1
 Coding sequence: 163..1590

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 CTGTTTAAGT ACATAGATGA AAATCAGGAT CGCTACATTA AGAACTCGC AAAATGGGTG 240
 GCTATCCAGA GTGTGTCTGC GTGGCCGGAG AAGAGAGGCG AAATCAGGAG GATGATGGAA 300
 70 GTTGTCTGTG CAGATGTTAA GCAGTTGGGG GGCTCTGTGG AACTGGTGA TATCGGAAAA 360
 CAAAAGCTCC CTGATGGCTC GGAGATCCCG CTCCCTCTTA TCTGTCTCGG CAGGCTGGGC 420
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10	GCTGTCCACG	GGTGAGCTA	CCCGTTGGGC	TTATGAGTGA	CCTGGAGTGA	CAGCTGAGTC	1800
	ACCCCTGGGA	AGTTCTCAGA	GTGGTCAGGA	TGGCTTGACC	TGCAGAAGAT	ACCCAAGGTC	1860
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	TAATCGAGCA	CTTTGGGAGG	CCAAGACAGG	AGGATCACTT	GAGGCCAGGA	GTCTGAGACA	1980
	AGCCTAGGCA	ACAAAACAAG	ACTCTGTCTC	TACAAAAAGT	TTAAGAAATG	AGCCAGACAT	2040
15	GGTGGTGAT	GCCTGTAGTC	CCAGCCACTC	AGAAGGCTGA	GGCAGGAGGA	TGCTTGAGA	2100
	CCAAGAGTTT	GAGCCTCGCG	TGAGCTGTGA	ATSCACCAAG	GCACTCAAGC	CTGGGCAATG	2160
	TAGCAAGATC	CTGTCTCTAC	AAGAAATTTT	TTAAAAATGA	GCCAAGTGCT	GTGGTGCAATG	2220
	CCTGTAGTTC	CAGCTACTCA	GGACACTGAC	GTAGGAGGGT	TGCTTGAGAC	TGAGAGTTGG	2280
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20	CATCTCAAAA	AAAAATAGTT	CTGGTTGTCA	TTGAATTTGG	ATAAACAGAG	AGCTTGATGC	2400
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	GAAAGAAATT	AGGGCTCTCT	CTGATCTCTC	GCTATCTGCG	GGTCTGTGCC	TTTTCTCAAG	2520
	ACCTTCACCA	TTACTGGCAT	TTTCTGTCT	TCTCTTTAGT	ATGATCCCTC	AAAACCTCAC	2580
25	TAACTGGAAG	GATGATTTTG	TCTCAGTTTG	TACTCCTAAA	TAAAAAGTAA	ACATGACACC	2640
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Seq ID NO: 101 DNA Sequence
Nucleic Acid Accession #: AF258592
Coding sequence: 93..1268

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	ACATAGATGA	AAATCAGGAT	CGCTACATTA	AGAAACTCGC	AAAATGGGTG	GCTATCCAGA	180
35	GTGTGTCTGC	GTGGCCGAGG	AAGAGAGCGC	AAATCAGGAG	GATGATGGAA	GTGCTGCTG	240
	CAGATGTTAA	GCAGTTGGGG	GGCTCTGTGG	AACTGGTGGA	TATCGGAAAA	CAAAAGGAGA	300
	TTCTGTGCAA	CGTCCGATTTC	TGCCCTGGAAG	GCATGGAGGA	GTCCAGCTCT	GAGGGCCTAG	360
	ACCAGCTGAT	TTTTGCCCCG	AAAGACACAT	TCTTTAAGGA	TGTGGACTAT	GTCTGCATTT	420
	CTGACATTA	CTGGCTGGGA	AAGAAGAAGC	CCTGCATCAC	CTACGCCCTC	AGGGGCATTT	480
40	GCTACTTTTT	CATCGAGGTG	GAGTGCAGCA	ACAAAGACCT	CCATTCTGGG	GTGTACGGGG	540
	GCTCGGTGCA	TGAGGCCATG	ACTGATCTCA	TTTTGCTGAT	GGGCTCTTTG	GTGGACAAGA	600
	GGGGGAACAT	CCTGATCCCC	GGCATTAAAG	AGGCCGTGGC	CGCCGTACAG	GAAGAGGAGC	660
	ACAAGCTGTA	CGACGACATC	GACTTTGACA	TAGAGGAGTT	TGCCAAGGAT	GTGGGGCGCG	720
	AGATCTTCCT	GCACAGCCAC	AAGAAAGACA	TCTCATGCA	CCGATGGCGG	TACCCGTCTC	780
45	TGTCCTCCCA	TGGCATCGAA	GGCGCTTCT	CTGGTCTGG	GGCCAAGACC	GTGATTCCCA	840
	GGAGGTGGT	TGGCAAGTTC	TCCATCAGGC	TGCTGCCGAA	CATGACTCCT	GAAGTGGTCG	900
	CCGAGCAGGT	CACAAGCTAC	CTAACTAAGA	AGTTTGCTGA	ACTACGCAGC	CCCAATGAGT	960
	TCAAGGTGTA	CATGGGCCAC	GGTGGGAAGC	CCTGGGTCTC	CGACTTCAGT	CACCCCTATT	1020
50	ACCTGGCTGG	GAGAGAGGCG	ATGAAGACAG	TTTTTGGTGT	TGAGCCAGAG	TTGACCAGGG	1080
	AAGGCGGCAG	TATTCCCGTG	ACCTTGACCT	TTCAGGAGGC	CACGGGCAAG	AACGTCAATG	1140
	TGCTGCCTGT	GGGGTCAGCG	GATGACGGAG	CCCACTCCCA	GAATGAAAAG	CTCAACAGGT	1200
	ATAACTACAT	AGAGGGAAAC	AAGATGCTGG	CCGCGTACCT	GTATGAGGTC	TCCCAGCTGA	1260
	AGGACTAGGC	CAAGCCCTCT	GTGTGCCATC	TCCAATGAGA	AGGAATCCTG	CCCTCACCTC	1320
	ACCCTTTTCT	AACCTGCCCA	GGGAAGTGGA	GGTTCCCTCT	TTCTTTCCCT	TCTTGTCAAG	1380
55	TCATCCATGA	CTTTAGAGAA	CAGACACAAG	TGTATCCAGC	TGTCACCGGG	TGGAGCTACC	1440
	CGTTGGGCTT	ATGAGTGACC	TGGAGTGACA	GCTGAGTCAC	CCTGGGTAAG	TTCTCAGAGT	1500
	GGTCAGGATG	GCTTGACCTG	CAGAAGATAC	CCAAGGTCCA	AAAGCACAAG	GTCTGCCGAA	1560
	AGTTCTGGTT	GTGCGCTGGG	CACCAACGGT	CACACCTATA	ATCGAGCACT	TTGGGAGGGC	1620
	AAGACAGGAG	GATCACTTGA	GGCCAGGAGT	CTGAGACAAG	CCTAGGCAAC	AAAACAAGAC	1680
60	TCTGTCTCTA	CAAAAAGTTT	AAGAAATGAG	CCAGACATGG	TGGTGTATGC	CTGTAGTCCC	1740
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	AGCTGTGAAT	GCACCAAGGC	ACTCAAGCCT	GGGCAATGTA	GCAAGATCCT	GTCTCTACAA	1860
	GAAATTTTTT	AAAAATGAGC	CAAGTGTGGT	GGTGATGCC	TGTAGTTCCA	GCTACTCAGG	1920
	ACACTGACGT	AGGAGGGTTG	CTTGAGACTG	AGAGTTGGAG	GCTGCGATGA	GCCATGAATG	1980
65	CCCCACTGCA	CTCCAGCTTG	GGCGACAGAA	CGAGACCCCA	TCTCAAAAAA	AATAAGTTCT	2040
	GGTTGTCAAT	GAATTTGGGAT	AAACAGAGAG	CTTGATGCTT	TCTGCTTCT	GTCTCAGGTG	2100
	ATGCAATTGCA	CATTTGGGAT	ATTGGAAAG	GAAATGAGGA	AAGAAATTAG	GGCCTCCTCT	2160
	GATCTCTCGC	TATCTGCGGG	TCCTGTCTCT	TTCTCAAGAC	CTTCACCAT	ACTGGCATTT	2220
	TCCTGTCTTC	TCTTTAGTAT	GATCCCTCAA	AACCTCACTA	ACTGGAAGGA	TGATTTTGTG	2280
70	TCAGTTTGTA	CTCCTAAATA	AAAAGTAAAC	ATGACACCTC	TAAAAAATAA	AAAAAATAA	2340
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Seq ID NO: 102 DNA Sequence
Nucleic Acid Accession #: Eos sequence

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	CAATAATTTT	CTTTTCTTTC	TTTAGGACAC	TTTCTAGAT	CTTTCCACTG	TTAAACCAAC	180
80	CATCCAGATC	TCCTAAACTC	TCTGAGAAC	TTAGAAATTA	ACTCTTTTCC	TCTTCCCTAT	240
	TTGGCTGGCG	TAATAGAGCA	GGCATGCCAT	ACTAAGCTTC	ACAGCTAGGT	GTCTCATATA	300
	TGCAATGACT	TCCTTTGGCA	GCCTAGTCAT	TGACAGCTGA	CTTTGAGTCA	AGAAAGTAAG	360
	TTTCTCTCT	CCTTTATGTT	TAATTTCTAT	TTAGGGAGAT	TCCTTATGAG	GGATACCTAT	420
	GAAGGCCACT	TTCTCTCTGC	TATGTGCTCA	GAGCTAACTC	CATATTTTCC	TGTAAGTTTA	480

TAAGTAGCTT GCAATTCAGT TAGGTGTCCA CCAATG

516

Seq ID NO: 103 DNA Sequence
Nucleic Acid Accession #: NM_018401.1
Coding sequence: 65..1309

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CGTGCAAGAG	CGAGACACTA	AGAAAATGTA	TGCAATGAAG	TACATGAACA	AGCAGAAGTG	240
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GCACCCCTTC	CTGGTCAATC	TGTGTACTC	CTTCCAGGAT	GAGGAGGACA	TGTTCATGGT	360
GGTGGACCTG	CTCCTGGGAG	GCGACCTGGG	CTACCATCTG	CAGCAGAATG	TGCATTTTAC	420
AGAGGGGACT	GTGAAACTCT	ACATCTGTGA	GCTGSCACTG	GCCCTGGAGT	ATCTTCAGAG	480
GTACCACATC	ATCCACAGAG	ACATCAAGCC	AGACAATATC	CTGCTGGATG	AACACGGACA	540
TGTTTCAATT	ACAGACTTCA	ACATAGCGAC	GCTAGTGAAA	GGAGCAGAAA	GGGCTTCTCT	600
CATGGCTGGC	ACCAAGCCCT	ACATGGCTCC	AGAAGTATTC	CAGGTGTACA	TGGACAGAGG	660
CCCGGATAC	TGCTACCTCT	TGCACTGGTG	GTCCCTGGGC	ATCACAGCCT	ATGAGCTGCT	720
GCGGGGCTGG	AGGCCGTACG	AAATCCACTC	GGTCACGCCC	ATCGATGAAA	TCCTCAACAT	780
GTTCAAGGTG	GAGCGTGTC	ACTACTCCTC	CACGTGGTGC	AAGGGGATGG	TGGCCCTGCT	840
GAGGAAGCTC	CTGAGCAAGG	ATCCTGAGAG	CGCGGTGTC	AGCCTTCATG	ACATACAGAG	900
CGTGCCCTAC	TTGGCCGACA	TGAACTGGGA	CGCGGTGTC	AAGAAGGCAC	TGATGCCCGG	960
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TCTAGAAATC	AAGCCACTTC	ACAAAAAGAA	GAAGCGATTG	GCAAGAAGAA	GATCCAGGGA	1080
TGGCACAAGG	GACAGCTGCC	CGCTGAATGG	ACACCTGCAG	CACCTGTTGG	AGACTGTCCG	1140
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GCTCTTGGAC	ACCGACAGCC	GAGGGGGAGG	CCAGGCCCAA	AGCAAGCTCC	AGGACGGGTG	1260
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GCTGGGAAGC	GTGGGTTCTG	GTCCCATCTC	CATGACTGAT	TCACGTGTGA	CCTCAGACAA	1500
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ATTCGCCAAA	GCAATCAAAC	CGTCATGACT	TTGCAATTG	GCACATCCTA	GCTTGTGTA	1740
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CTGGCAGGCC	ACAGTCTCTG	GCTTGTAAAG	TGGTGCAGCA	TGCAGACCAG	ACTTGTCCCC	1920
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AAAGTTTATT	TCAGGAGGAA	AATGGGTTC	CACAAAAGC	AAACTACATT	CTGATCTGCT	2340
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TGGAGTCAGG	TTTGTTTCA	GAATCCAGCC	CTGCTGGCTA	CTAACTAACT	GGGAGACCTT	2460
AGGCAAGACA	TGCAATCCGT	CTGAATGGCA	GTTTCTCAT	TTTTAAACAG	GGATAATAAA	2520
ACTAATATTG	CAGGGGAGTT	ACAGGGTTAA	ATAAGATCCT	GTGTGTAACC	CCAAGCATTG	2580
GATGACTCAT	AGAATGGCCT	TTTTTGTGAG	CATAATCGTC	ATCATTATTT	AGATACCTTC	2640
TTCTTCACT	CACCCAGCAG	GTCAAGTTTC	TGTGCAAAAC	AACTGTTTAA	GGATTCTTCC	2700
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ATTTTATTTT	TTTAAAAAAG	AAATAGTCAG	TGTTTCTCTC	CTTCAACCG	AGACTATTTC	2940
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CATCAACAAC	CGTCTGCTC	CCCACCTCCC	CCAGGAAATA	AGGGGCTGTC	TCCTCTCCCT	3060
ACTGTGACCC	TGGAGGCTCT	TAAGATGATG	ATGGTTTTTT	TTATGGGCT	GAGTTACAGA	3120
ATTAGGGGCA	GGAGCTGGAA	GTGCGCCTAG	GAACACCAGA	TTTCTGGT	CTGTTCAAGT	3180
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Seq ID NO: 104 DNA Sequence
Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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AGGCCGTCAG	TGTCTCTTTC	AAGGAGCTCA	TACAGAGATT	TGGGATCGCG	TACAGCGACA	240
CAGCCTGGAT	CTCCTCCATC	CTGCTGCCCA	TGCTCTACGG	GACAGGTCCG	CTCTGCAGTG	300
TGTGCGTGAA	CCGCTTTGGC	TGCGGGCCCG	TCATGCTTGT	GGGGGCTCTC	TTTGCGTGGC	360
TGGGCATGGT	GGCTGCGTCC	TTTTGCGGGA	GCATCATCCA	GGTCTACCTC	ACCACTGGGG	420
TCATCACCGG	TTTGGGTTTG	GCACTCAACT	TCCAGCCCTC	GCTCATCATG	CTGAACCGCT	480
ACTTCAGCAA	CGGGCGCCCC	ATGGCCAAAG	GGCTGGCGGC	AGCAGGTAGC	CCTGCTCTCC	540
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TCCTCATCCT	GGGCGGCGTG	CTGCTCAACT	GCTGCGGTGT	TGCGGCACCT	ATGAGGCCCC	660
TGGTGGTCAC	GGCCACGCGG	GGCTCGGGGC	CGCCGCGACC	CTCCGCGGCG	CTGCTAGAGC	720
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TGGGGCTCTT	CGTCCGCGCC	GTGTTGCTGG	TGAGCTACGC	CAAGGACCTG	GGCGTGCCCG	840
ACACCAAGGC	CGCTTCCCTC	CTCACCATCC	TGGGCTTCAT	TGACATCTTC	GCGCGGCGCG	900
CCGCGGGCTT	CGTGGCGGGG	CTTGGGAAGG	TGCGGCCCTA	CTCCGTCTAC	CTCTTCAGCT	960
TCTCCATGTT	CTTCAACGGC	CTGCGGACC	TGGCGGGCTC	TACGGCGGGC	GACTACGGCG	1020

	GCCTCGTGGT	CTTCTGCATC	TTCTTTGGCA	TCTCTACGG	CATGGTGGGG	GCCCTGCAGT	1080
	TGGAGGTGCT	CATGGCCATC	GTGGGCACCC	ACAAAGTTCTC	CAGTGCCATT	GGCCTGGTGC	1140
	TGCTGATGGA	GGCGGTGGCC	GTGCTCGTCG	GGCCCCCTTC	GGGAGGCAAA	CTCCTGGATG	1200
	CGACCCACGT	CTACATGTAC	GTGTTTCATC	TGGCGGGGCG	CGAGGTGCTC	ACCTCCTCCC	1260
5	TGATTTTGCT	GCTGGGCAAC	TTCTTCTGCA	TTAGGAAGAA	GCCCCAAGAG	CCACAGCCTG	1320
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	CCGCAGACAG	GCTGGCAGGG	CAGGTGCTGC	GTGGGGCCCT	CTCCAGCCCG	TCCTACCCCTG	1860
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	CAGCCCGGGA	GATGAAATC	CAAGAGAAAA	CAGCCCATTC	CTCAACAATG	TCGAGGTGGA	180
	ACAAGAGAGC	TTCTTTGAAG	GGAAGAACAT	GGCACTTTTC	GAGGAGGAGA	TGGACAGTAA	240
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	GGTGGAGCAC	GAGGAGGACG	AGGAGAGCCG	GCGGCGGGAG	GCCAAGGCTC	CGCGCATGGG	360
30	CACCTTCATC	GGCGTCTACC	TGCCGTGCC	GCAGAACATC	CTGGGCGTCA	TCCTCTCTCT	420
	GGCGCTGACG	TGGATCGTGG	GGGTGGCTGG	TGTCTTGGAG	TCCTTCTCTA	TCGTGGCCAT	480
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Seq ID NO: 113 DNA Sequence

Nucleic Acid Accession #: NM_002011.2

Coding sequence: 157..2565

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Seq ID NO: 116 DNA Sequence

Nucleic Acid Accession #: NM_016551.1

Coding sequence: 38..1750

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Nucleic Acid Accession #: NM_003820.1
Coding sequence: 294..1145

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Seq ID NO: 118 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 42..1070

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	CTTTAAACA	CCTATTCTCT	CCCGATGGGG	CATCGTCTA	AAGCTTTGGG	GGAGTGGGGG	1440
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Seq ID NO: 119 DNA Sequence
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Seq ID NO: 123 DNA Sequence
 Nucleic Acid Accession #: Eos sequence

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	GTATGAATTC	CAGGTGGGCC	CAATGGGGGA	GGGGCTGGTG	GGCCTGGGGA	CCCTGGTCCT	2520
30	AGGTCTGGAG	TGGCCCTACG	AAGTCAGCAA	TGGCAAGTGG	CTGCTGTATC	CCACGGAGAT	2580
	CACGTCTCAT	GAGCAATGGGT	CCTGGCCCTG	CCGACCACTT	GGAGACCTTA	TCAACCTCT	2640
	CAACCTCACT	CTTCTGACCC	CTGGGGACAG	GCCATCATCC	CCACAGGCGA	GGGCGGACCA	2700
	GCTGGATCCA	GGGGGAGGCC	AGGGCCCCCC	ACCTGTCACT	CTGGCTGCTG	CCAAAAAAGC	2760
	CAAGTCTGAG	ACTGTGCTGA	CCTGTGCCAC	AGGGCGTGCC	CACGTGTGTG	GGCTAGAGTG	2820
35	CCCCATCCCT	GATGCCCCCG	TTGTCAACAA	CGTGACTGTG	AAGGCACGAG	TGTGGAACAG	2880
	CACCTTCATC	GAGGATTACA	GAGACTTTGA	CCGAGTCCGG	GTAATGGCTG	GGGCTACCTT	2940
	ATTCTCTCGA	ACCAGCATCC	CCACCATCAA	CATGGAGAA	AAGACCACTG	GGTTCTCTGT	3000
	GGACATTGAC	TCCGAGCTGG	TGGAGGAGCT	GCCGGCCGAA	ATCGAGCTGT	GGCTGGTGCT	3060
	GGTGGCCGTG	GGTGACGGGC	TGCTGCTGCT	GGGGCTGATC	ATCCTCTGTC	TGTGGAAGTG	3120
40	TGACTTCTTT	AAGCGGACCC	GCTATTATCA	GATCATGCCC	AAGTACCAAG	CAGTGCGGAT	3180
	CCGGGAGGAG	GAGCGCTACC	CACCTCCAGG	GAGCACCTTG	CCCACCAAGA	AGCACTGGGT	3240
	GACCACTGGG	CAGACTCGGG	ACCAATACTA	CTGACGTCTT	CCCTGATCCC	ACCCCTCTCT	3300
	CCCCAGTGTG	CCCCCTTCTT	CCTATTATAT	ATAAGTTATG	CCTCTGACAG	TCCACAGGGG	3360
	CCACCACCTT	TGGCTGGTAG	CAGCAGGCTC	AGGCACATAC	ACCTCGTCAA	GAGCATGCAC	3420
45	ATGCTGTCTG	GCCTCTGGGA	TCTTCCACAA	GGAGGGCCAG	CGCTGTGGAC	CTTACAACGC	3480
	CGAGTGCACT	GCATTCTCTG	GCCCTAGATG	CACGTGGGGC	CCACTGTCTG	TGGACTGTGC	3540
	TGGTGTCATC	CGGATGGTGT	ATGGGCTCGC	CGTGTCTCAG	CCTCTGCCAG	CGCCAGCGCC	3600
	AAACAAGACC	AAAGAGCTTC	CCACCAAGAG	CGGGAGGAAA	AGGCCCTCGT	AATGTGGTGA	3660
	CACCTCCCCCT	TTACACCTTG	GATCCATCTT	GAGAGCCACA	GTCACCTGGT	TGACTTTGCT	3720
50	GTCAAAACTA	CTGACAGGGA	GCAGCCCCCG	GGCCGCTGGC	TGGTGGGCCC	CCAATTGACA	3780
	CCCATGCCAG	AGAGGTGGGG	ATCCTGCTTA	AGGTTGTCTA	CGGGGGCACT	TGGAGGACCT	3840
	GGCGTGCTCA	GACCAACAGC	CAAAAGAACT	AGAAAGAAAG	ACCCAGAAAG	CTTGCTTTCC	3900
	TGCATCTCTG	TGAAGCTCTT	CTCCTTGSCC	ACAGACTGAA	CTCGCAGGGA	GTGCAGCAGG	3960
	AAGGAACAAA	GACAGGCAAA	CGGCAACGTA	GCCTGGGCTC	ACTGTGCTGG	GGCATGGCGG	4020
55	GATCTCTCAC	AGAGAGGAGG	GGACCAATTC	TGGACAGACA	GATGTTGGGA	GGATACAGAG	4080
	GAGATGCCAC	TTCTCACTCA	CCACTACCA	CCAGCCTCCA	GAAAGGCCCA	GAGAGACCTT	4140
	GCAAGACCAA	GGAGGGAGCC	GACACTTGAA	TGTAGTAATA	GGCAGGGGGC	CCTGCCACCC	4200
	CATCCAGCCA	GACCCAGCT	GAACCATGCG	TCAGGGGCCCT	AGAGGTGGAG	TTCTTAGCTA	4260
	TCCTTGCTTT	TCTGTGCCAG	CCTGGCTCTG	CCCCCTCCCC	ATGGGCTGTG	TCCTAAGGCC	4320
	CATTTGAGAA	GCTGAGGCTA	GTTCCAAAAA	CCTCTCTCTG	CCCCTGCTGT	TTGGCAGCCC	4380
60	ACTCCCGAGC	CCACAGCCCC	TCCATGGTAC	TGTAGCAGGG	GAATTCCCTT	CCCCCTCTTG	4440
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Seq ID NO: 126 DNA Sequence

Nucleic Acid Accession #: NM_003786

Coding sequence: 71..4654

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70	CCTCGGCCCC	ATGGACGCCC	TGTGCGGTTT	CGGGGAGCTC	GGCTCCAAAGT	TCTGGGACTC	120
	CAACTGTGCT	GTGCACACAG	AAAACCCGGA	CCTCACTCCC	TGCTTCCAGA	ACTCCCTGCT	180
	GGCTGGGTG	CCCTGCATCT	ACCTGTGGGT	CGCCTGCCCC	TGCTACTTGC	TCTACTTGCG	240
	GCACCATTTG	CGTGGCTACA	TCATCTCTCT	CCACCTGTCC	AAGCTCAAGA	TGGTCTCTGG	300
	TGTCCTGTCT	TGCTGCTGCT	CCTGGGCGGA	CTTTTCTTAC	TCCTTCCATG	GCCTGGTCCA	360
75	TGGCGGGGCC	CCTGCCCTTG	TTTTCTTTGT	CACCCCTTGG	GTGGTGGGGG	TCACCATGCT	420
	GCTGGCCACC	CTGCTGATAC	AGTATGAGCG	GCTGCAGGGC	GTACAGTCTT	CGGGGGTCTT	480
	CATTATCTTC	TGGTTCCTGT	GTGTGGTCTG	CGCCATCGTC	CCAATTCGGT	CCAAGATCCT	540
	TTTAGCCCAAG	GCAGAGGGTG	AGATCTCAGA	CCCCCTCCCG	TTCAACACCT	TCTACATCCA	600
	CTTTGCCCTG	GTACTCTCTG	CCCTCATCTT	GGCCTGCTTC	AGGGAGAAAC	CTCCATTTTT	660
80	CTCCGCAAA	AATGTGAGCC	CTAACCCCTA	CCCTGAGACC	AGCGCTGGCT	TTCTCTCCCG	720
	CCTGTTTTTG	TGGTGGTTCA	CAAAGATGGC	CATCTATGGC	TACCGGCATC	CCCTGGAGGA	780
	GAAGGACCTC	TGGTCCCTAA	AGGAAGAGGA	CAGATCCAG	ATGGTGGTGC	AGCAGCTGCT	840
	GGAGGCATGG	AGGAAGCAGG	AAAAGCAGAC	GGCAGCAGAC	AAGGCTTCAG	CAGCACCTGG	900
	GAATAATGCC	TCCGGCGAGG	ACGAGGTGCT	GCTGGGTGCC	CGGCCAGGCG	CCCGGAAGCC	960
	CTCCTTCTCT	AAGGCCCTGC	TGGCCACCTT	CGGCTCCAGC	TTCTCATCA	GTGCTGCTTT	1020

5	CAAGCTTATC CAGGACCTGC TCTCCTTCAT CAATCCACAG CTGCTCAGCA TCCTGATCAG 1080
	GTTTATCTCC AACCCCATGG CCCCCTCTCG GTGGGGCTTC CTGGTGGCTG GGCTGATGTT 1140
	CCTGTGCTCC ATGATGCACT GCCTGATCTT ACAACACTAT TACCACTACA TCTTTGTGAC 1200
	TGGGGTGAAG TTTCGTACTG GGATCATGGG TGTCTCTAC AGGAAGGCTC TGGTTATCAC 1260
	CAACTCAGTC AAACTGCGGT CCACTGTGGG GGAAATTGTC AACCTCATGT CAGTGGATGC 1320
	CCAGCGCTTC ATGGACCTTG CCCCCTTCTT CAATCTGCTG TGGTCAGCAC CCCTGCAGAT 1380
	CATCCTGGCG ATCTACTTCC TCTGGCAGAA CCTAGGTCCC TCTGCTCTGG CTGGAGTGGC 1440
	TTTCATGGTC TTGCTGATTC CACTCAACGG AGCTGTGGCC GTGAAGATGC GCGCCTTCCA 1500
	GGTAAAGCAA ATGAAATTGA AGGACTCGCG CATCAAGCTG ATGAGTGAGA TCCTGAACGG 1560
10	CATCAAGGTG CTGAAGCTGT ACGCCTGGGA GCCCAGCTTC CTGAAGCAGG TGGAGGGCAT 1620
	CAGGCAGGGT GAGCTCCAGC TGTGTGGCAC GCGCGCTTAC CTCCACCA CAACCACTT 1680
	CACCTGGATG TGCAGCCCTT TCTGTGTGAC CCTGATCACC CTCTGGGTGT ACGTGTACGT 1740
	GGACCCAAAC AATGTGTGGG ACGCCGAGAA GGCCTTTGTG TCTGTCTCCT TGTTTAAATAT 1800
	CTTAAGACTT CCCCTCAACA TATTCCTGAG CCAAGAGGAA CTTGACCCCC AGAGTGTGGA 1860
15	GTCTCTGAAA CGGATCCAGC AATTCTCTGAG CCAAGAGGAA CTTGACCCCC AGAGTGTGGA 1920
	AAGAAAGACC ATCTCCCCAG GCTATGCCAT CACCATACAC AGTGGCACCCT TCACCTGGGC 1980
	CCAGGACCTG CCCCCTCTTC TGACAGCCCT AGACATCCAG GTCCCGAAAG GGGCAGTGGT 2040
	GGCGCTGGTG GCGCCTGTGG GCTGTGGGAA GTCTCCCTG GTGTCTGCCC TGCTGGGAGA 2100
	GATGGAGAAG CTAGAAGGCA AAGTGACAT GAAGGGCTCC GTGGCCTATG TGCCCCAGCA 2160
20	GGCATGGATC CAGAACTGCA CTCTTCAGGA AAACGTGCTT TTCCGCAAG CCCTGAACCC 2220
	CAAGCGCTAC CAGCAGACTC TGGAGGCTGT TGCTTGTCTA GCTGACCTGG AGATGTCTGC 2280
	TGGTGGGATG CAGACAGAGA TTGGAGAGAA GGGCATTAACT CTGTCTGGGG GCCAGCGGA 2340
	GCGGCTCAGT CTGGCTCGAG CTGTTTACAG TGATGCGCAT ATTTTCTTGC TGGATGACCC 2400
	ACTGTCCGGG GTGAGCTCTC ATGTGGCCAA GCACATCTTT GAACCACTCA TCGGGCCAGA 2460
25	AGGCGTGTCT GCGAGCAAGA CCGAGTGTCT GGTGACCCAC GGCATTAGCT TCCTGCCCA 2520
	GACAGACTTC ATCATTTGTC TAGCTGATGG ACAGGTGTCT GAGATGGGCG CGTACCCAGC 2580
	CCTGCTGAGC GCGAACGGCT CCTTTGCCAA CTCTCTCTGC AACTATGCCC CGATGAGGA 2640
	CCAAGGGCAC CTGGAGGACA GCTGGACCCG GTTGAAGGT GCAGAGGATA AGGAGGCACT 2700
	GCTGATTGAA GACACTCA GCAACCAAC GATCTGACA GACAATGATC CAGTCACTA 2760
30	TGTGGTCCAG AAGCAGTTTA TGAGACAGCT GAGTGCCTG TCCTCAGATG GGGAGGGACA 2820
	GGGTGGGCTT GTACCCCGGA GGCACCTGGG TCCATCAGAG AAGGTGCAGG TGACAGAGGC 2880
	GAAGGCAGAT GGGGCACTGA CCCAGGAGGA GAAAGCAGCC ATTGGCACTG TGGAGCTCAG 2940
	TGTGTTCTGG GATTATGCCA AGGCGGTGGG GCTCTGTACC ACGCTGGCCA TCTGTCTCCT 3000
	GTATGTGGGT CAAAGTCCGG CTGCCATTGG AGCCAATGTG TGGCTCAGTG CCTGGCAAAA 3060
35	TGATGCCATG GCAGACAGTA GACAGAACAA CACTTCCCTG AGGCTGGGCG TCTATGCTGC 3120
	TTTAGGAATT CTGCAAGGGT TCTTGGTGAT GCTGGCAGCC ATGGCCATGG CAGCGGGTGG 3180
	CATCCAGGCT GCCCGTGTGT TGCACCAAGC ACTGCTGCAC AACAAGATAC GCTGCCACA 3240
	GTCCCTCTTT GACACACAC CATCAGGCCG CATCCTGAAC TGCTTCTCCA AGGACATCTA 3300
40	TGTGTTGAT GAGGTTCTGG CCCCCTGTCT CACTATGCTG CTCAATTCTT TCTTCAACGC 3360
	CATCTCCACT CTGTGGTCA TCATGGCCAG CACGCGCTC TTCACTGTGG TCATCTGCC 3420
	CCTGGCTGTG CTCTACACCT TAGTGACGCG CTCTATGCA GCCACATCAC GGCAACTGAA 3480
	GCGGCTGGAA TCAGTCAGCC GCTCACCTAT CTACTCCAC TTTTCGGAGA CAGTACTGG 3540
	TGCCAGTGTG ATCCGGGCTT ACAACCGCAG CCGGGATTTT GAGATCATCA GTGATACTAA 3600
45	GGTGGATGCC AACCAGAGAA GCTGCTACCC CTACATCATC TCCAACCGGT GGCTGAGCAT 3660
	CGGAGTGGAG TTCGTGGGGA ACTGCGTGGT GCTCTTTGCT GCACTATTG CCGTCATCGG 3720
	GAGGAGCAGC CTGAACCCGG GGCTGGTGGG CCTTCTGTG TCCTACTCCT TGCAGGTGAG 3780
50	ATTTGCTCTG AACTGGATGA TACGAATGAT GTCAGATTG GAATCTAACA TCGTGGCTGT 3840
	GGAGAGGCTC AAGGAGTACT CCAAGACAGA GACAGAGGCG CCCTGGGTGG TGGAAAGCAG 3900
	CCGCCCTCCC GAAGGTTGGC CCCCACGTGG GGAGGTGGAG TTCCGGAATT ATTCTGTGCG 3960
	CTACCGGCGG GGCCTAGACC TGGTGCTGAG AGACCTGAGT CTGCATGTGC ACGGTGGCGA 4020
	GAAGGTGGGG ATCGTGGGCG GCACTGGGCG TGGCAAGTCT TCCATGACCC TTTGCCCTGT 4080
	CGCATCTCTG GAGGCGGCAA AGGGTGAAT CCGCATTTGAT GGCCTCAATG TGGCAGACAT 4140
	CGGCTCCAT GACTCGGCT CTGAGCTGAC CATCATCCCG CAGGACCCCA TCCTGTTCTC 4200
55	GGGAGCCCTG CGCATGAACC TGGACCCCTT CGGAGCTAC TCAGAGGAGG ACATTGGTGG 4260
	GGCTTTGGAG TGTGCCACC TGACACAGTT TGTGAGCTCC CAGCGGCGAG GCTGGACTT 4320
	CCAGTGCTCA GAGGGCGGGG AGAATCTCAG CGTGGGCCAG AGGCAGCTCG TGTGCCCTGG 4380
	CCGAGCCCTG CTCGCAAGA GCGCATCCT GGTTTTAGAG GAGGCCACAG CTGCCATCGA 4440
	CCTGGAGACT GACAACCTCA TCCAGGCTAC CATCCGACCC CAGTTTGATA CCTGCACTGT 4500
	CCTGACCATC GCACACCGGC TTAACACTAT CATGGAATAC ACCAGGGTCC TGGTCTGGA 4560
60	CAAAGGAGTA GTAGCTGAAT TTGATTCTCC AGCCAACCTC ATTGCAGCTA GAGGCATCTT 4620
	CTACGGGATG GCCAGAGATG CTGGACTTGC CTAAATATA TTCTGAGAT TTCTCTCTGG 4680
	CCTTCTCTGG TTTTCATCAG GAAGGAAATG ACACCAATA TGTCCGCAGA ATGGACTTGA 4740
	TAGCAACAC TGGGGGCACC TTAAGATTTT GCACCTGTAA AGTGCCTTAC AGGGTAACTG 4800
65	TGCTGAATGC TTTAGATGAG GAAATGATCC CCAAGTGGTG AATGACACGC CTAAGGTAC 4860
	AGCTAGTTTG AGCCAGTTAG ACTAGTCCCC CGGTCTCCCG ATTCCCACT GAGTGTATT 4920
	TGCACACTGC ACTGTTTCA AATAACGATT TTATGAAATG ACCTCTGTCC TCCCTCTGAT 4980
	TTTTCATATT TTCTAAAGT TTGTTTCTG TTTTAAATA AAAAGCTTTT TCCTCTGGA 5040
	ACAGAGACA GCTGCTGGGT CAGGCCACCC CTAGGAACCT AGTCTGTAC TCTGGGTGC 5100
70	TGCTGAATC CATTAAAAAT GGGAGTACTG ATGAAATAAA ACTACATGTT CAACAGTAAA 5160
	AAAAAAAAA AAAAAA 5176

Seq ID NO: 127 DNA Sequence
Nucleic Acid Accession #: NM_002701.1
Coding sequence: 102..899

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	TCCTTGGGGC	CACACGTAGG	TTCTTGAATC	CCGAATGGAA	AGGGGAGATT	GATAACTGGT	180
80	GTTTATATGT	TCTTACAAGT	CTTCTGCCCT	TTAAATCCCA	GTCCAGGAC	ATCAAAGCTC	240
	TGCAGAAAGA	ACTCGAGCAA	TTTGCCAAGC	TCCTGAAGCA	GAAGAGGATC	ACCCTGGGAT	300
	ATACACAGGC	CGATGTGGGG	CTCACCCCTG	GGGTTCTATT	TGGGAAGGTA	TTACGCCAAA	360
	CGACCATCTG	CGCTTTTGG	GCTCTGCAGC	TTAGCTTCAA	GAACATGTGT	AAGCTGCGG	420
	CCTTGCTGCA	GAAGTGGGTG	GAGGAAGCTG	ACAACAATGA	AAATCTTCAG	GAGATATGCA	480

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GCCAGAAGGG CAAGCGATCA AGCAGCGACT ATGCACAACG AGAGGATTTT GAGGCTGCTG 720
GGTCTCCTTT CTGAGGGGGA CCAGTGTCTT TTCTCTGGC CCCAGGGCCC CATTTTGGTG 780
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GAACACAAAG GGTGGGGCCA GGGGAGTTTG GGGCACTGG TTGGAGGGAA GGTGAAGTTC 1080
AATGATGCTC TTGATTTTAA TCCACATCA TGTATCACTT TTTTCTTAAA TAAAGAAGCT 1140
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Seq ID NO: 128 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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AAATAAGTAT ATCTGTCAAA AATCATATTT TTATGAGATG TGTCATACT GGTCTCGTGT 60
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AGAAACCAAG TGAATGAAG GAAATATGT AACATTAGGC ATTGATGGAA GAGGACTAGA 240
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TCAGACTTCC TATGATAAAT TAAATGTGCC AGTACCAGAG ACTCCAGGAA AAACCAAGAA 360
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GTAGCAAAAA TAAGAGTGAG AACTCCCACT AATAAAAAAGT GAGAGTCTCA AAGGGGGAAA 1620
ATGAGGAAAG AGAGCGACCC TCTCATATTG TCTATATTG TTTTATACTC AGTACCTGTT 1680
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TGTTCTGTTT CTCTCTGACT GCCCGTGCA TCGAGCCCTG TCACGTACCG CCTGCTTGCT 1920
CAAAATCAATC ACGACCTTTT CATGTGAAAT GTTTAGTGTG GTGAGCCCTT AAAAGGGACA 1980
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AATAAGCCCT TCCTTCTAC AAAAAAAA 2068

Seq ID NO: 129 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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Seq ID NO: 130 DNA Sequence

Nucleic Acid Accession #: NM_005458.1

Coding sequence: 461..3286

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ACGCGGCCCC CCTTCTCCGC GTTGTCTGCG TTGCTCCCG CCTCCGCGAC TCCGCTCGCT 240
CCCACCCCTT CCGCGCGTGA TTGATCCGTC ACGGCGCGCG CCGCTGCGCG CCGCGCGCGC 300
GCGGCGGTTT TGAGCCGAGC CGGAACCTTA GCCCGAGACG GAGCGCGGCG CCGGCGCGCG 360
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	CGGGCGCGG	CCGAGCAGC	CGCGCTCTC	CATCATGGG	CTCATGGCG	TCACCAAGGA	660
5	GGTGGCCAAG	GGCAGCATCG	GGCGCGGTG	GCTCCCGCC	GTGGAATCG	CCATCGAGCA	720
	GATCGCAAC	GAGTCACTCC	TGCGCCCTA	CTTCTCGAC	ATAAAATACG	GGCTTAACCA	780
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	CTTGATGGTG	TTTGGAGGG	TCTGTCCATC	CGTCACATCC	ATCATGTGAG	AGTCCCTCCA	900
	AGGCTGGAAT	CTGGTGCAGC	TTTCTTTTGC	TGCAACCAAG	CCTGTCTAG	CCGATAAGAA	960
10	AAAAATACCT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	GCGGTGAATC	CAGCCATTCT	1020
	GAAGTTGCTC	AAGCACTACC	AGTGAAGCG	CGTGGGCAG	CTGACGCAAG	ACGTTCAAGG	1080
	GTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	GGCGAGGACA	TTGAGATTTT	1140
	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCACTGTC	AAAAAGCTGA	AGGGGAATGA	1200
	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	GCAAAAGTGT	TCTGTTGTGC	1260
15	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCAGTGGATC	ATTCGGGCTG	GGTACGAGCC	1320
	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAACTCATCC	GGATTTGAG	CCCTGAGCT	1380
	GCTTGTCTGC	ATGGAGGGCT	ACATTGGCGT	GGATTTGAG	CCCTGAGCT	CCAAGCAGAT	1440
	CAAGACCATC	TCAGAAAGA	CTCCACAGCA	GTATGAGAGA	GAGTACAACA	ACAAGCGGTC	1500
	AGGCGTGGG	CCGACCAAGT	TCCACGGGTA	CGCTACGAT	GGCATCTGGG	TCAATGCCAA	1560
20	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	CGGCACGAG	GGATCCAGGA	1620
	CTTCAACTAC	ACGACACACA	CGCTGGGCG	GATCATCTCT	AATGCCATGA	ACGAGACCAA	1680
	CTTCTTGGG	GTACGCGGTC	AAGTTGTATT	CCGGAATGGG	GAGAGAATGG	GGACCATTA	1740
	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	GAGTACAACG	CTGTGGCCGA	1800
	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	TCCGAACCAA	CAAAAGACAA	1860
25	GACCATCATC	TGGAGCAGC	TGCGGAAGAT	CTCCCTACTT	CTCTACAGCA	TCCTCTCTGC	1920
	CCTCACCATC	CTCGGGATGA	TCATGGCCAG	TGCTTTTCTC	TTCTTCAACA	TCAAGAACCG	1980
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75	ACGCTTTTGT	TACATTGCAT	TTGCTTTTAT	TAAAATACAA	AATTAACAAA	ACAAAAAAC	3360
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	TTCTAGTTTT	AGACTTTAGT	TTGTTTTTTT	TTTTTCACTA	AAATCTTAAA	ACTTACTCAG	3480
	CTGGTTGCCA	ATAAGGGGAG	TTTTCATATC	ACCAATTGTT	AGCAAAATTG	AATTTTTTCA	3540
	TAAACTAGAA	TGTTAGACAC	ATTTTGGTCT	TAATCCATGT	ACACTTTTTT	ATTTCTGTAT	3600
80	TTTTCCACTT	CACGTGAAAA	ATAGTATGTG	TACATAATGT	TTTATTGGCA	TAGTCTATGG	3660
	AGAAGTGCAG	AAACTTCAGA	ACATGTGTAT	GTATTATTG	GACTATGGAT	TCAGGTTTTT	3720
	TGCATGTTTA	TATCTTTCGT	TATGGATAAA	GTATTTACAA	AACAGTGACA	TTTGATTCAA	3780
	TTGTTGAGCT	GTAGTTAGAA	TACTCAATTT	TTAATTTTTT	TAATTTTTTT	ATTTTTTATT	3840
	TTCTTTTTGG	TTTGGGGAGG	GAGAAAAAGT	CTTAGACAAA	ATGTTTTTCA	TAATTTGTAC	3900
	CAAAAAAATA	AAAAAGGAAA	GGAAAGAAA	GGGTGGCCTG	ACACTGGTGG	CACTACTAAG	3960
	TGTTGTTTTT	TTAAAAAATA	AAATGAAAAA	AAAAAGCTT	TTAACTGGA	GAGACTTCTG	4020

ACAACAGCTT TGCCTCTGTA TTGTGTACCA GAATATAAAT GATACACCTC TGACCCACAGC 4080
 GTTCTGAATA AAATGCTAAT TTTGGAAAAA AAAAAAAAAA AA 4122

Seq ID NO: 133 DNA Sequence
 Nucleic Acid Accession #: NM_016941.1
 Coding sequence: 8..1864

1 11 21 31 41 51
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 10 GAAGGCCATG GTCTCCCCAC GGATGTCCGG GCTCCTCTCC CAGACTGTGA TCCTAGCGCT 60
 CATTTTCCTC CCCGAGACAC GGCCCGCTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG 120
 GCGGGTCCA GGCCTTGGGG CCCCGGGTCC CCCTGCAGC GCCCGGCTCC CCTGCCGCTC 180
 CTTCTTCAGA GTCTGCCTGA AGCCTGGGCT CTCAGAGGAG GCCGCCGAGT CCCCGTGGGC 240
 CCTGGGCGCG GCGCTGAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300
 15 GCGTGATCTC CCACTGCCCG ACGGGCTCTT GCAGGTGCCC TTCGGGAGC CCTGGCTGG 360
 CACCTTCTCT TTCTATCATG AAACCTGGAG AGAGGAGTTA GGAGACCAGA TTGAGGGGCC 420
 CGCTCTGAGC CTGCTGGCCG GGTGGCTGG CAGCGGGCGC TTGGCAGCG GAGGCCGCTG 480
 GGCCCGGGAC ATTACGCGCG CAGGCGCCTG GGAGCTGCGC TTCTCGTACC GCGCGCGCTG 540
 CGAGCGGCTC GCGTGGGGA CCGCGTGCAC GCGCTCTGCG CGTCCGCGCA GCGCCCCCTC 600
 GCGGTGCGGT CCGGACTGCG GCCCTGCGC ACCGCTCGAG GACGAATGTG AGGCGCCGCT 660
 20 GGTGTGCGGA GCAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCGG 720
 ATGCTAGAGG GGCCTGACTG GACCCTCTG CACGGTCCCT GTCTCCACCA GCAGCTGCCT 780
 CAGCCCCAGG GCGCCGTCTC CTGCTACCAC CGGATGCCCT GTCCCTGGGC CTGGGCCCTG 840
 TGACGGGAAC CCGTGTGGCA ATGGAGGCAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900
 25 CACTGCCCG CCGGGACTCT ACGGGCTGCG GTGTAGGGTG AGCGGGGTGA CATGTGCAGA 960
 TGGACCTCTG TTCAAGCGCG GCTTGTGTGT CGGGGGTGCA GACCCTGACT CTGCTACAT 1020
 CTGCCACTGC CCACCTGGTT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGGTCAG 1080
 CCTGCAGCCA TGCCGCAATG GCGGACTCTG CCTGGACCTG GGCACGCCCC TGCGCTGCCG 1140
 CTGCGCGCGC GGCTTGGCGG GTCTCTGCTG CGAGCAGCAC CTGGAGGACT GCGCGGGCGG 1200
 30 CGCTCTCGCT AACGGCGGCA CGTGTGTGGA GGGCGGCGCG GCGCACCGCT GCTCCTGCGC 1260
 GCTGGGCTTC GGGCGCGCGG ACTGCCGCGA GCGCGCGGAC CCGTGGCGCG GCGCGCCCTG 1320
 TGCTCACGGC GCGCGCTGCT ACGCCACTT CTCCGGCTC GTCTGCGCTT GCGCTCCCGG 1380
 CTACATGGGA GCGCGGTGTG AGTTCCTCAGT GCACCCCGAC GGCAGCAAGC CCTTGCCTGC 1440
 GGGCCGCGCG GGCTCTCAGC CCGGGGACCC TCAGCGCTAC CTTTTCCTC CCGCTCTGGG 1500
 35 ACTGCTCGTG GCGCGGGCGG TGGCGGCGCG TGCGCTCTTG CTGGTCCAGC TGCGCGCGCG 1560
 TGGCACTCC CAGGATGCTG GGTCTCGCTT GCTGGCTGGG ACCCGGAGC GGTCACTGCA 1620
 CGCACTCCCG GATGCACTCA ACAACCTAAG GACGAGAGAG GGTTCGGGG ATGGTCCGAG 1680
 CTGTCCTGTA GATTGGAATC GCCCTGAAGA TGTAAGCCCT CAAGGGATTG ATGTCATATC 1740
 TGCTCTCTCC ATCTACGCTG GGGAGGTAGC GACGCCCTT TCCCCCGCG TACACACTGG 1800
 40 GCGCGCTGGG CAGAGGCAAC ACTGCTTTT TCCCTACCTT TCCTCGATTG TGTCCGTGAA 1860
 ATGAATTGGG TAGAGTCTCT GGAAGGTTT AAGCCCATTT TCAGTTCTAA CTTACTTTCA 1920

Seq ID NO: 134 DNA Sequence
 Nucleic Acid Accession #: FGENESH prediction
 Coding sequence: 1..411

1 11 21 31 41 51
 | | | | |
 45 ATGTGTCAGG CTTTCTCTG GGTGCTAGGG AACTGTGGC TTCTCAAAAA TGCCCGTTGT 60
 CTGCAGCCAT ACCCACTGTA ACATGCCCAA TCTTGCTGTA TCTCAGAAGC TAAAGCAGGT 120
 CAGGCCCACT TACCCTTGG ATGGGTGAAG TGGCCCTTGC ACTTGAGGAG CTCACTGTCC 180
 50 AAAAGGTTGG AAAGGAAGTA CCCAGCCTA TTGAATGGGG AAATTGAAGC ACAGATATGT 240
 AAAACATCTT CTCTAGAGTT ACCCAGCTGT GATCTGGTGA CAGCTGATGG TTCCACTGAA 300
 GTAACATCT CGGAAATCT CCCTGCTGTT GGATTCCATA TCTGTCAACA GCAGGACTCT 360
 CATGTAGAAG GCATGGTTAA CATCTCCAAA GCCTCTTCTG GCCAAATGTA G 411

Seq ID NO: 135 DNA Sequence
 Nucleic Acid Accession #: NM_024812.1
 Coding sequence: 184..621

1 11 21 31 41 51
 | | | | |
 60 GAGAGGGCCC GGACTAGGGG CGGCGGGCAC CGCAGGAGCT CGCGCGGCT GCAGCGCGGG 60
 CGGAGCGGGG GACGCGATGT GCGCGCGCGC GCCTCTCTGC GGGCGGGGGC TGCGCTCCG 120
 GGGCTGAGCC GCGCGCAGAG CCGACAGCCG AGCAGCGGCT GGGCGCTCCC GCGCGCAGG 180
 AGGATGGGCT GCGCGGGGAG CCGGGCGGAT GCCATCGAGC CCCGCTACTA CGAGAGCTGG 240
 65 ACCCGGGAGA CAGAATCCAC CTGGCTCACC TACCCGACT CGGACGCGCC GCCCAGCGCC 300
 GCGCGCCCGG ACAGCGGCCC CGAAGCGGGC GGCCTGCACT CGGCGATGCT GGAAGATGGA 360
 CTGCCCTCCA ATGGTGTGCC CCGATCTACA GCGCCAGGTG GAATACCCAA CCCAGAGAAG 420
 AAGACGAAGT GTGAGACCCA GTGCCCAAAT CCCCAGAGCC TCAGCTCAGG CCCTCTGACC 480
 CAGAAACAGA ATGGCCTTCA GACCACAGAG GCTAAAAGAG ATGCTAAGAG AATGCCTGCA 540
 70 AAAGAAGTGA CCATTAATGT AACAGATAGC ATCCAACAGA TGGACAGAAG TCGAAGAATC 600
 ACAAGAAGT GTGTCAACTA GCAGAGAGTC CAAGCAGAAG GGCAGATGGA CTTCTTCAGT 660
 GTCCTTCACG GCACTGGATC CCATCAAAGA ACCTTGAAGA AGTGGCTGCC CCTTGTCTGA 720
 CCTGAATTCT ACTGAGTCCC TGGCAAGACC GTCTTACCTG GCAGCAAACT GCTGCTGAT 780
 TTGTGGGAC CTTCTGAGCC TTCTACTTAT CATGTAAATG TATTGGCACA GTGCTTACAT 840
 75 ATGTTAATAA ACTGCAATG TGCACTTCTG TGTGCTCTT TGCAACTCCT GTAATACGGT 900
 CTGGTGTAAA AGTAGTGAGT TAAAGCTACA GGTGAGTTTA TGAACAGAA AAGTAGGAAT 960
 GCATTTTCTG GGTGAAAGAG TCACACCTTA GTGCTATAAC TCTCCTGCCC ATGATAGTGT 1020
 ATTCTGTTTC AGGCAAGCTT ATTCTTTCCT TCCTTCATT TAAATATTGT CATTACAAAT 1080
 CTTACCAAGT TCACTTAAAA GCTGGCTTTC ATCCAACCTT AAACCCACAT ATTGAAAAAA 1140
 80 TCAAGGTACA CGAAACTCC TTGTTATCCT TGTTCCTTA GCTTGGTATG AGACAGATCG 1200
 GATCCAGTTT CCCATGCACC AACCCACTGC CCATGGCATG TCTTTGGGAG GTGCTGTGTA 1260
 AGCAGTCATA CCTGCTCCTC ATCTGCTCTG AAGTCTCTCC TATTCCAGTG TCCATGTTGG 1320
 CCTCCAGTCT TTAATGTCAAC CATGCTTGTG GCAATGCAAT CCAATAAAGG ATACCCCTCA 1380
 GGGCTCAGCT AGACATTGCA ATTTTGATA GCTTCCAGT TCCCTTTGCT TGTCTCTGT 1440
 ACTGCTTCTC CTCTCTACCG GGTCACTTGT CAATTGTATA TCAAGATTG AACACTGCGT 1500

	AGGAGAGGGA	GATGATCCAG	AGACATGTGG	CAGCAGGCAT	GGCTTCCCCT	TGGCCTCTCT	1560
	GTACACTGCC	CCAGGACTGT	CATTTGGCA	TCTGCAAGG	AATCACTTTA	GAAAGCCAGC	1620
	ACCTGGTTGA	TGTGTATTCA	TACTGACATT	AGATTGATGT	GCACCTGCATT	AGAAATGAGG	1680
	TAGCTGACAC	AGAAAAAGGA	TGTTTTGATA	GGAATAATTT	TCTAGTATGT	CTTGAAACAT	1740
5	GTTCATCTGG	AAGTATTTTC	TCCAAAGTA	ATGTAGCATG	ATTTTTCAG	GATTGTAAAC	1800
	ATGCGTGGGA	TTGGGAAAGA	TAGGACTAAA	GTGTGCCAA	ACTATATCAA	TAAATTCCAT	1860
	GTTTAGCAGA	AATAGGCAGC	CTATTGGTGT	TATGTTTATG	TAACATAGTC	CAGAGAACTG	1920
	ACATGCAGGT	CAAAAGTCAG	ATACGCAACC	TCCTTATCTG	CTAACTCTGT	TATTTCTCAA	1980
	ACACAAGTGG	GTAGTGTCTAT	TTTTCTTCC	TTCTTCCAT	TGGCAGATTG	TATATTTATT	2040
10	CACAAAACAT	TAAATGTCCA	TCTGTGCCA	GSTACTATGC	AGATGTTGAG	GGATTGGGG	2100
	TCTGGTTAGT	CGTGACTATC	TATCCTGAAT	CTAACAGTGA	CTTCATAACT	AGGAGACTGA	2160
	ATTAGACCCCT	TAAAGGTATAG	TGTGTGTTGC	AAATCACTCT	GCAATGGAAA	CTTTTATATT	2220
	CAGGGTAGGT	TTGTGTTCTA	AAC TAGGTGT	TCTAATCAAT	GTACAAGACT	TTACCATACA	2280
	CGCAACTATA	GTTTTCTTAA	ACCTTCATCA	TTTTGTGATT	CTTTGAGAAA	GGGCTTTTAG	2340
15	GAACCTTATG	TTCTAAAAAA	TGTTTTTAAC	AATAATAAGA	TAAAGAAAA	ACCTGTGATT	2400
	CATATGTCCC	CAGTGGCATT	ACTCAGCAGG	AGCCCCCAGC	TGCCAAAGGT	TGGCAGTGAT	2460
	CCTGCAAGTT	CAAGGGCTCT	TTCTCCCTGG	GGATGTGCTT	TGTGGCTTCT	CTTTACAGCT	2520
	TTGTTTCTGC	ATCAGTTTCA	TGCTGCATGT	TGTTTGGAA	TTATCACCTT	AAGAAAGTGT	2580
	CTCTGTTTTA	TATAGAAACA	CTTTCTCACT	TACAGGGGAG	AAGGAAATGC	AGGGCAGCATG	2640
20	ATCTGGCCCT	CCCAGAAACA	ATCTGGATT	CACGGAGACA	GCAACCAGAA	GTTAAACCTA	2700
	GTGACTAAAA	ATGCATCTCG	CTACTTTTC	ATGTATGTAT	GAGACAGAAA	CTAATCCTTA	2760
	CTATCCTATT	AGGATACCAC	TTTTCAATGC	AAAGTTTGTG	TCAATAAAGT	CATTAATTTT	2820
	AAACAT						2826
25	Seq ID NO: 136 DNA Sequence						
	Nucleic Acid Accession #: XM_040550.1						
	Coding sequence: 82...4158						
	1	11	21	31	41	51	
30	CCTTGGTTTC	CGTTGCAGAT	TCCCACAAC	CCATGCTGTG	TGCTGCAGGC	TGGTCTGAA	60
	CCCAGATCTC	TGGCTGAGAG	GATGGGGGCA	GATGGGGAAA	CAGTGGTTCT	GAAGAACATG	120
	CTCATTTGCA	TCAACCTGAT	CCTTCTGGGC	TCCATGATCA	AGCCTTCAGA	GTGTGAGCTG	180
	GAGGTCAACA	CAGAAAGGGT	CCAGAGACAG	TCAGTGGAGG	AGGAGGGAGG	CATTGCCAAC	240
	TACAACACAT	CCAGCAAGA	GCAGCCTGTG	GTCTTCAACC	ACGTGTACAA	CATTAACTGT	300
35	CCCTTGGACA	ACCTCTGCTC	CTCAGGGCTA	GAGGCCCTCT	CTGAGCAGGA	GGTGAGTGCA	360
	GAAGACGAGA	CTTGGCAGA	GTACATGGGC	CAGACCTCAG	ACCACGAGAG	CCAGGTCAAC	420
	TTTACACACA	GGATCAACTT	CCCCAAAAAG	GCCTGTCCAT	GTGCCAGTTC	AGCCAGAGTG	480
	CTGCAGGAGC	TGCTGAGCCG	GATCGAGATG	CTGGAGAGGG	AGGTGTGCGT	GCTGCGAGAC	540
40	CAGTGCACAG	CCAACCTGCT	CCAAGAAAGT	GCTGCCACAG	GACAACTGGA	CTATATCCCT	600
	CAGTGCACAG	CCACCGGCAA	CTTTAGCTTT	GAGTCTGTG	GCTGCATCTG	CAACGAAGGC	660
	TGTTTGGGCA	AGAATTGCTC	GGAGCCCTAC	TGCCCGCTGG	GTTGCTCCAG	CCGGGGGGTG	720
	TGTTGAGATG	GCCAGTGCAT	CTGTGACAGC	GAGTACAGCG	GGGATGACTG	TTCCGAACCTC	780
	TGTTGAGATG	GCCAGTGCAT	CTCCCGGGGG	CTCTGCGTGG	ACGGGGAGTG	TGCTGTGCAA	840
	CGGTGCCCAA	CAGACTGCAG	CTCCCGGGGG	CTCTGCGTGG	ACGGGGAGTG	TGCTGTGCAA	900
45	GAGCCCTACA	CTGGCGAGGA	CTGCAGGGAA	CTGAGGTGCC	CTGGGGAGTG	TTCCGGGAAG	960
	GGGAGATGTG	CCAACGGTAC	CTGTTTATGC	GAGGAGGGCT	ACGTTGTGTA	GGACTGCGGC	1020
	CAGCGGCAGT	GTCTGAATGC	CTGCAGTGGG	CGAGGACAAT	GTGAGGAGGG	GCTCTGCGTC	1080
	TGTGAAGAGG	GCTACCGAGT	CCCTGACTGC	TCAGCAGTTG	CCCTCCAGA	GGACTTGCGA	1140
	GTGGCTGGTA	TCAGCGACAG	GTCCATTGAG	CTGGAATGGG	ACGGGGCCGAT	GGCAGTGACG	1200
	GAATATGTGA	TCTCTTACCA	GCCGACGGCC	CTGGGGGGCC	TCCAGCTCCA	GCAGCGGGTG	1260
50	CCTGGAGATT	GGAGTGGTGT	CACCATCAGC	GAGCTGGAGC	CAGGTCTCAC	CTAACACATC	1320
	AGGCTCTACG	CTGTCAATTG	CAACATCCTC	AGCCTTCCCA	TCAGCTTCAT	TCCAAAGAAC	1380
	CATCTCTCCA	CTCTCAAGG	GCTACAATT	AAGACGATCA	CAGAGACCAC	CGTGGAGGTG	1440
	CAGTGGGAGC	CCTTCTCATT	TTCTTCTGAT	GGGTGGGAAA	TCAGCTTCAT	TCCAAAGAAC	1500
55	AATGAAGGGG	GAGTGATTGC	TCAGGTCCCC	AGCGATGTTA	CGTCTTTTAA	CCAGACAGGA	1560
	CTAAAGCCTG	GGGAGGAATA	CATTGTCAAT	GTGGTGGCTC	TGAAAGAAACA	GGCCCCGAGC	1620
	CCCCCTACTC	CGGCCAGCGT	CTCCACAGTC	ATTGACGGCC	CCACGCAGAT	CCTGGTTGCG	1680
	GATGTCTCGG	ACAATGTGGC	TTTTGTGGAG	TGGATTCCCC	CTCGAGCCAA	AGTCGATTTC	1740
	ATTCTTTTGA	AATATGGCCT	GGTGGGCGGG	GAAGGTGGGA	GGACCACCTT	CGGCTGCGAG	1800
	CCTCCCTTGA	GCCCAATACT	AGTGACGGCC	CTGGGCGCTG	GCTCCCGATA	CGAGGTGTCA	1860
60	GTCAAGTCCG	TCCGAGGGAC	CAACGAGAGC	GATTCTGCCA	CCACTCAGTT	CACAACAGAG	1920
	ATCGATGCCC	CCAAGAACTT	GCGAGTTGGT	TCTCGCACAG	CAACCAAGCT	TGACCTCGAG	1980
	TGGGATAACA	GTGAAGCCGA	AGTTCAAGAG	TACAAGGTTG	TGTACAGCAC	CCTGGCGGGT	2040
	GAGCAATATC	ATGAGGTACT	GGTCCCCAGG	GGCATTGGTC	CAACCAAGCT	GGCCACCCTG	2100
	ACAGATCTGG	TACTGGCAC	TGAGTATGGA	GTTGGAATAT	CTGCCGTCTC	GAACCTCAG	2160
65	CAAGCGTGC	CAGCCACCAT	GAATGCCAGG	ACTGAACTTG	ACAGTCCCCG	AGACCTCATG	2220
	GTGACAGCCT	CCTCGGAGAC	CTCATCTGCC	CTCATCTGGA	CCAAGGCCAG	TGGCCCATTT	2280
	GACCACTACC	GAATTACCTT	TACCCATCCC	TCTGGGATTG	CCTCAGAACT	CACCGTACCC	2340
	AAGGACAGGA	CCTCATAAC	ACTAACAGAT	CTAGAGCCTG	GGGCAGAGTA	CATCATTTCC	2400
	GTCAGTCTG	AGAGGGGTGC	GCAGCAGAGC	TTGGAGTCCA	CTGTGGATGC	TTTCAAGGC	2460
70	TTCCGTCCCA	TCTCTCATCT	GCACTTTTCT	CATGTGACCT	CCTCCAGTGT	GAACATCACT	2520
	TGGAGTGATC	CATCTCCCCC	AGCAGACAGA	CTCATCTTCA	ACTACAGCCC	CAGGGATGAG	2580
	GAGGAAGAGA	TGATGGAGGT	CTCCCTGGAT	GCCACCAAGA	GGCATGCTGT	CCTGATGGGC	2640
	CTGCAACCCG	CCACAGAGTA	TATTGTGAAC	CTTGTGGCTG	TCCATGGCAC	AGTGACCTCT	2700
	GAGCCCATTT	TGGGCTCCAT	CACCACAGGA	ATTGATCCCC	CAAAAGACAT	CACAATTAGC	2760
75	AATGTGACCA	AGGACTCAGT	GATGGTCTCC	TGGAGCCCTC	CTGTTGCATC	TTTCTGATTAC	2820
	TACCGAGTAT	CATATCGACC	CACCCAAAGT	GGACGACTAG	ACAGCTCAGT	GGTGCCCAAC	2880
	ACTGTGACAG	AATTCAACAT	CACCAGACTG	AACCAGCTA	CCGAATACGA	AATCAGCCTC	2940
	AACAGCGTGC	GGGGCAGGGA	GGAAAGCGAG	CGCATCTGTA	CTCTTGTGCA	CACAGCCATG	3000
	GACAAACCTG	TGGATCTGAT	TGCTACCAAT	ATCACTCCAA	CAGAAGCCCT	GCTGAGTGG	3060
80	AAGGCACCAG	TGGGTGAGGT	GGAGAACTAC	GTCATTGTTT	TTACACACTT	TGCAGTCTGT	3120
	GGAGAGAGCA	TCCTTGTGTA	CGGAGTCAGT	GAGGAATTTT	GGCTTGTGTA	CCTGCTTCTT	3180
	AGCAACCACT	ATACTGCCAC	CATGTATGCC	ACCAATGGAC	CTCTCACCAG	TGGCACCATC	3240
	AGCACCACCT	TTTCTACTCT	CCTGGACCCT	CCGGCAAAAC	TGACAGCCAG	TGAAGTCACC	3300
	AGACAAAGTG	CCCTGATCTC	CTGGCAGCCT	CCAGGGCAG	AGATTGAAAA	TTATGTCTTG	3360

	ACCTACAAAT	CCACCGATGG	AAGCCGCAAG	GAGCTGATTG	TGGATGCAGA	AGACACCTGG	3360
	ATTGACTTGG	AGGGCTGT	GGAGAACACA	GAATACACGG	TGCTCTGCA	GGCAGCACAG	3420
	GACACCAAGT	GGAGCAGCAT	CACCTCCACC	GCTTTTCA	CAGGAGGCCG	GGTGTTCCT	3480
	CATCCCAAG	ACTGTGCCCA	GCATTTGATG	AATGGAGACA	CTTTAGTGG	GGTTTACCCC	3540
5	ATCTTCTCA	ATGGGGAGCT	GAGCCAGAAA	TTACAAGTGT	ACTGTGATAT	GACCAACGAC	3600
	GGGGGGCGCT	GGATTGTATT	CCAGAGGCGG	CAGAATGGCC	AAACTGATT	TTTCCGAAA	3660
	TGGGTGATT	ACCGTGTGG	CTTCGGGAAC	GTGGAGGATG	AGTTCTGGCT	GGGGCTGGAC	3720
	AATATACACA	GGATCACATC	CCAGGGCCGC	TATGAGCTGC	GGTGGACAT	GGGGGATGGC	3780
	CAAGAGGCG	CCTTCGCTC	CTACGACAGG	TTCTCTGTG	AGGACAGCAG	AAACCTGTAC	3840
10	AAACTCCGCA	TAGGAAGCTA	CAACGGCACT	GCGGGGACT	CCCTCAGCTA	TCATCAAGGA	3900
	CGCCCTTTCT	CCACAGAGGA	TAGAGACAAT	GATGTTGCAG	TGACTAATCT	TGCCATGTGC	3960
	TACAAGGGAG	CATGTGTGTA	TAAGAACTGC	CACCGGACCA	ACCTCAATGG	GAAGTACGGG	4020
	GAGTCCAGGC	ACAGTCAGGG	CATCAACTGG	TACCAATTGA	AAGGCCATGA	GTTCTCCATC	4080
	CCCTTTGTGG	AAATGAAGAT	GCGCCCTAC	AACCAACGTC	TCATGGCAGG	GAGAAAAACGG	4140
15	CAGTCTTAC	AGTTCGTAGC	AGTGGGCGGC	TGCAAGCCAA	CCAATATTTT	CTGTCAATTTG	4200
	TTTGTATTTT	ATAATATGAA	ACAAGGGGGG	AGGGTAATAG	CAATGTGTTT	TGCAACATAT	4260
	TAAGATGATG	TGAAGGAAGC	AGGGATGTGC	CAGGAATCCG	CTGGCTAACA	TCTGCTTTG	4320
	GTTTCTGTCT	CCCTGGAGCC	TGACCCCTCAG	TCTCCATTCT	CCCTCTCACC	CAGGCTCTCT	4380
	CAACCTTAC	CTCCTTTCCC	ACCAAGGAGG	AGAAGTAGGA	AGTTTCTTA	AAGGGCCAAT	4440
20	TCAAAGCCAA	GTGCTGGGT	GCAGATTGTT	ATGTTGACAG	GCACACACAT	TTTTCTACCC	4500
	TTCTTCTGAG	ATGTCCTCTG	CCTTCCAGGT	ATTGTGATT	TTGTACACAG	CTGACATGGC	4560
	CAGGTTCTCA	CATCTGCCCA	GAGAAAAGAG	CCTCAGCAAG	AGAGTTTTCG	CAACAATTCC	4620
	CCTTAAAGG	AAACAGATCA	ACTACACCGC	ATCCCAACAA	CCCAGTTCT	TTTCTCTCT	4680
25	TCCTTCCTTC	CTCCTTCT	TCTTCTCTGC	CTTCCC			4716

Seq ID NO: 137 DNA Sequence
Nucleic Acid Accession #: NM_005883.1
Coding sequence: 1714..8625

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	GGCTGGGCAT	GGATGGTGA	CCTCAGCTGG	AACATGGGGC	TGAGCCAGA	CCTCAGGGTC	120
	TCCTGCGGTG	TAGCCCCCAA	CCCCAAGCCT	GATCCCCACC	GGAGACCTGA	ACAGCCTTGG	180
	ACATCATCGG	ATCAGGGTGG	GAGGTGCCAG	CCTCTGCCAE	CTGACTTCCA	GTCCCTGTGC	240
35	CCCTCCACC	CTGCCCTTGG	GCACTCCTGC	CCTGCAGGTT	CCTCAGAGGG	GCAACCCAAA	300
	GCCAGAGAGG	GGCGGGTCTT	GTCCGGCCTC	CAGCCTGGAC	TTCCAGCCCC	CTCTGGGGCA	360
	GCATCTGGGT	CCAGACCTTC	GGTTCTAGG	GCCTCGTTTC	TCCTCTGGG	AACAGCCAAA	420
	TGGTGTCTCC	TGAGACTCAG	GACAGACCAA	GAAGAAGCCG	GATGACATGG	CAAGCCACAC	480
40	ACTGCTCCC	CTGAGCAGGA	CGGACAGCC	CGACTCCATC	CTCCACCTG	CGACTGAGCC	540
	CCCAACCCCTA	CTCTGTCTCC	AGCCGTGCCC	CTGTGACAT	TTGGTGGGA	GGGAGGGGA	600
	TGAGGGGGCA	CCTGGGGGTC	AGAGAACAAA	TGAGGGGTGA	ATACATGTGT	GTGGCCAGGT	660
	GGAGGAGGGA	GGGAGGAGC	AGGTGGGCTG	GACAGGGCCG	GTGTGAGGAA	GGGGCTCAGG	720
	CTGGCAGGGG	GAGGTGGCAA	GAGGGATGGG	CTGCCATTGG	TGGTCTGAGA	CAAGGCCGGA	780
	GGGAGGAGGC	GAGCGTGTAT	GGGAAAGGAA	CAAAGAGGGA	AGGGGGCGT	GAAGGGGTT	840
45	CGGCGGGAG	GGCGAGCCG	AGGGAGGAG	CGCGGCCAG	CTGGACAGAG	GGAGGAGGCC	900
	AGGCCAGAGC	CAGAAGACCG	CCAGAGGCAC	AAAGAAGCCA	GCGCGCTGGC	GGAGTCAAGG	960
	GATGGGCGAG	AGACTCGCGG	GGCCAGCAGG	GACCACTGA	AGGCTGCGCA	GGGGGTCCGG	1020
	GCCACACAGG	TAGCCACCTT	GAGCTCAGCC	ACCGATGGAG	GGTCTGGGG	CTGCTGCGGT	1080
50	GATGGCGGTG	GGCTTGGGTC	CATCTGTCTT	GCCTTTCTG	CACAGCTTAG	GTGTCAACCA	1140
	CTGGCCTTGG	TGGTGTTTTC	ATTGTCCATC	GGCAGGACA	GCTGGTGGTC	TGTCTGCCCC	1200
	CCCTGTCTGG	CTGTGAGCCT	CTGGGCAGGC	TGCTTTTAT	GGGGAGGGT	CCTGTCTGTC	1260
	TGTCTGTGCG	CCTCTCTGCG	TGTGAGCCTG	GGGGTGTCTG	GCTGGCCAGT	CGGCTGTCTG	1320
	GGTTAGGCTG	TCCAGCTGT	CTGAGTGT	GTCCGGCTGT	CAGGATGTGT	CCTGGGGGCT	1380
55	GGGAAGGAGA	GGCGACCCCA	TNGTCTGTCT	GTGACTGGT	CAGTTGGAGC	TTGAGCTGTC	1440
	TGTACGTCTG	TCTGTGTGTC	CATCTGTCTC	CCCTTGGGGC	CACCTCTCAC	TCCACCTGCC	1500
	CCTCTGCGCC	CCGATTGCCC	TGGCCAGCAC	CACGTGGGCC	TGTACTTGTG	CACACCAAGT	1560
	ACTCTGCTGC	GAGACCCCCC	CCCAACCCAG	GATCAGGCAG	GACGGCTGGG	GCTTAGGTCA	1620
	GGGGCGGTCT	GTCCGGAAGG	CATCACCGCG	CCCTCCCCAG	ACCATCAGCT	GAACCTCTG	1680
60	ACCCTGTGAT	CCCAGACGCT	GCAGGAGCTG	AAGATGGCGA	GCTCCGTGGC	GCCCTACGAG	1740
	CAGCTGGTGA	GGCAGGTGGA	GGCCTTGAAG	GCTGAGAAAC	GCCACCTGAG	GCAGGAGCTA	1800
	AGGGACAAC	CCAGCCACCT	GTCCAACTGT	GAGACAGAGA	CGTCCGGCAT	GAAGGAGGTC	1860
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Seq ID NO: 138 DNA Sequence
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Coding sequence: 1801..3933

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Coding sequence: 102..1103

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Coding sequence: 76..2781

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Seq ID NO: 142 DNA Sequence
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Coding sequence: 1..1641

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Nucleic Acid Accession #: NM_022123.1
Coding sequence: 76..2781

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AGGAGTTTGT	GAGCGAGGTG	GATGTGCTGG	TGTTTGTGGT	GGACTCGGT	GACGACTGC	540
GGCTGGCCCTG	GGCCGACAG	GAGCTGCACA	AGCTGCTGGA	CAAGGACCT	GACCTGCTG	600
TGCTGCTGGT	GGCCAAACAG	CAGGACCTGA	GCGAGGCCAT	GAGTATGGG	GAGCTGCAGC	660
GGGAGCTGGG	TCTACAGCT	ATCGATAACC	AGCGGAGGT	TTTCTCTTG	GCAGCCAGCA	720
TTGCCCTCG	AGGACCCACC	TTTGAAGAGC	CTGGCACGCT	GCACATCTGG	AAACTGCTCT	780
TGGAGCTCCT	CTCTTAGCT	GGAGCTCTCC	TGCTTGCCAC	CTGCCTGTCA	AGACCATAGT	840
TGTACTGCTG	CTGCTTCATT	GCCAGACTGG	GCCTGGGGCA	AGAGCCACAT	GGCAGCATT	900
CCCTTTTCCC	CTCCTTTGCC	TTTCAAGAGC	AGGCGCTGGG	CAAGGCCAAG	AACCATGCAG	960
AAGCCTTCT	GGTAGGTTGG	CCGTGAAGCC	GAAGCAGGGA	GGTGGGTGAG	ACAGAGGGTG	1020
GGGAGGATAG	TGCTGGCTG	ATTCCAGGCT	GGAATGTGGA	TCCAGCTTTC	CCTTCTCTTA	1080
CCTGTACAGT	GAGATGCTCA	GTGGGCTCAA	TCCTCCACTA	CAGGTCCCGG	TACCTGAGGA	1140
ACCAAGTGTAG	GTGTCAGAA	TACTCTAGA	GCCTCAAGGT	CTCCAGTCC	AGAAACAGTC	1200
TGGTGACGCT	TGTCCTTCT	CATGTGGCA	GCCTCTGAGT	GGTGACACAG	CAAGCCTTTG	1260
TTCTGTCTCT	GCATTGTCCA	GGCCAGCTC	CACCTAAGTG	ACTTGTGGCC	TTGTGCAATC	1320
TCTGCTCTC	TGACCCGAGG	GCCATTATTT	TTAAAGGGAG	GTGGTTTCT	AATTGGGAGA	1380
TGCCCTTCCC	AGCCATGGGA	GTGTGAAGTG	CTAGGATGAA	CCTGGCCATC	CTAGCAAGGA	1440
GCTTTCTGAA	GACCTCCCTG	CCTTCCCTG	AGCCAGGCC	TGGCCCGCCA	GCCTCTCTTG	1500
ACTACAGAAT	AACTGATATT	CACCCACCAA	ACAGAAAAG	TGAAGGCTGG	GTTTTCCCC	1560
TCTAATCTGG	AGGCAAGCTG	CTGCTCTCGT	ACTAATGTG	CCAGTGCCCA	TGTTTACAGA	1620
AGTCAGGGGA	AGGAAGGAGC	CTGTGCTCCT	GGGACGACAG	TCAACTGGAG	CTAGGTGTTG	1680
ACCTCAGAAC	TGCATTTTAT	TTATTAATTT	ATAAGCAGAA	CAGGCCACAG	TTCTAGGCTC	1740
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AAAAATAGCT	GAATCATGAA	TGACAATGAG	ATAACATACA	GATGTCAGTG	GAGACAAAGT	1860
TGTGGGTTCC	TCCTCCACC	TGGCTTTGAG	GCTGTGCTG	ATATCATAGT	ACTTTACATG	1920
GATTACAGTG	AACTGAAACG	CCACCACTTG	GCCACGAGTG	TTGAAAGGT	GCAATTTCTT	1980
TCTGGGTAGA	TAAGAAATGA	CTCTGGGAGA	GGATTTCCCT	TATGTGAATC	TAGGTAAAAA	2040
GATGAAAAAA	AATTGTATTA	TGTGATCTTA	AGGACAGGAA	TAGCAGACCA	GCCACCGGGA	2100
TGGCCTTGGG	TACATCACTC	AGCCTTCTG	GACCCAAATT	TTCCCAAGTG	AAAGCCAAAGT	2160
TGGACTGAAT	TTCTGGAGTT	CTCATCAGTG	CACATTCCAT	AGTTCTCCAG	TGCTTGGCGA	2220
TCAGCCCAAT	TGAAGGACTG	GCTCTGACT	GACACTTATT	ATCGGTACAG	GCAAGAGGGA	2280
GCCTGTGTG	TGTTAGGGAC	CACATAATCA	ACAACCACAA	ATGGATTTTT	TTTTTAAGAG	2340
GAGCTGTGCA	CCTCAATTTG	CTGTCTAGTT	GAGAATAGAG	ATTGTGTGCC	TTCAATTTCAT	2400
TTTCATTGCT	TTGTAGTATT	TTATGTATG	CATGTACCAT	AATTTATTTA	TCCAGTTGGA	2460
ATTTATCTCT	GCAAGAGATT	GCAGTAAGTC	TCCAGCTGAA	TTTCTTTTCA	GGGACTAGC	2520
CAGTTGCACC	AACAATATT	AGTGAGTAAT	CCGTCTTTT	TCCACTAATG	TAAATGCCAC	2580
TTTTATTATT	TATTAATATG	CCTTAAATAT	TGTGTCTACT	TCCAGACTT	GCTCTTCTG	2640
TCCATTATC	TTTCTATTTC	TGAATTTGCA	ATGAACAGTT	TATTATTGTC	ACTTTATAAT	2700
ACACTTTAAG	ATCTGGCAGA	GTTTGTCTCC	CGCAATTCTC	TTTCTTTTTC	AGAACTTTTC	2760
TTGATTTCCT	TGCATGATCT	TTGGAATCAG	CTTGTCAAGA	TCCAAAATAA	TCCTGTGGT	2820
ATGTTTGTCT	GTATCCCAT	AAAATTATAG	ATGAAAAG			2858

Seq ID NO: 147 DNA Sequence
Nucleic Acid Accession #: NM_021077.1
Coding sequence: 37..402

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CGCGCGCCCG	AACGAAGCG	CGGCCCCGGC	ACAGCCATGG	CCCGGCGGGC	GGGGGGCGCT	60
CGGATGTTG	GCAGCTCTCT	GCTCTTCGCC	CTGCTCGCTG	CGGCGGTGCG	CCCGCTCAGC	120
TGGGATCTCC	CGGAGCCCCG	CAGCCGAGCC	AGCAAGATCC	GAGTGCACTC	GCGAGGCAAC	180
CTCTGGGCCA	CCGTCACATT	CATGGGCAAG	AAGAGTCTGG	AGCCTTCCAG	CCCATCCCAT	240
TGGGGACAGC	TCCCCACACC	TCCCTGAGG	GACCAGCGAC	TGCAGCTGAG	TCATGATCTG	300
CTTCGAATCC	TCCTGCTAAA	GAAGGCTCTG	GGCGTGAGCC	TGACGCGCCC	CGCACCCCAA	360
ATCCAGTACA	GGAGGCTGCT	GGTACAAAAT	CTGCAGAAAT	GACACCAATA	ATAGGGGACG	420
ACACAACAGC	GTGGCTTAGA	TTGTGCCAC	CCAGGGAAGG	TGCTGAATGG	GACCTGTTG	480
ATGGCCCCAT	CTGGATGTA	ATCCTGAGCT	CAATCTCTG	TTACTTCATT	ACTGTGATT	540
CTGGCTGGGT	CACCAAGAAAT	ATCGCTGATG	CAGACACAGA	TTATGTTCT	GCTGTATTTC	600
CTGCTTCCCT	GTGAAATGG	TGAATAAAC	CTTGCTCTT			639

75
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Seq ID NO: 148 DNA Sequence
Nucleic Acid Accession #: NM_002055.1
Coding sequence: 15..1313

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AGAGCCAGAG	CAGGATGGAG	AGGAGACGCA	TCACCTCGCG	TGCTCGCGCG	TCCTACGTCT	60
CCTCAGGGGA	GATGATGGTG	GGGGGCTCTG	CTCTGCGCG	CCGTCTGGGT	CCTGGCACCC	120
GCCTCTCCCT	GGCTCGAATG	CCCTCCAC	TCCCGACCCG	GGTGGATTTC	TCCCTGGCTG	180
GGGCATCTAA	TGCTGGCTTC	AAGGAGACCC	GGGCGACTGA	GCGGGCAGAG	ATGATGGAGC	240
TCAATGACCG	CTTTGCCAGC	TACATCGAGA	AGGTTGCTT	CCTGGAACAG	CAAAACAGG	300
CGCTGGCTGC	TGAGCTGAAC	CAGCTGCGGG	CCAAGGAGCC	CACCAAGCTG	GCAGACGTCT	360

	ACCAGGCTGA	GCTGCGAGAG	CTGCGGCTGC	GGCTCGATCA	ACTCACCGCC	AACAGCGCCC	420
	GGCTGGAGGT	TGAGAGGGAC	AATCTGGCAC	AGGACCTGGC	CACTGTGAGG	CAGAAAGCTCC	480
	AGGATGAAAC	CAACCTGAGG	CTGGAAGCCG	AGAACAACTT	GGCTGCTTAT	AGACAGGAAG	540
	CAGATGAAGC	CACCTTGGCC	CGTCTGGATC	TGGAGAGGAA	GATTGAGTCG	CTGGAGGAGG	600
5	AGATCCGGTT	CTTGAGGAAG	ATCCACGAGG	AGGAGGTTCC	GGAACTCCAG	GAGCAGCTGG	660
	CCGACAGACA	GGTCCATGTG	GAGCTTGAGC	TGGCCAAGCC	AGACCTCACC	GCAGCCCTGA	720
	AAGAGATCCG	CACGCAATAT	GAGGCAATGG	CGTCCAGCAA	CATGCATGAA	GCCGAAGAGT	780
	GGTACCGCTC	CAAGTTTGCA	GACCTGACAG	ACGCTGTGTC	CCGCAACGCG	GAGCTGCTCC	840
	GCCAGGCCAA	GCACGAAGCC	AACGACTACC	GGCGCCAGTT	GCAGTCTTTG	ACCTGCGACC	900
10	TGGAGTCTCT	GCGCGGCAAG	AACGAGTCCC	TGGAGAGGCA	GATGCGCGAG	CAGGAGGAGC	960
	GGCAGCTGGG	GGAGGGCGCC	AGTTATCAGG	AGGCGCTGGC	GCGGCTGGAG	GAAGAGGGGG	1020
	AGAGCCCTCA	GGACGAGATG	GCCCGCCACT	TGCAGGAGTA	CCAGGACCTG	CTCAATGTCA	1080
	AGCTGGCCCT	GGACATCGAG	ATGCCCACTT	ACAGGAAGCT	GCTAGAGGGC	GAGGAGAAAC	1140
	GGATCAACAT	TCCCGTGCAG	ACCTTCTCCA	ACCTGCAGAT	TGAGAGAAAC	AGCCTGGACA	1200
15	CCAAGTCTGT	GTGAGAAGGC	CACCTCAAGA	GGAAACATCG	GGTGAAGACC	GTGGAGATGC	1260
	GGGATGGAGA	GGTCATTAAAG	GAGTCCAAGC	AGGAGCACAA	GGATGTGATG	TGAGGCGAGGA	1320
	CCCACTCTGT	GGCTCTGTGC	CCGTCTCATG	AAGGGCCCGA	GCAGAAGCAG	GATAGTTGCT	1380
	CGGCTCTGTC	TGGCACAATT	CCCCAGACCT	GAGCTCCCCA	CCACCCGAGC	TGCTCCCTCT	1440
	CCTCTCTGT	CCCTAGGTCA	GCTTGTGTC	CTAGGCTCCG	TCAGTATCAG	GCCTGCCAGA	1500
20	CGGCACCCAC	CCAGCACCCA	GCAACTCCAA	CTAAACAAGAA	ACTCACCCCC	AAGGGCAGTC	1560
	TGGAGGGGCA	TGGCCAGCAG	CTTGGCTTAG	AATGAGGAGG	AAGGAGAGAA	GGGGAGGAGG	1620
	GCGGGGGGCA	CCTACTACAT	GGCCCTCCAC	ATCCCTGATT	CCTGTTGTGA	TGGAAACTGT	1680
	TGCCAGAGAT	GGAGGTTCTC	TGGGAGTATC	TGGGAACTGT	GCCTTTGAGT	TCTCTCAGGC	1740
	TGCTGGAGGA	AAACTGAGAC	TCAGACAGGA	AAGGGAAGGC	CCACAGACA	AGGTAGCCCT	1800
25	GGCCAGAGGC	TGTGTTTGTG	TTTTGTTTTT	TATGAGGTGG	GATATCCCTA	TGCTGCCTAG	1860
	GCTGACCTTG	AATCTCTGGG	CTCAAGCAGT	CTACCCACCT	CAGCCTCCTG	TGTAGCTGGG	1920
	ATTATAGATT	GGAGGCCACCA	TGCCAGCTC	AGAGGGTTGT	TCTCTAGAGC	TGACCCCTGAT	1980
	CAGTCTAAGA	TGGGTGGGGA	CGTCTGCCA	CCTGGGGCAG	TCACCTGCCC	AGATCCCGAG	2040
	AGGACCTCCT	GAGCGATGAC	TCAAGTGTCT	CAGTCCACCT	GAGCTGCCAT	CCAGGGATGC	2100
30	CATCTGTGGG	CACGCTGTGG	GCAGGTGGGA	GCTTGTATTCT	CAGCACTTGG	GGGATCTGTT	2160
	GTGTAGCTGG	AGAGGGATGA	GGTGTGGGA	GGGATAGAGG	GGGGCTGCCT	GGCCCCCAGC	2220
	TGTGGGTACA	GAGAGGTCAA	CCCCAGGAGG	ACTGCCCCGT	GCAGACTGGA	GGGGAACGCTG	2280
	GTAGAGATGG	AGGAGGAGGC	AATTGGGATG	GCACATAGGA	TACAAGTAGG	GGTGTGGGTT	2340
	GACCAGTTGC	ACTTGGCCCT	TGSATTGTGG	GAATTAAGGA	AGTGACTCAT	CCTCTTGAAG	2400
35	ATGCTGAAAC	AGGAGAGAAA	GGGGATGTAT	CCATGGGGGC	AGGGCATGAC	TTTGTCCCAT	2460
	TTCTAAAGGC	CTCTCTCTTG	CTGTGTCTAT	CCAGGCCCGC	CCAGCCTCTG	AGCCCCCTGG	2520
	ACTGCTGCTT	CTTAACCCCA	GTAAGCCACT	GCCACAGCTC	TGACCCCTCT	CACCCCATAG	2580
	TGACCGGCTG	CTTTTCCCTA	AGCCAAGGGC	TCTTGGCGTC	CCTTCTTACT	CACACACAAA	2640
	ATGTACCCAG	TATTTCTAGT	AGTGCCCTAT	TTTACAATTG	TAAAACTGAG	GCACGAGCAA	2700
40	AGTGAAGACA	CTGGCTCATA	TTCTTGACAG	CTGGAGGCGG	GGTGCTCAGG	GCTGACACGT	2760
	CCACCCCATG	GCACCCACTC	TGCTTTGACT	GAGCAGACTG	GTGAGCAGAG	TGGTGGGATC	2820
	TGTGCCACAG	GATGGGACTG	GGAGGGCCCA	CTTCAGGGTT	CTCCTCTCCC	CTCTAAAGGC	2880
	GAAGAAGGGT	CCTTCCCTCT	CCCCAAGACT	TGTTGTCTCT	TCCCTCCACT	TCTTCTGCTC	2940
	ACCTGCTGCT	GCTGCTGCTG	CTAATCTTCA	GGGCACTGCT	GCTGCCCTTA	GTCGCTGAGG	3000
45	AAAAATAAAG	ACAAATGCTG	CGCCTTAAA	AAA			3033

Seq ID NO: 149 DNA Sequence
Nucleic Acid Accession #: L29126.1
Coding sequence: 445..1845

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	CGTCTGCCAG	CTTGGTGGGC	TCCTTGGCCC	GCAGCTGGTT	CAGCCTCAGC	AGCCAGCCGC	180
55	TTGTTTTGCT	GTTCAGAGAA	GCGAACCTTC	TGATGTAGC	TGGCAAAGCG	GATTGTAGCT	240
	CCATCATCTC	TGCCCGCTCA	CTGGCCCGGG	TCTCCTTGAA	GCCAGCATTG	AGTGCCCGAG	300
	CCAGGGAGAA	ATCCACCCGG	GTCCGAGTGG	AGGGGGCATT	CGAGCCAGGG	AGAGGCGGGT	360
	GCAGGACCCA	GACGCGCGCC	AGGAGCCAGG	CCCCCACC	TCATCTCCCC	TGAGGAGACG	420
	TAGGAGCGGC	GAGCAGCGGA	GGTGATGCGT	CTCTCTCCA	GCCTGTCCGG	CTCGTCGGTG	480
60	TGCTCCGATG	CTGAAGAATA	CCAGCCTCCT	ATATGGAAAT	CATACCTATA	TCAGTTACAG	540
	CAAGAGGCAC	CTGCTCCCAA	GAGAATCAAT	TGTCTCGGG	AGGTGGAAAA	CAGACCAAAA	600
	TATTATGGAA	GAGAGTTTCA	TGGGATCATC	TCTCGGGAGC	AGGCGGATGA	GCTTCTTGGA	660
	GGCGTGGAGG	GTGCTTACAT	CCTTAGAGAA	AGCCAGCGGC	AACCAGGATG	CTACACGCTG	720
	GCTCTCAGGT	TTGAAACCA	GACCTTAAAC	TACAGGCTCT	TCCAGGACGG	GAACACATTT	780
65	GTGGGTGAGA	AGAGGTTTGA	GTGATTTCAT	GATCTGGTGA	CAGATGGCTT	GATAACACTG	840
	TACATAGAAA	CAAAAGCTGC	CGAGTACATT	TCAAAAATGA	CAACTAACCC	CATCTATGAA	900
	CACATTGGAT	ATGCCACCCT	ACTCAGAGAA	AAAGTATCCA	GAAGGCTGAG	CAGGTCTAAA	960
	AATGAACCAA	GAATAACAAA	CGTCACACAT	GAAGAACACA	CAGCGGTGGA	AAAGATCTCC	1020
	TCCCTGGTTC	GAAGGGCTGC	CCTCACACAC	AACGACAACC	ACTTCAATTA	TGAGAAGACA	1080
70	CACAACCTTA	AGGTCCACAC	GTTCGAGGC	CCCACTGGT	GTGAATATTG	TGCCAATTTT	1140
	ATGTGGGGGC	TCATCGCCCA	AGGGGTCCGG	TGCTCAGACT	GTGGATTGAA	CGTACACAAA	1200
	CAGTGTTCGA	AGCACGTTCC	CAATGACTGC	CAACTGATC	TCAAGAGGAT	CAAGAAAGTG	1260
	TACTGTGTGT	ACCTCACAAC	ACTTGTGAAG	GCTCACAACA	CTCAGAGACC	CATGTTGGTA	1320
	GACATATGCA	TTGCGGAAAT	TGAAGCAAGA	GGATTAAAT	CGGAAGGCCT	TTACAGAGTC	1380
75	TCTGGGTTCA	CTGAACACAT	TGAAGATGTC	AAAAATGGAT	TTGACAGAGA	TGGTGAAAAG	1440
	GCCGATATAT	CTGCCAATGT	CTATCCAGAC	ATAAACATCA	TCACTGGAGC	CCTTAAACTG	1500
	TATTTACAG	ACCTTACCCT	CCCTGTCTAT	ACATATGATA	CCTATTCCAA	ATTATATAGT	1560
	GCAGCAAAAA	TCTCCAATGC	AGATGAGAGG	CTGGAAGCCG	TCCATGAAGT	GCTGATGCTG	1620
	CTGCCTCCTG	CCCACTATGA	AACCCCTCCG	TACCTAATGA	TCCACCTCAA	AAAGGTTACT	1680
80	ATGAATGAAA	AAGACAATTG	CATGAATGCA	GAATAATCTG	GGATCGTGTG	TGGGCCCACT	1740
	CTGATGAGGC	CCCCTGAGGA	CAGCACCCCT	ACCACCCCTG	ATGATATGCG	GTACCAAAAG	1800
	CTGATTGTGC	AGATTTTAAAT	AGAAAAACGAA	GACGTTTTAT	TCTAATCCAT	CAGGGAATAG	1860
	AGCTGAATGG	CCGAGCACCA	TCAAGTTGAC	ACAGCTAAGG	ATAAAACATT	TCTTACCCT	1920
	TGATTTGTTT	TCCAAGCAAG	TGCTAGAATT	TGCTGGACTG	CAGAGGATCG	CTGAGTGGGG	1980

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CCCCTCAGGT TGGGTCTTTT GCTGTGCTTC CTATGTATGT CTGGTTTGCT GGAAGAGTGA 2100
TTAATACATC TTTAATTTAT TAAAAACAA TGTAGACCTT TAAACTTCAG TCTTATTGGG 2160
AATAAAGGG AACTTAATTTC ATACAGGTAC TTGATACAGT TATACATTTT CCACCTACAA 2220
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AGAATGTTGT TATTTTAGCA ATAGAACTCA ATGCAGATGC ATTGGTTATT ACCTGTGTGA 2340
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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: XM_113553.1
Coding sequence: 25..939

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1 11 21 31 41 51
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AGTTCGGCTC TAGGTTCCAT GTCCCAACT ACATCTTCCC AGATTTTGGC CAGAAAAAGA 180
CGGAGAGGAA TAATTGAGAA GCGCCGACGA GACCGGATCA ATAACTGTTT GTCTGAGCTG 240
AGAAGGCTGG TACCCAGTGC TTTTGAGAA GAGGGATCTG CTAAGCTAGA AAAAGCCGAG 300
ATCCTGCAGA TGACCGTGA TCACTGAAA ATGCTGCATA CGGCAGGAGG GAAAGGTTAC 360
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CGACTGGTTT CGCATCTCAA CAATACGCT TCCAGCGGG AGCCCGCGAG CGGCGGCCAC 540
GCGGGCTCTG GACACATTCC CTGGGGGACC GTCTTCGGAC ATCAACCGCA CATCGCGCAC 600
CCGCTGTTGC TGCCCCAGAA CGGCCACGGG AACCGCGGCA CCACGGCTC ACCCAAGGAA 660
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CCTAGCGGCA GCCTCGGACC GGTGCTCCCT GTGGTCACCT CGCCTCCAA ACTGTGCGCC 780
CCTCTGCTCT CCTCAGTGGC CTCCCTGTGG GCCTTCCCCT TCTCTTTCGG CTCCTTCCAC 840
TTACTGTCTC CCAATGCACT GAGCCCTTCA GCACCCACGC AGGCTGCAAA CCTTGGCAAG 900
CCCTATAGAC CTTGGGGGAG GGAGATCGGA GCTTTTAA GAACTGATGT AGAATGAGGG 960
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GAACTGTGGT TGCCAAGGTA TTTAAAGGG CTTTCTGCTC TCCTCTCTT TGATTTATTT 1980
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Seq ID NO: 151 DNA Sequence
Nucleic Acid Accession #: NM_001936.2
Coding sequence: 178..2589

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CACTGGTGGT CTCGGGATGG CACGAGACTC GCCTACGCGC CCATCAATGA TTCCTGTGTC 960
CCCATCATGG AGCTCCACAC TTACACCGGC TCCATCTACC CCACCGTGAA GCCTTACCAC 1020
TATCCCAAGG CTGGAAGTGA GAACCCAGC ATTTCCCTAC ACGTTATTGG CTTAAATGGA 1080
CCCAACCATG ATCTGGAGAT GATGCCGCTC GATGATCCAC GGATGAGGGA GTACTACATC 1140
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CGAAAGTTTT TCTTCATCAG AGCCATCCCC CAGGAGGAGC GAGGGAAATT CTATCACATC 1380
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5 GTGCACAACA CAACAGATAA GAAAAAATG TTTGACCTAG AAACAAATGA ACATGTCAAG 1740
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 GGCAGCGGCT TCCAAGGGAC CAAGCTCCTG CACGAAGTGA GCGCGCGCTG GGGCTTGCTG 2040
 GAGGAGAAGG ACCAGATGGA GGCGGTGCGG ACGATGCTGA AGGAGCAGTA CATTGACAGG 2100
 AGCGCGGTGG CCGTGTCTGG GAAGGATTAC GGTGGCTACC TGAGCACCCTA CATCTCCCA 2160
 10 GCAAAGGGAG AAAATCAAGG CCAGACATTG ACCTGCGGCT CTGCTCTCTC TCCAATAACA 2220
 GACTTCAAAG TCTATGCCTC TGCGTTTTCG GAGAGGTACT TGGGCTTCCA TGGACTTGAC 2280
 AACAGAGCAT ACGAGATGAC CAAGGTAGCC CATCGAGTCT CCGCGCTGGA AGAACAGCAG 2340
 TTCCTGATCA TTCATCCACC TGCCGATGAA AAAATTCA TTCCAGCACAC AGCAGAACTC 2400
 ATTACACAAC TAATTAGGGG AAAGGCTAAT TACAGCTTAC AGATTACCC GGACGAAAGC 2460
 15 CATTACTTTA CCAGTCCAG CCTCAAAACAG CATCTGTACC GGTCCATCAT CAACTTCTTC 2520
 GTGGAATCTG TCCAGTCCCA GGACAACTG CCGACAGTCA CAGCGAAAGA GGACGAGGAG 2580
 GAGGACTAAG CTCAGGTGCG TCTAAGCACA AACGTGGCTC TTTCTACAAC CAGATGCAAC 2640
 CGAGGGAATT CCTCGCCCTC CCTCTTCCCT CGGAGGGGCG GGGCGGGGCG GGGCGGGTGG 2700
 TTCCATAGCA TGTGTGCTC GGATGCGGAA GGCAGTTTGG CTTGGGAAAC AAGCTCCTTC 2760
 20 CCGCGGGTGA TCACTCAGCG CCTCCATGGC ACCAGGGACA ACGCTGTCCC CGCAGCAGCG 2820
 CCTCTCCCG GCGCCCGAGA GACCGGCACG CCAACGGCCC TCCCGCAAGG AACAGAGCAA 2880
 AGGATGGTGG CCGCAGGCC CACGCGAGCC CACAGGACAC CGGCCCTTAG ATTCCAGCCA 2940
 CCAAGCGGAA GCATGAGACC GCGCCCACT AGCCTCTGTG TTCCGTTAG GGACATCA 3000
 CCTGTCTCA CGTCGAGTG CCATGGACGC AGCAGTTACA GCACCATGTG TTTAGCAGTG 3060
 25 CGTGTCTATA TATGGGCTTG CTACTTCTGT TAATGAGGAC GTTCAACATG GTGAGGGGCT 3120
 ACAAGAAACG GCTTTTCTGT ACAGAGTCTT ACTGTAGCTA CGTAAATGGT TAACCTGATA 3180
 GAATTAACCT GTATTCTTCT ATGGTTTAA CTTGATGCTC CACTGTCTCC GTCATGGGGT 3240
 TGTTTTCTG TTTGGGGTGG GGCCTTGTCT CCTTTCTCT TCTCCAGTCC ACGTGTAGAC 3300
 TTTGGGCTTG ATGAAGAAGC AGATCGGAAG TAACTGCTCC CTCCTCAAGG TTGTCTTCAG 3360
 30 ACGTCTTGGG GAGCTTCTTA AACACTGAGG GGAAGACAG CCAATAGCAC CCATTAAAGC 3420
 AAATACCTAA ATAAACCTC TCTCCCACTC AGCTATGCTA GGGCTTGGCT GTAGGTGTGC 3480
 ACTGTCTATT TACATCCGTC CTTACAACCA TCCTTGTCTC CCTTGTACC GTATCAAGCT 3540
 CTTTCCCATG ACATTGTGTT 3560

35 Seq ID NO: 152 DNA Sequence
 Nucleic Acid Accession #: XM_087461.1
 Coding sequence: 236..1138

1 11 21 31 41 51
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 40 CCGCGCGCGG GCGCGCGGG GAACCCCAAA CGCAACCGGG TCTGGAGGGA TCCCGCGCGC 60
 GAGCCAGCCG CCGTCAACGC CTCGCGCGCG CCCCTGCGGG CTTGGCAGGC GCCCGCGCGG 120
 CCGCAGCTGC GCCCGCGCG CCGCTCCGCG GGTCCACCGG TGAGCTCGCC GCGCGGTGCG 180
 CCGCTCGCCA TGCAACCGCC GCGCGCTCG CGCGCGTAGG CGCCCGCGCG AGGCCATGCT 240
 GCGCTGCTGC GCGCGCTGCG TGCGCGCGCG CTGCGCGCTG CCGCGCGTCC GCGCGCGGGC 300
 45 CGCGGAGCGG CCGCGCTCC TCGGGGTGCC TCCAATGCT TCAGTCAACG CGTCTCTCGC 360
 GCGGAGCCCA TCGCGCGCGG CTGCTGGGCC TCGCGCGCCC CCGGCGCCCC CGAGCGCCCG 420
 GCGCGGAGGG AGCGCGCGCG GCGCGCGCGG CCTGTGCAAC ATCAGCGTGC AGCGGCAGAT 480
 GCTGAGCTCG CTGCTGCTGC GCTGGGGCGG CCGCGCGGGC TTCCAGTGGC ACCTACTGCT 540
 CTTCTCCACC AACCGCGACG GCGCGCTTTT CTGCGCGGCC GCCTTCCACC CGGTGCGGCC 600
 50 GCGCGTCTGC ATCGAGCACC TGGGGCTGGG GCGCGCGCGG CGCGCAGCAG ACCTGCGCCT 660
 CTGGTGGGCG TGGCGCTGCG TGCGCGGTGC CGCACCGGCG CGCTCCGCG CCGCGCGCGC 720
 CCGCAGCGCC GCGCGCGCCA CCGCGCGGGC GCGCACCGCG CTGCCAGCCT ACCCGCGGCG 780
 CGAGCGCGCC GGGCGCTGCT GGCTGCAGGG CGAGCGCGCT CATTTCTGCT GCCTAGACTT 840
 CAGCTTGGAG GAGCTGCAGG GCGAGCGCGG CTGGCGGCTG AACGTAAGC CCATTGAGTC 900
 55 CACGCTGGTG GCGTGTCTCA TGACCTGGT CATCGTGGTG TGGAGCGTGG CCGCCCTCAT 960
 CTGGCGGGTG CCGCATGCG CCGGCTTCT GCGCAACGGC ATGGAACAGC GCGGAGCCAC 1020
 CGCGAGCACC ACCGAGCCA CCGCGCGCGG AGTGCCCGCA GGGACCAACG CAGCGCGCGC 1080
 CGCGCGCGCG GCTGCGCGCG CCGCGCGCGG CGTCACTTGG GGGGTGGCGA CCAAGTGACC 1140
 CGCTCGCTCC CTCTCTGTG CCGCTCTGTG TCCGCGCGCG CGGTGCGCTT TCCGCGCGGA 1200
 60 GACTCGGCGG GTGTGCTCG TGCTGTAGTT ATCGTTAGTT CCTCTTCCCG AGATGGGGCC 1260
 GCGGAGAGAG CCGAGCGCCT TTGAAAGCA AGGTTTGTGC TGCGCTTCCA GTTCCGAAAA 1320
 GCAGATGTTT AAGCCCTTGG ACTGAGGGTG GATCGCAGC TCCGAAGACG GAGAGGAGGG 1380
 AAATGGGGCC CTTTCCCTTC TATTGCATCC CCTGCGCGCA CTCCTTCCCC GCACCCACGT 1440
 GCGCTAGATT CATGGCAGAA AATGACCAAA TCCTGTGTAT TTGTTTTATA TATTTAATAA 1500
 65 CTGTTTTAAA TGAAGTTTT AGTAAAAAAA ATACAAAAA AAAAGATTAA ATTGCTATTG 1560
 CTGTAGTAAG AGAAGCTCTT TGTATCTGAA CATAGTTGTA TTTGAAATTT GTGGTTTTTT 1620
 AATTTATTTA AAATTTGGGG GAGGGCATGG GAAGSATTTA ACACCGATAT ATTGTTACCG 1680
 CTGAAATGA ACTTATGAA CCTTTTCCAA GTTGATCTAT CCAGTGACGT GGCCTGTGGG 1740
 GCGTTTCTTC TTGTACTTAT GTGGTTTTTT GCGTTTTAAT ACAGACATT TCCTCC 1796

70 Seq ID NO: 153 DNA Sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 1-843

1 11 21 31 41 51
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 75 ATGGATCTCC AAGGAAGAGG GGTCCCCAGC ATCGACAGAC TTCGAGTTCT CCTGATGTTG 60
 TTCCATACAA TGGCTCAAAT CATGGCAGAA CAAGAAGTGG AAAATCTCTC AGGCCTTTCC 120
 ACTAACCTCG AAAAAGATAT ATTTGTGGTG CGGGAATAAT GGAAGACGTG TCTCATGGCA 180
 GAGTTTGCAG CCAAAATTTAT TGTACCTTAT GATGTGTGGG CCAGCAACTA CGTAGATCTG 240
 80 ATCAGAAAC AGGCCATAT CGCATTGACC CGGGGAGCTG AGGTGAAGGG CCGCTGTGGC 300
 CACAGCCAGT CGGAGCTGCA AGTGTCTGCG GTGGATCGCG CATATGCACT CAAAATGCTC 360
 TTTGTAAAGG AAAGCCACAA CATGTCCAAG GGACCTGAGG CGACTTGGAG GCTGAGCAAA 420
 GTGCAGTTTG TCTACGACTC CTCGGAGAAA ACCCACTTCA AAGACGCAGT CAGTGCTGGG 480
 AAGCACACAG CCAACTCGCA CCACTCTCTC GCCTTGGTCA CCGCGCTGCG GAAGTCTCTAT 540
 GAGTGTCAAG CTCACAAAC CATTTCACTG GCCTCTAGTG ATCCGACAGG GACGCTCACC 600

5
 ATGATCCTGT CTGCGGTCCA CATCCAACTT TTTGACATTA TCTCAGATTT TGTCTTCAGT 660
 GAAGAGCATTA AATGCCAGT GGTAGAGCGG GAGCAACTGG AAGAAACCTT GCCCCTGATT 720
 TTGGGGCTCA TCTTGGGCTT CGTCATCATG GTAACTCTCG CGATTACCA CGTCCACCAC 780
 AAAATGACTG CCAACCAGGT GCAGATCCCT CGGGACAGAT CCCAGTATAA GCACATGGGC 840
 TAG 843

Seq ID NO: 154 DNA Sequence
 Nucleic Acid Accession #: NM_144586
 Coding sequence: 261..686

10
 1 11 21 31 41 51
 | | | | |
 GGCACGAGGC CGGAGGCGCG GTGCTCGGCC CGGAGCGCG AGCGGGAGGA GCAGAGACCC 60
 GCAGCCGGGA GCCCGAGCGC GGGCGATGCA GGCTCCGCGA GCGGCACCTG CGGCTCTCTT 120
 AAGCTAAGAC CGTGTCTCTC GCGGCAGCAG CGCGGGCCCC AGCAGCCTCG GCAGCCACAG 180
 15 CCGCTGAGC CGGGGACGCC TCCGCTGCTG TCGCCTCTCT TGATGCGCTT GCCCTCTCCC 240
 GGCCCGGGGA CTCGCGGAGA ATGTGGGTCC TAGGCATCGC GGCAACTTTT TCGCGATTGT 300
 TCTTGCTTCC AGGCTTTGCG CTGCAAAATCC AGTGCTACCA GTGTGAAGAA TTCCAGCTGA 360
 ACAACGACTG TCCTCCCCCC GAGTTCATTG TGAATTGCAC GGTGAACGTT CAAGACATGT 420
 20 GTCAGAAAGA AGTCATGGAG CAAAGTGCAG GGATCATGTA CGCAAGTCC GTGTCATCAT 480
 CAGCGGCGCT TCTCATCGCC TCTGCGGGGT ACCAGTCTCT CTGCTCCCCA GGGAAACTGA 540
 ACTCAGTTTG CATCAGCTGC TGCAACACCC CTCTTTGTAA CGGGCCAAAG CCCAAGAAAA 600
 GGGGAAGTTC TGCTCGGCC CTGAGGCCAG GGCTCCGCAC CACCATCTCT TTCTCTCAAT 660
 TAGCCCTCTT CTGCGCACAC TGCTGAAGCT GAAGGAGATG CCACCCCTCT CTGCATTGTT 720
 25 CTTCCAGCCC CTGCCCCCAA CCCCCACCT CCTGAGTGA GTTTCTTCTG GGTGTCCTTT 780
 TATTCTGGGT AGGGAGCGGG AGTCCGTGTT CTCTTTGTTT CCGTGCAAAA TAATGAAAGA 840
 GCTCGGTTAA GCATTCTGAA TAAATTGAG CTGACTGAA TTTTCAATG TACTTGAAGG 900
 AAGGAGGTGG AGTGAAGATT CACCCCAAAA AAAAAA 946

Seq ID NO: 155 DNA Sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

30
 1 11 21 31 41 51
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 TTGGGGGTTT ATTCTCTTCC CTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60
 35 AGTGCACTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120
 TCCCTCCACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAAATGAC CCAAAATAAA 180
 TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 GCGGTAGCTG TTTCATTTTT CTTCGTTGAA GTCTTCACCT ACGGCATCAT CAAGACATT 300
 40 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCTCGCCAC AGTCCCTGAGC 420
 AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTCAG CACCGGGATG 480
 GTGGCCGCTT CTTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
 45 AAAAGAGCTT CCATAGTCAC TGCAAGTGTG TCCACAGGAG AATGTTTTCG TGTGTTTGCT 660
 TTCGCACCCG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720
 GTGGGCTTAC TACAGTTAAA CATTGTATC TTGGAGCAC TGCTCAGACC CATCATTATC 780
 AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAAATC GGAAGAAGC GCAGTATATG 840
 CTTGAAATAG AGAAAACAGC AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900
 50 ACCTCACTTA AATAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
 TTCTCCATT TGAAGAGCAA AAGTTTATT TGTATGCAT TATTTGGTCT CTTTGCAACA 1080
 CTGGGATTCT TTGCACCTTC CTTGTACATC ATTCCTCTGG GCATTAGTCT GGGCATTGAC 1140
 CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGCGCCATTG CAGAAGTTT CGGAAGGATC 1200
 55 GGAGCTGGTT TTGCTCTCAA CAGGGAGCCC ATTGTAAGA TTACATTGA GCTCATCTCG 1260
 GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGCTCA 1320
 ATGTATGCA GCATATTTTT TGGGTTTATG GTTGAACAA TAGGAGGACT CACATTCCAC 1380
 TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440
 ATCTTCTATC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
 60 CAAAGTAAGA TCTACAGCAG GGCTTCTAC TCTGCGCAG CTGGCATGGC CTTGGCTGCT 1560
 GTGTGCTCG CCTCGGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACTCAGGT 1620
 GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1680
 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740
 ACTTTCTTAC AACCAACGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAAGGGG 1800
 65 ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACCTACA TTTTAAAGGG 1860
 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTIT TGTTTTGTIT TGTTTTAAAG 1920
 TTTTITTTTT TGCTTGTITT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCCATATA 1980
 TAAATCTGGC TGTATTCACT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTTACA 2040
 70 TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
 TAAATGATTT TCTTTTTTTC TTTTCTTCT TCTATGGTC TTGTCTGAAT AAACCTACTCT 2160
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAATGAA ATTGGCCAGT C. 2212

Seq ID NO: 156 DNA Sequence
 Nucleic Acid Accession #: NM_004833.1
 Coding sequence: 246..1277

75
 1 11 21 31 41 51
 | | | | |
 TCAGCCAATT AGAGCTCCAG TTGTCACTCC TACCCACACT GGGCCTGGGG GTGAAGGGAA 60
 GTGTTTATTA GGGGTACATG TGAAGCCGTC CAGAAGTGTG AGAGTCTTTG TAGCTTTGAA 120
 80 AGTCACCTAG GTTATTGGG CATGCTCTCC TGAGTCTCTT GCTAGTTAAG CTCTCTGAAA 180
 AGAAGGTGGC AGACCGGTT TGCTGATCGC CCCAGGGATC AGGAGGCTGA TCCCAAGTT 240
 GTCAGATGGA GAGTAAATAC AAGGAGATAC TCTTGCTAAC AGGCTTGGAT AACATCACTG 300
 ATGAGGAATC GAGTAGGTTT AAGTCTTTTC TTTCAGACGA GTTTAATATT GCCACAGGCA 360
 AACTACATAC TGCAACACGA ATACAAGTAG CTACCTTGAT GATTCAAAT GCTGGGGCGG 420
 TGTCTGCAGT GATGAAGACC ATTGTAATT TTCAGAAATT GAATTATATG CTTTGGCAA 480

AACGTCCTTCA GGAGGAGAAG GAGAAAAGTTG ATAAGCAATA CAAATCGGTA ACAAACCAA 540
 AGCCACTAAG TCAAGCTGAA ATGAGTCTCTG CTGCATCTGC AGCCATCAGA AATGATGTCG 600
 CAAAGCAACG TGCTGCACCA AAGTCTCTCTC CTGATGTTAA GCCTGAACAG AACAGATGG 660
 TGGCCAGCA GGAATCTATC AGAGAAGGGT TTCAGAAGCG CTGTTTGCCA GTTATGGTAC 720
 5 TGAAGCAAA GAAGCCCTTC ACGTTTGAGA CCAAGAAGG CAAGCAGGAG ATGTTTCATG 780
 CTACAGTGGC TACAGAAAAG GAATTTCTCT TGTAAAAGT TTTTAATACA CTGCTGAAAG 840
 ATAAATTCAT TCCAAAGAGA ATAATTATA TAGCAAGATA TTATCGGCAC AGTGGTTTCT 900
 TAGAGGTAAA TAGCGCTCA CGTGTGTAG ATGCTGAATC TGACCAAAAG GTTAATGTCC 960
 CGCTGAACAT TATCAGAAA GCTGGTGAAA CCGGGAAGT CAACACGCTT CAACTCAGC 1020
 10 CCCTTGAAC AATTGTGAAT GGTGTTGTTG TAGTCCAGAA GGTAACAGAA AAGAAGAAAA 1080
 ACATATTATT TGACCTAAGT GACAACACTG GGAATATGGA AGTACTGGGG GTTAGAAACG 1140
 AGGACACAAT GAAATGTAA GAAAGAGATA AGTTTCGACT TACATTCTTC ACCTGTCAA 1200
 AAAATGGAGA AAACTACAG CTGACATCTG GAGTTCATAG CACCATAAAG GTTATTAAGG 1260
 CCAAAAAAA AACATAGAGA AGTAAAAAG ACCAATTCAA GCCAACTGGT CTAAGCAGCA 1320
 15 TTTAATTGAA GAATATGTGA TACAGCCTCT TCAATCAGAT TGTAAAGTAC CTGAAAGCTG 1380
 CAGTTCCAG GCTCTCTCT CACCAAAAT AGGATAGAAT AATTGCTGGA TAAACAAAT 1440
 CAGAATATCA ACAGATGATC CCAATAAACA TCTGTTCTC ATTCC 1485

Seq ID NO: 157 DNA Sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 | | | | |
 25 TTCCTTTTCA GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GCCTATAGCC 120
 TTGGCTGTGA TATTGTGTGG TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTTGA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAAATGACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 30 AAAGGACAAC GATGCCCTAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCTGAAAT GAATGACAAT CAGAATTCCA 600
 35 CTGCCCAAAG GAGTCCAGCA ATTAATATGGA TTTCTAGGAA AAGCTACCTT AAGAAGGCT 660
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTATT ATACATTCAAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACAATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGTTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAG 900
 40 CATCTATGTC TCGTAAAGCA TTCTCTAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAAAATATCA TGTATGACAT CAATATGTAG GGAACATTTC TTATGCATCA TTTGGTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTCCA TAACCAAATT AGCAGCACCG GTCTTAAATT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 45 TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTTGAAA 1260
 TACAAAATGT TTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAAT TATACCTAGC 1320
 AATCATTCTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTCTC 1380
 TTGTTATGTC CTATATACTG TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTTT TAAAAAAA AAA 1493

Seq ID NO: DNA Sequence 158
 Nucleic Acid Accession #: NM_002562.1
 Coding sequence: 27..1814

1 11 21 31 41 51
 | | | | |
 55 AAAACGCAGG GAGGAGGGCT GTCACCATGC CGGCCTGCTG CAGCTGCAGT GATGTTTTCC 60
 AGTATGAGAC GAACAAGTCT ACTCGGATCC AGAGCATGAA TTATGGCACC ATTAAGTGGT 120
 TCTTCCACGT GATCATCTTT TCCTACGTTT GCTTTGCTCT GGTGAGTGAC AAGCTGTACC 180
 AGCGGAAAGA GCCTGTCTATC AGTTCTGTGC ACACCAAGGT GAAGGGGATA GCAGAGGTGA 240
 60 AAGAGGAGAT CGTGGAGAA GTGAGTGAAGA AGTTGGTGCA CAGTGTCTTT GACACCGCAG 300
 ACTACACCTT CCGTTTGCAG GGGAACTCTT TCTTCGTGAT GACAAACTTT CTCAAAAACG 360
 AAGGCCAAGA GCAGCGGTTG TGTCCCGAGT ATCCCAACCG CAGGACGCTC TGTTCCTCTG 420
 ACCGAGGTTG TAAAAAGGGA TGGATGGACC CGCAGAGCAA AGGAATTACG ACCGGAAGGT 480
 GTGTAGTGCA TGAAGGGAAC CAGAAGACCT GTGAAGTCTC TGCCGTGTGC CCCATCGAGG 540
 65 CAGTGGAAAG GGCCCCCGG CCGTCTCTCT TGAACAGTGC CGAAAACCTC ACTGTGCTCA 600
 TCAAGAACAA TATCGACTTC CCGGCCACCA ACTACACCAC GAGAAACATC CTGCCAGGTT 660
 TAAACATCAC TTGTACCTTC CACAAGACTC AGAATCCACA GTGTCCCAT TCCGAGTACG 720
 GAGACATCTT CCGAGAAACA GCGGATAATT TTTAGATGT GGCAATTACG GCGGAATAA 780
 TGGGCATTGA GATCTACTGG GACTGCAACC TAGACCGTTG GTTCCATCAC TGCCATCCCA 840
 AATACAGTTT CCGTCGCTT GACGACAAGA CCACCAACGT GTCCTGTGAC CTGGCTTACA 900
 70 ACTTCAGATA CGCCAAGTAC TACAAGGAAA ACAATGTTGA GAAACGGACT CTGATAAAAG 960
 TCTTCGGGAT CCGTTTGTAC ATCTGTGTTT TTGGCACCGG AGGAAAAATT GACATTATCC 1020
 AGCTGGTTGT GTACATCGGC TCAACCTCTC CTAATCTGG GCTGTGCTC CCATATTAT CCCTGGTGCA 1140
 ACTTCTCAT CGACACTTAC TCCAGTAACT GCTGTGCTC CCATATTAT CCCTGGTGCA 1140
 75 AGTGTGTCA GCTCTGTGTG GTCAACGAAT ACTACTACAG GAAGAAGTGC GAGTCCATTG 1200
 TGGAGCCAAA GGAGCATATTA AAGTATGTGT CCTTTGTGGA TGAATCCCACT ATTAGGATGG 1260
 TGAACAGCA GCTACTAGGG AGAAGTCTGC AAGATGTCAA GGGCCAAGAA GTCCCAAGAC 1320
 CTGCGATGGA CTTACAGAT TGTCCAGGC TGCCCTGGC CTTCCATGAC ACACCCCGA 1380
 TTCTGGGACA ACCAGAGGAG ATACAGCTGC TTAGAAAGGA GGCGACTCCT AGATCCAGGG 1440
 ATAGCCCCGT CTGCTGCCAG TGTGGAAGCT GCCTCCCATC TCAACTCCCT GAGAGCCACA 1500
 80 GGTGCTGGA GGAGCTGTGC TGCCGGAATA AGCCGGGGGC CTGCATCACC ACCTCAGAGC 1560
 TGTTCAGGAA GCTGCTCTG TCCAGACACG TCCTGCAGTT CCTCTGCTC TACCAGGAGC 1620
 CCTTGTGGC GCTGGATGTG GATTCCACA ACAGCCGGCT GCGGCACTGT GCCTACAGGT 1680
 GCTAOGCCAC CTGGCGCTTC GGCTCCAGG ACATGGCTGA CTTTGCCATC CTGCCAGCT 1740
 GCTGCCGCTG GAGGATCCGG AAAGAGTTTC CGAAGAGTGA AGGGCAGTAC AGTGGCTTCA 1800

AGAGTCCTTA CTGAAGCCAG GCACCGTGGC TCACGTCTGT AATCCCACT TTT 1853

Seq ID NO: 159 DNA Sequence

Nucleic Acid Accession #: NM_001793.2

Coding sequence: 54-2543

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1 11 21 31 41 51
| | | | |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCGCGTCCG GGCAGCTGCT TCACCCCTCT 60
CTCTGCGACC ATGGGGCTCC CTGCTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120
CTGGCTGCGAG TGGCGGCGCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
CTTGAGGCGG GAGAGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
CTGCCCTGGG CAGAGCCAGC CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
TGAAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTCA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTGCTGTGA GAGAAAGGAG CAGGCTGTTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCAGCG TGTGTGAGAG AATGGTGCCCT CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAAGT 780
GACAGCCACG GATGAGGATG ATGCCATCTA CACTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAGG ACCCACAGA CCTCATGTTT ACCATTCACT GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGAAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCACTC ACGGCAGTGG CAGTAGTGGA 1020
GATCCCTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATAT 1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGAGCGCCCT 1140
CAACTCACC GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCAATT 1200
TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCCTG ACAACCCAGG AGGGTTTGGG 1260
TTTTGAGGCC AAAAACAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
ACTGTGTGTT GTCCCACTCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCATCTGCGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
TGTGGGCACC CTGACCGTG AGGATGAGCA GTTTGTGAGG AACAACTCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAACT 1680
ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTTG AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGGCACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCCTG CTGGTGTGTC TTTTGTGGT 2100
GAGAAAGAAG CCGAAGATCA AGGAGCCCTC CTACTCCCA GAAGATGACA CCGGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGAGC TGGCAACCAAC 2280
CATCATCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAG TCGCAACTT 2340
TATAATTGAG AACCTGAAG CGGCTAACAC AGACCCCA CAACCCGCTC ACGACACCTT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGAGCGCGCG TCCCTGAGCT CCCTCACTTC 2460
CTCGGCTTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGTCC TGCAGGGCTG 2580
GGGACCAAACT GTGAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTCGGAG CTGTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTGTCTTCC TTAGCCCTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACTCTCCAC CTGGGCCAGG GTTGCTCTCAG AGGCCAAGTT TCCAGAAAGC 2820
TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGTCT GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTTAAAT GCTATCTTCA AAAAGTTAGG GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTCCAGAC CCCAATGCCT CCCATTCCGA 3060
TGGATCTCTG CGTTTATTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTTCCCT 3120
60 GTTGGCTTGC TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA 3205

Seq ID NO: 160 DNA Sequence

Nucleic Acid Accession #: NM_002571.1

Coding sequence: 99..587

65
70
75
80

1 11 21 31 41 51
| | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACTG GAGATCGTTC TGACAGATG GGAGAAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAACGA GGGCAGCGTG CTGATACTG ACTACGACAA TTCTCTGTTT CTCTGCTAC 420
AGGACACCA CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGTGGT 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCT 600
CCAGGAAGAC CAGACTCCCA CCCTTCACA CTCCAGAGC AGTGGGACTT CCTCTGCC 660
TTTCAAGAA TAACCACAGC TCAGAAGAGC ATGACGTGGT CATCTGTGTC GCCATCCCT 720
TCCTGCTGCA CACTGCAAC ATTGCCATGG GAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAAC CTTGAGCAT G 811

Seq ID NO: 161 DNA Sequence

Nucleic Acid Accession #: NM_001327.1

Coding sequence: 89..631

	1	11	21	31	41	51	
5	AGCAGGGGGC	GCTGTGTGTA	CCGAGAATAC	GAGAATACT	CGTGGGCCCT	GACCTTCTCT	60
	CTGAGAGCCG	GGCAGAGGCT	CCGAGGCCAT	GCAGGCCGAA	GGCCGGGGCA	CAGGGGGTTC	120
	GACGGGCGAT	GCTGATGGCC	CAGGAGGCCC	TGGCATTCTCT	GATGGGCCAG	GGGGCAATGC	180
	TGGCGGCCCA	GGAGAGGGCG	GTGCCACGGG	CGGCAGAGGT	CCCGGGGGCG	CAGGGGCAGC	240
	AAGGGCTCTG	GGGCCGGGAG	GAGGCGCCCC	CGGGGTCCG	CATGGCGGGC	CGGCTTCAGG	300
	GCTGAATGGA	TGCTGCAGAT	GCGGGGCCAG	GGGCCGGAG	AGCCGCCTGC	TTGAGTTCTA	360
10	CCTCGCCATG	CCTTTCCGGA	CACCCATGGA	AGCAGAGCTG	GCCCGCAGGA	GCCTGGCCCA	420
	GGATGCCCA	CCGCTTCCCG	TGCCAGGGGT	GCTTCTGAAG	GAGTTCAGTG	TGTCGGGCAA	480
	CATACTGACT	ATCCGACTGA	CTGCTGCAGA	CCACGCCCAA	CTGCAGCTCT	CCATCAGCTC	540
	CTGTCTCCAG	CAGCTTTCCT	TGTTGATGTG	GATCACGCAG	TGCTTCTGTC	CGGTGTTTTT	600
	GGCTCAGCCT	CCCTCAGGGC	AGAGGGGCTA	AGCCAGCCT	GGCGCCCCCT	CCTAGGTTCAT	660
15	GCCTCTCTCC	CTAGGGAATG	GTCCAGCAC	GAGTGGCCAG	TTGTTGTGG	GGGCTTGATT	720
	GTTTGTGCT	GGAGGAGGAC	GGCTTACATG	TTTGTTCCTG	TAGAAAATAA	AACTGAGCTA	780

Seq ID NO: 162 DNA Sequence

Nucleic Acid Accession #: NM_020994

Coding sequence: 53..459

	1	11	21	31	41	51	
	CCTCGTGGGC	CCTGACCTTC	TCTCTGAGAG	CCGGGCAGAG	GCTCCGGAGC	CATGCAGGCC	60
	GAAGGCCAGG	GCACAGGGGG	TTCCAGGGGC	GATGCTGATG	GCCAGGAGG	CCCTGGCATT	120
25	CTGATGGCC	CAGGGGGCAA	TGCTGGCGCG	CCAGGAGAGG	CGGTGCCAC	GGGCGGCAGA	180
	GGTCCCCGGG	GCGCAGGGGC	AGCAAGGGCC	TGGGGCCGA	GAGGAGGGCG	CCCGCGGGGT	240
	CCGATAGCGG	GTGCGGCTTC	TGCGCAGGAT	GGAAGGTGCC	CCTGCGGGGC	CAGGAGGGCG	300
	GACAGCCGCC	TGCTTCAGTT	CCGACTGACT	GCTGCAGACC	ACCGCCAATC	GCAGCTCTCC	360
	ATCAGCTCCT	GTCTCCAGCA	GCTTTCCTTG	TTGATGTGGA	TCACGCAGTG	CTTTCGCCCC	420
30	GTGTTTTTGG	CTCAGGCTCC	CTCAGGGCAG	AGGCGCTAAG	CCCAGCTGG	CGCCCCCTTC	480
	TAGGTATGCG	CTCCTCCCTC	AGGGAATGGT	CCCAGCACGA	GTGGCCAGTT	CATTGTGGGG	540
	GCCTGATTGT	TTGTGCTGG	AGGAGGACGG	CTTACATGTT	TGTTTCTGTA	GAATAATAAG	600
	CTGAGCTA						608

Seq ID NO: 163 DNA Sequence

Nucleic Acid Accession #: NM_006928.2

Coding sequence: 1..1986

	1	11	21	31	41	51	
40	ATGGATCTGG	TGCTAAAAAG	ATGCCTTCTT	CATTGGCTG	TGATAGGTGC	TTTGCTGGCT	60
	GTGGGGGCTA	CAAAAGTACC	CAGAAACCAG	GACTGGCTTG	GTGTCTCAAG	GCAACTCAGA	120
	ACCAAGCGCT	GGAAACGGCA	CTGTATCCA	GAGTGACAG	AAGCCAGAG	ACTTGACTGC	180
	TGGAGAGGTG	GTCAAGTGTG	CCTCAAGGTC	AGTAATGATG	GGCCTACACT	GATTGTGTGA	240
	AATGCTCCT	TCTCTATTGC	CTTGAACCTC	CCTGGAAGCC	AAAAGGTATT	GCCAGATGGG	300
45	CAGGTTATCT	GGGTCAACAA	TACCATCATC	AATGGAGGCC	AGGTGTGGGG	AGGACAGCCA	360
	TGTATATCCC	AGGAACTGA	CGATGCCTGC	ATCTCCCTG	ATGGTGGACC	TTGCCCATCT	420
	GGCTCTGGT	CTCAGAAGAG	AGCTTTGTT	TATGTCTGGA	AGACCTGGGG	CCAATACTGG	480
	CAAGTTCTAG	GGGCCCCAGT	GTCTGGGCTG	AGCATTGGGA	CAGGCAGGGC	AATGCTGGGC	540
	ACACACACCA	TGGAAGTGAC	TGTCTACCAT	CGCGGGGAT	CCCGGAGCTA	TGTGCCCTCT	600
50	GCTCATTCCT	GCTCAGCCTT	CACCATTACT	GACCAAGTGC	CTTCTCCGT	GAGCGTGTC	660
	CAGTTGCGGG	CCTTGGATGG	AGGGAACAAG	CACCTCCTGA	GAAATCAGCC	TCTGACCTTT	720
	GCCTCTCAG	TCCATGACCC	CAGTGGCTAT	CTGGCTGAAG	CTGACCTCTC	CTACACCTGG	780
	GACTTTGGAG	ACAGTAGTGG	AACCCGTATC	TCTCGGGCAC	TTGTGGTCAC	TCATACTTAC	840
	CTGAGGCGTG	GGCCAGTCC	TGCCAGGTTG	GTCTGCAGG	CTGCCATTCC	TCTCAGCTCC	900
55	TGTGGCTCCT	CCCCAGTTCC	AGGCACACCA	GATGGGCACA	GGCCAACTGC	AGAGGCCCTC	960
	ACACCCACAG	CTGGCCAACT	GCCTACTACA	GAAGTTGTGG	GTAATACACC	TGGTCAGGGC	1020
	CCAATGTCAG	AGCCCTCTGG	AACCACATCT	GTGCAGGTGC	CAACCACTGA	AGTCATAAGC	1080
	ACTGCACCTG	TGCAGATGCC	AACTGCAGAG	AGCACAGGTA	TGACACCTGA	GAAGGTGCCA	1140
	GTTCAGAGG	TGATGGGTAC	CACACTGGCA	GAGATGTCAA	CTCCAGAGGC	TACAGGTATG	1200
60	ACACCTGCAG	AGGTATCAAT	TGTGGTGGCT	TCTGGAACCA	CAGCTGCACA	GGTAACAACCT	1260
	ACAGAGTGGG	TGGAGACCAC	AGCTAGAGAG	CTACCTATCC	CTGAGCTGTA	AGGTCCAGAT	1320
	GCCAGCTCAA	TGATGTCTAC	GGAAAGTATT	ACAGGTTCCC	TGGGCCCTCT	GCTGGATGGT	1380
	ACAGCCACCT	TAAGGCTGGT	GAAGAGACAA	GTCCCCCTGG	ATTGTGTTCT	GTATCGATAT	1440
	GGTTCTTTT	CCGTACCCCT	GGACATTGTC	CAGGATATTG	AAAGTGCCGA	GATCCTGCAG	1500
65	GCTGTGCCGT	CCGGTGAGGG	GGATGCATT	GAGCTGACTG	TGTCCTGCCA	AGGCGGGCTG	1560
	CCCAAGGAAG	CCTGCATGGA	GATCTCATCG	CCAGGGTGCC	AGCCCTCTGC	CCAGCGGCTG	1620
	TGCCAGCCTG	TGCTACCCAG	CCCAGCCTGC	CAGCTGGTTC	TGCACCATAT	ACTGAAGGGT	1680
	GGCTCGGGGA	CATATGCTCT	CAATGTGTCT	CTGGCTGATA	CCAACAGCCT	GGCAGTGGTC	1740
	AGCACCCAGC	TTATCATGCC	TGGTCAAGAA	GCAGGCCTTG	GGCAGGTTCC	GCTGATCGTG	1800
70	GCATCTTGG	TGGTGTGAT	GGCTGTGGTC	CTTGCACTTC	TGATATATAG	GCGCAGACTT	1860
	ATGAAGCAAG	ACTTCTCCGT	ACCCAGTTG	CCACATAGCA	GCAGTCACTG	GCTGCGTCTA	1920
	CCCCGATCT	TCTGCTCTTG	TCCCATTTGG	GAGAATAGCC	CCCTCTCTAG	TGGGCAGCAG	1980
	GTCTGA						1986

Seq ID NO: 164 DNA Sequence

Nucleic Acid Accession #: NM_001922.2

Coding sequence: 415..1974

	1	11	21	31	41	51	
80	GCAATTAAG	TCAAGAGCTA	AGGAGGGAGG	GAGAGGGTTT	AGAAATACCA	GCATAATAAG	60
	TAGTATGACT	GGGTGCTCTG	TAAATTAAC	CAATTAGACA	AAGCCTGACT	TAACGGGGGA	120
	AGATGGTGAG	AAGCGTACC	CTCATTAAT	TTGGTTGTTA	GAGGCGCTTC	TAAAGAAATT	180
	AAGTCTGTGA	TTGTTTGA	TCACATAAAA	TTGTGTGTGC	ACGTTTATGT	ACACATGTGC	240
	ACACATGTAA	CCTCTGTGAT	TCTTGTGGGT	ATTTTTTTAA	GAAGAAAGGA	ATAGAAAGCA	300

5
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 15
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 25
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 35

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AAGAAAAATA AAAAACTACTG AAAAGAAAAG ACTGAAAGAG TAGAAGATAA GGAGAAAAAGT 360
ACGACAGAGA CAAGGAAAGT AAGAGAGAGA GAGAGCTCTC CCAATTATAA AGCCATGAGC 420
CCCCCTTGGT GGGGGTTTCT GCTCAGTTGC TTGGGCTGCA AAATCCTGCC AGGAGCCCGAG 480
GGTCAGTTCC CCCAGTCTCG CATGACGGTG GACAGCCTAG TGAACAAGGA GTGCTGCCCA 540
CGCCTGGGTG CAGAGTGGCG CAATGTCTGT GCCTCTCAGC AAGGCCGGGG GCAGTGCACA 600
GAGGTGGGAG CGACACAAGG GCCTGGAGT GGTCCCTACA TCCTACGAAA CCAGGATGAC 660
CGTGAGCTGT GGCCAAGAAA ATTCTTCCAC CGSACCTGCA AGTGACACAGG AAATCTTGCC 720
GGCTATAATT GTGGAGACTG CAAGTTTGGC TGGACCGGTC CCAACTGCGA GCGGAAGAAA 780
CCACCATGTA TCTGGAGAAA CATCCATTCC TTGAGTCCTC AGGAAAAGAG GCAGTTCTTG 840
GGCGCCTTAG ATCTCGCGAA GAAGAGAGTA CACCCGACT ACGTGATCAC CACACAACAC 900
TGGCTGGGCC TGCTTGGGCC CAATGGAAAC CAGCCGAGT TTGCCAACTG CAGTGTATTAT 960
GATTTTTTTG TGTGGCTCCA TTATTATTCT GTTAGAGATA CATTATTAGG ACCAGGACGC 1020
CCCTACAGGG CCATAGATTT CTCACATCAA GGACCTGCAT TTGTTACCTG GCACCGGTAC 1080
CATTGTGTGT GTCTGGAAAG AGATCTCCAG CGACTCATTG GCAATGAGTC TTTTGCTTTG 1140
CCCTACTGGA ACTTGGCCAC TGGGAGGAAC GAGTGTGATG TGTGTACAGA CCAGCTGTTT 1200
GGGCGCAGCA GACCAGACGA TCCGACTCTG ATTAGTCGGA ACTCAAGATT CTCAGCTGG 1260
GAAACTGTCT GTGATAGCTT GGATGACTAC AACCACCTGG TCACCTTGTG CAATGGAAAC 1320
TATGAAGGTT TGCTGAGAAG AAATCAAATG GGAAGAAAAC GCATGAAATT GCCAACCTTA 1380
AAAGACATAC GAGATTGGCT GTCTCTCCAG AAGTTTGACA ATCTCCCTTT CTTCAGAAC 1440
TCTACCTTCA GTTTCAGGAA TGCTTTGAA GGGTTTGATA AAGCAGATGG GACTCTGGAT 1500
TCTCAAGTGA TGAGCCITCA TAATTGGTT CATTCTCTCC TGAACGGGAC AAACGCTTTG 1560
CCACATTGAG CCGCCAATGA TCCCATTTTT GTGGTTCTTC ATTCTTTTAC TGATGCCATC 1620
TTTGATGAGT GGATGAAAAG ATTTAATCCT CCGTCAGATG CCTGGCCTCA GGAGCTGGCC 1680
CCTATTGGTC ACAATCGGAT GTACAACATG GTTCTTTCT TCCTCCAGT GACTAATGAA 1740
GAACTCTTTT TAACTCTAGA CCAACTGGGC TACAGCTATG CCAATGATCT GCCAGTTTCA 1800
GTTGAAGAAA CTCCAGGTTG GCCCACAAC CTCTTAGTAG TCATGGGAAC ACTGGTGGCT 1860
TTGGTTGGTC TTTTGTGCT GTTGGCTTTT CTTCATATA GAAGACTTCG AAAAGGATAT 1920
ACACCCCTAA TGGAGACACA TTAAAGCAGC AAGAGATACA CAGAAGAAGC CTAGGCTGCT 1980
CATGCTTATC CTAAGAGAAG AGGCTGGCCA AGCCACAGTT CTGACGCTGA CAATAAAGGA 2040
ACTAATCTCT ACTGTTCTCT CTGAGTTGA AGATCTTTGA CATAGGTTCT TCTATAAGTA 2100
TGATGATCTC ATTCAGAAGA TGCTTAGCTG TAGTTTCCCG TTTGCTTGCT TGTTTAACAA 2160
ACCCAACCTA AGTGCTTGAG GCTACCTCTA CCTTCAAATA AAGATAGACC TGACAATTG 2220
TGATATCTAA TAATAACCCC CCCCCAATA TTGATTAAGC CTCTCCTTT TCTGAAAGCA 2280
TTTAAAAAAA A
  
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Seq ID NO: 165 DNA Sequence
 Nucleic Acid Accession #: XM_059422.3
 Coding sequence: 207..1400

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 65
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 75
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1 11 21 31 41 51
| | | | |
TGTTGGGCTG CCCGGGCTGC GCGGCGTCTG CAGGCGCCAC CGCTGCCTCT TTCCGGCTGT 60
GACCTCTCTC GCGGCGGCTG CTTGGCTGCG TCCTCGACT CCCCGGCGCG CCGAGACCAG 120
GCTCCCGCTC CGGTGCGGCG CGCACCGCCC TCCGCGGCGG CCCCCTGGGG ATCCAGCGAG 180
CGGGGTGCTC CTTGGTGGAA GGAACCATGA ACTGGCATCT CCCCCTCTTC CTCTTGGCGT 240
CTGTGACGCT GCCTTCCATC TGCTCCCACT TCAATCCTCT GTCTCTCGAG GAACTAGGCT 300
CCAACACGGG GATCCAGGTT TTCAATCAGA TTGTGAAGTC GAGGCTCAT GACAACATCG 360
TGATCTCTCC CCATGGGATT GCGTCGGTCC TGGGGATGCT TCAGTCTGGG GCGGACGGCA 420
GGACCAAGAA GCAGCTCGCC ATGGTGATGA GATACGGCGT AAATGGAGTT GGTAAAAATAT 480
TAAAGAAGAT CAACAGGCCC ATCGTCTCCA AGAAGAATAA AGACATTGTG ACAGTGCGTA 540
ACGCGGTGTT TGTTAAGAAT GCCTCTGAAA TTGAAGTGCC TTTTGTTACA AGGAACAAAG 600
ATGTGTTCCA GTGTGAGGTC CGGAATGTA ACTTTGAGGA TCCAGCCTCT GCCTGTGATT 660
CCATCAATGC ATGGGTAAAA AATGAAACCA GGGATATGAT TGACAATCTG CTGTCCCGAG 720
ATCTTATTGA TGGTGTGCTC ACCAGACTGG TCCTCGTCAA CGCAGTGTAT TTCAAGGGTC 780
TGTTGAAATC ACGGTTGCCA CCGGAGAACA CAAAGAAACG CACTTTCTGT GCAGCGGAGC 840
GGAAATCCTA TCAAGTGCCA ATGCTGGCCC AGCTCTCCGT GTTCCGGTGT GGGTCGACAA 900
GTGCCCCCAA TGATTATTGG TACAACCTCA TTGAACCTGCC CTACACGGG GAAAGCATCA 960
GCATGCTGAT TGCACCTGCC ACTGAGAGCT CCACTCCGCT GTCTGCCATC ATCCACACA 1020
TCAGCACCAA GACCATAGAC AGCTGGATGA GCATCATGGT GCCCAAGAGG GTGCAAGTGA 1080
TCCTGCCCAA GTTCACAGCT GTAGCACAAA CAGATTGTA GAGCGCGCTG AAGTTCTTG 1140
GCATTACTGA CATGTTTGAT TCATCAAAGG CAAATTTTGC AAAATAACA AGGTGAGAAA 1200
ACCTCCATGT TTCTCATATC TTGCAAAAAG CAAAAATTGA AGTCAGTGAA GATGGAACCA 1260
AAGCTTCAGC AGCAACAAC TCAATTCTCA TTGCAAGATC ATCGCCTCCC TGGTTTATAG 1320
TAGACAGACC TTTTCTGTTT TTCAATCGAC ATAATCCTAC AGGTGCTGTG TTATTCAATG 1380
GGCAGATAAA CAACACCTGA AGAGTATACA AAAGAAACCA TGCAAGCAA CGACTACTTT 1440
GCTACGAAGA AAGACTCCTT TCCTGCATCT TTCATAGTTC TGTTAAATAT TTTGTACAT 1500
CGCTCTTTTT TCAAACTAG TTCTTAGGAA CAGACTCGAT GCAAGTGTG CTGTTCTGGG 1560
AGGTATTGGA GGGAAAAAAC AAGCAGGATG GCTGGAACAC TGTAAGTAGG AATGAATAGA 1620
AAGGCTTGCA GATGCTTAAA AGATTCTTTA AACTACTGAA CTGTACCTA GGTTAACAAC 1680
CCTGTTGAGT ATTTGCTGTT GTTCCAGTTC AGGAATTTTT GTTTGTTTT GTCTATATG 1740
GCGGCTTTTT AGAAGAAATT TAATCAGTGT GACAGAAAAA AAAATGTTTT ATGGTAGCTT 1800
TTACTTTTTA TGAAAAAAAA ATTATTGCTC TTTTAAATTC TTTTCCCTCA TCCCTCTCCA 1860
AAGTCTGAT AGCAAGCGTT ATTTGGTGG TAGAAACGGT GAAATCTCTA GCCTCTTTGT 1920
GTTTTGTGTG TTGTGTTGTG TGTTGTTTAA TATAATGCAT GTATTCACTA AAATAAAATT 1980
TAAAAAATC CTGCTCTGCT AGACAAGGTT GCTGTTGTGC AGTGTGCTG TCACTACTGG 2040
TCTGTACTCC TTGGATTGTC ATTTTGTGAT TTTGTACAAA GTAAAAATAA ACTGTTATGA 2100
GTAGT
  
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Seq ID NO: 166 DNA Sequence
 Nucleic Acid Accession #: XM_040512.3
 Coding sequence: 382..1302

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1 11 21 31 41 51
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GGGCGCGCGG GGCAGGAGGA GTTGAGGAG GACGATGCCT TTATCAGCGT GCAGGTGCCG 60
GCGCGCCGCT TTTTGGGCTC CGGACCCCC GGGAGTGGGA GCGGCGAGTG GCGACGCTC 120
  
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	AAC	TG	TCC	GA	AGG	ATC	CG	CTT	CT	CA	GG	CGA	CTT	GC	AG	AACTAC	180
	AG	CC	CG	CCG	AG	CC	CG	AG	CC	CG	AG	CC	CG	AG	CC	CG	240
	TCC	CG	AG	CCG	AG	CC	CG	AG	CC	CG	AG	CC	CG	AG	CC	CG	300
5	AAC	GC	CCCTC	TCC	GG	AG	ATG	TCC	GA	AG	ATG	TCC	GA	AG	ATG	TCC	360
	AAG	AT	TCC	AT	CA	AG	AA	CAT	G	CG	CA	AG	CA	AG	CA	AG	420
	AT	CA	GT	GG	CA	GA	AT	CC	TT	CT	GT	AG	TAT	TT	CA	GT	480
	CA	AG	T	CG	GG	AG	AT	G	GA	CG	AG	GA	AG	CA	AT	CA	540
	G	AG	AT	CA	TT	G	AT	G	GT	G	AG	CT	G	T	T	CA	600
10	CA	AT	T	CT	GT	T	AC	CC	CA	AA	TG	CT	T	GA	AA	AT	660
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	AC	CC	AG	GG	GA	GC	CT	CA	CA	AG	CT	CA	CA	AG	CT	CA	780
	CT	CT	TT	GG	AT	G	AT	G	GC	CT	TT	GG	AT	G	AT	G	840
	T	AC	AT	GA	CA	AG	T	GA	CA	AG	T	GA	CA	AG	T	GA	900
15	AC	CT	CA	AG	GA	AG	TT	CC	TC	AC	AT	TA	AG	CT	GA	CT	960
	CG	AG	AT	GC	TT	GC	GC	AG	AG	GC	TT	GC	GC	AG	AG	GC	1020
	GC	CT	TT	CG	TT	CA	TT	GA	AA	AG	CT	CG	CT	TC	AA	AG	1080
	CT	GT	GT	CG	TT	GC	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	1140
	GA	AG	T	CA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	AT	1200
20	AT	TG	CC	TT	GC	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	AT	1260
	GA	AG	T	CA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	AT	1320
	CC	AG	GG	CC	CA	TT	CT	CA	GC	TT	GG	TT	GA	CA	GC	TT	1380
	AA	AG	T	GA	AA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	1440
	AC	T	GA	AA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	AT	1500
25	CC	T	CA	AG	CA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	1560
	T	AG	CG	AG	AA	AG	TT	GA	CA	AA	AT	GC	TT	GA	CA	AA	1620
	AG	CG	T	GG	T	CC	AG	AT	CT	GT	T	CC	AG	AT	CT	GT	1680
	AC	CG	GG	GA	AG	AT	CT	GT	T	CC	AG	AT	CT	GT	T	CC	1740
	CA	AG	AG	T	GT	G	CA	AA	AT	GC	TT	GA	CA	AA	AT	GC	1800
30	GT	GG	T	GT	G	CA	AA	AT	GC	TT	GA	CA	AA	AT	GC	TT	1860
	C	AG	T	CC	CG	CC	TT	T	AC	AG	CA	AG	CA	AG	CA	AG	1920
	CA	AT	T	AT	T	CT	AG	AT	T	CT	AG	AT	T	CT	AG	AT	1980
	TC	CT	CC	AC	CC	TT	AG	AA	AT	GC	TT	GA	CA	AA	AT	GC	2040
	T	AA	AG	AG	GC	AG	T	CT	GT	AG	T	CT	GT	AG	T	CT	2100
35	CG	CT	CT	GT	AA	CT	CT	CT	GT	AA	CT	CT	CT	GT	AA	CT	2160
	CC	AG	T	GT	GA	AT	GG	T	GG	GC	CG	CC	CG	CC	CG	CC	2220
	GT	G	CA	T	CA	GA	AT	T	CA	GA	AT	T	CA	GA	AT	T	2280
	AC	CC	CA	GA	AT	T	CA	GA	AT	T	CA	GA	AT	T	CA	GA	2340
	T	G	CG	T	TT	GA	AG	CT	GA	AA	AT	GC	TT	GA	AG	CT	2400
40	CG	T	G	CG	CC	AG	GC	T	GT	CA	AG	GC	T	GT	CA	AG	2460
	TC	GT	AT	GT	AG	CA	CT	GT	CG	CA	CT	GT	CG	CA	CT	GT	2520
	A	AG	T	CC	CC	CT	GT	AG	AG	CT	GT	AG	AG	CT	GT	AG	2580
	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	2587

Seq ID NO: 167 DNA Sequence																
Nucleic Acid Accession #: BC008826																
Coding sequence: 188..2695																
	1	11	21	31	41	51										
50	GGC	CAGGAGG	TCCG	GGCCTCT	GGACTAGGAA	CCGACAGCCC	CCCTCCCGCC	GTCCTCCCTC								60
	CTCT	CTCCAG	CCGTTT	TGGG	GAGGGCTACT	CCACGCTCCG	GATAGTTTCC	GAGGGTCTATC								120
	CGTC	CCGAC	TCCG	CTTTCC	GTTTGCCTCT	CCCTGGATA	TAATTTCCGA	GGCAAGCTGC								180
	CCCC	GAGTAT	ACCACG	CTGG	CCGGCCGTCT	CCCGACGATG	ATCGCGCGCC	CCCGCGGGCA								240
	GAAC	TACCCG	GTAG	CCGGT	CTGGA	AGTGTCCATC	CCCTCCGGCC	AGGGCGCGGT								300
55	CAAC	CAGCTC	GGCGGG	CTTT	TTATCAACGG	CAGCGCCGTG	CCCAACACCA	TCCGCCACAA								360
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	TGGT	GCCATC	GGCGG	CAGCA	AGCCCAAGT	GACAAAGCCT	GAGCTGGAGA	AGAAAATTCA								540
	GGAT	ACA	GAATG	CAAA	CGGGCATGTT	CAGCTGGGAA	ATCCGAGACA	AAATTACTCA								600
60	GAAG	CGCGGT	TGTG	ATCGAA	ACACCGTGCT	GCGATGAGT	TCCATCAGCC	GCATCTGAGG								660
	AGCT	AAATTT	GGGA	AAAGTG	AAGAGGAGGA	GGCCGACTTG	GAGAGGAAGG	AGCGCAGAGGA								720
	AAGC	GAGAAG	AAGCG	CAAA	ACAGCATCGA	CGGCATCTCTG	AGCGAGCGAG	CCTCAGCAAC								780
	CCAAT	CAGAT	GAAG	CGCTCTG	ATATTGACTC	TGAACCAAGT	TTACCACTAA	AGAGGAAACA								840
	GCGC	AGAAG	CGA	ACCACT	TCACAGGCA	ACAGCTGGAG	GAACTGGAGC	GTGCTTTTGA								900
65	GAG	AACTAT	TAC	CTTGACA	TTTATACTAG	GGAGGAATCT	CCCGACGAGC	CGAAGCTCAC								960
	CGAG	CGCCGA	TG	CAGGTCT	GGTTTAGACA	CAGCTGGTCA	AGATGGAGGA	AGCAAGCTGG								1020
	GGC	CAATCA	CTG	ATGGCTT	TCAACCATCT	CATTCGCGG	GGGTTCCCTC	CCACTGCCAT								1080
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	CAGC	ATGGA	TTT	TTCAGC	ATACACAGAC	CTTTGTGCCT	CGCTCGGGGC	CTCTCAAA								1320
	CAT	GAACCC	ACC	ATTGGCA	ATGGCTCTC	ACCTCAGAAT	TCAATTCGTC	ATAATCTGTC								1380
	CCT	CAACAG	AAG	TTTATC	GTTGTGAGAA	TGAAGGAAC	GGAAAAGTT	CTTGGTGGAT								1440
	GCT	CAATCCA	GAG	GGTGGCA	AGAGCGGGAA	ATCTCTAGG	AGAAGAGAGT	CATCCACATG								1500
75	CA	ACAACAGT	AAAT	TTGCTA	AGAGCCGAAG	CCGAGCTGCC	AGAAAGAAAG	CATCTCTCCA								1560
	GTCT	GGCCAG	GAG	GGTGCTG	GGGACAGCCC	TGGATCACAG	TTTTCAAAT	GGCCTGCAAG								1620
	CCCT	GGCTCT	CAC	AGCAATAT	ATGACTTTGA	TAACTGGAGT	ACATTTGCCC	CTCGAAGTAG								1680
	CTCA	AAATGT	AGT	ACTAATG	TGTGGAGACT	CTACACCAT	ATGACGCAAG	AGGATGATCT								1740
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	CA	ACTTCTC	TCAT	CACCAA	CATCATTAAC	TGTTTGGACC	CAGTCTCTAC	CTGGACCAAT								1920
	GAT	GACAGC	ACG	CGGTGCT	ACTCGTTTGC	GCCCAACAA	ACCAATTTGA	ATTCACCCAG								1980
	CCC	AAATCTAC	CAAAA	ATAAT	CATATGGCCA	ATCCACGATG	AGCCCTTTAG	CCCGATAGCC								2040
	TAT	CAAACTC	CT	CAGGACA	ATAAGTTCGAT	TTATGGAGGT	ATGAGTCAAT	ATAATCTGTC								2100
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	CTCCTCCGTG	AGCAGCTGCA	ATGGCTATGG	CAGAATGGGC	CTTCTCCACC	AGGAGAAGCT	2520
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	CCCAGCCCCA	TGGAGTCTCT	CCGAGGGAAG	GCGCGCGCGG	GCCCCCGCGG	CCCCGCGAGG	300
	CCACTGCCCC	TGCTCGCCTA	TCTGCTGGCA	CTGGCGGCTC	CGCGCGGGGG	CGCGGACGAG	360
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65	CTGCAGTATC	GGGAGGACCC	CAGATTACAG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
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Nucleic Acid Accession #: XM_063670.1

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Seq ID NO: 171 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1-2094

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 GTGCTGAGCG CAGCAGCTGT GCGCTGCTCT ACCGATGCT GCTCCAGCGC CCGCGGAGT 420
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 GCGCCCTCA CTTGGGTGGC CGTGCGGCTG CTGGGGGCG CTTTTCAGTA GTGCGCGGCC 540
 55 ACCGGGAGC CGGCTTCTCG GCAGCGCCTG TGCCCTGGCC GCAACCGCAG CTGCGCGGCC 600
 GAGCTGCGCG TGTGCGCTGT CAACAGGCC AAGCGCTCGG ACGTGACGGA CCTCCTGAAG 660
 GATCTGAAGG CTCAGTGCAG GGTGTTGGGC TGGATCTTGA TAGCAGTTGT TATCATCATT 720
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 60 GCAACTGAAT TGGCAAAAGA GAATATTAAA TGTTCCTTTG AGGGCTCGCA TCCAAAAGAA 900
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 ATCAGGTCTA CTGAAGGAGA TAQGGTGATT CTTGTTCTTG GCTTTGTAGA TTCATCTGGT 1080
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 TATTGCTTTA TTAATAAATA AACATTGGTA TTTT 1175

65 Seq ID NO: 174 DNA Sequence
 Nucleic Acid Accession #: NM_032211.5
 Coding sequence: 152..2422
 1 11 21 31 41 51
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 75 TCTGTTCTCT CTGCTGCTAG GCCAGCCCCC TCCAGCAGG CCACAGTCAC TGGGCACCA 240
 TAAGCTCCGG CTGGTGGGCC CAGAGAGCAA GCCAGAGGAG GGGCGCCTGG AGGTGCTGCA 300
 CCAGGGCCAG TGGGGCACCG TGTGTGATGA CAACTTTGCT ATCCAGGAG CCACAGTGGC 360
 TTGCGCCAG CTGGGCTTGG AAGCTGCCTT GACCTGGGCC CACAGTGCCA AGTACGGCCA 420
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 80 CCAAGTCCGG TCTAATGGCT GGGAGTCCAG TGACTGCAGT CACTCAGAAG ACGTAGGGGT 540
 GATATGCCAC CCGCGGCGCC ATCGTGGCTA CCTTCTGAA ACTGTCTCCA ATGCCCTGG 600
 GCCCCAGGCC CGGCGGCTGG AGGAGGTGCG GCTCAAGCCC ATCTTGTCCA GTGCCAAGCA 660
 GCATAGCCCA GTAGCCGAGG GAGCCGTGGA GGTGAAGTAT GAGGGCCACT GCGCGCAGGT 720
 GTGTGACCA GGTGAGCA TGAACAACAG CAGGTTGGTG TGGCGGATGC TGGGCTTCCC 780
 CAGCGAGGTG CCGTGCAGCA GCCACTACTA CAGGAAAGTC TGGGATCTGA AGATGAGGGA 840

	CCCTAAGTCT	AGGGCTGAAGA	GCCTGACGAA	TAAGAACTCC	TTCTGGATCC	ACCAGGTAC	900
	CTGCCCTGGG	ACAGAGCCCC	ACATGGCCAA	CTGCCAGGTG	CAGGTGGCTC	CAGCCCGGGG	960
	CAAGCTGCGG	CCAGCTGTCC	CAGGTGGCAT	GCATGCTGTG	GTCACTGTGT	TGGCAGGGCC	1020
5	TCACCTCCCG	CCACCGAAGA	CAAAGCCACA	ACGCAAGGGG	TCCTGGCCAG	AGGAGCCGAG	1080
	GGTGGCGCTG	CGCTCCGGGG	CCCAGGTGGG	CGAGGGCCGG	GTGGAAGTGC	TCATGAACCG	1140
	CCAGTGGGGC	ACGGTCTGTG	ACCACAGGTG	GAACCTCATC	TCTGCCAGTG	TCGTGTGTGG	1200
	TCAGCTGGGC	TTTGGCTCTG	CTCGGGAGGC	CCTCTTTGGG	GCCCGGCTGG	GCCAAAGGGT	1260
	AGGGCCCATC	CACCTGAGTG	AGGTGCGCTG	CAGGGGATAT	GAGCGGACCC	TCAGCGACTG	1320
	CCCTGCCCTG	GAAGGGTCCC	AGAATGGTTG	CCAACATGAG	AATGCTGCTG	CTGTCAAGTG	1380
10	CAATGTCCCT	AACATGGGCT	TTCAGAATCA	GGTGCCTTGG	GCTGGTGGGC	GTATCCCTGA	1440
	GGAGGGGCTA	TTGGAGGTGC	AGGTGGAGGT	GAACGGGGTC	CCACGCTGGG	GGAGCGTGTG	1500
	CAGTGAAGAC	TGGGGGCTCA	CCGAAGCCAT	GGTGGCTGCG	CGACAGCTCG	GCCTGGGTTT	1560
	TGCCATCCAT	GCCTACAAGG	AAACCTGGTT	CTGGTGGGGG	ACGCCAAGGG	CCCAGGAGGT	1620
	GGTGATGAGT	GGGGTGGCT	GCTCAGGCAC	AGAGCTGGCC	CTGCAGAGT	GCCAGAGGCA	1680
15	CGGGCCGGTG	CAGTGTCTCC	ACGGTGGCGG	GCCTTCCTG	GCTGGAGTCT	CCTGCATGGA	1740
	CAGTGCACCA	GACCTGGTGA	TGAACGCCCA	GCTAGTGCAG	GAGACGGCCT	ACTTGGAGGA	1800
	CGCGCGCTCG	AGCCAGCTGT	ATTGTGCCCA	CGAGGAGAAC	TGCTCTTCCA	AGTCTGGCGA	1860
	TCACATGGA	TGGCCCTACG	GATACCGCCG	CCTATTGGCG	TTCTCCACAC	AGATCTACAA	1920
	CTTGGGCGGG	ACTGACTTTC	GTCCAAAGAC	TGACCGCAT	AGCTGGGTTT	GGCACCAGTG	1980
20	CCACAGGCAT	TACCACAGCA	TTGAGGTCTT	CACCCACTAC	GACCTCTCTA	CTCTCAATGG	2040
	CTCCAAGGTG	GCTGAGGGGC	ACAAGGCCAG	CTTCTGTCTG	GAGGACACAA	ACTGCCCCAC	2100
	AGGACTGCAG	CGCGCGTACG	CATGTGCCAA	CTTTGGAGAA	CAGGGAGTGA	CTGTAGGCTG	2160
	CTGGGACACC	TACCGGCATG	ACATTGATTG	CCAGTGGGTG	GATATCACAG	ATGTGGGCCC	2220
	CGGGAATTAT	ATCTTCCAGG	TGATTGTGAA	CCCCCACTAT	GAAGTGGCAG	AGTCAGATTT	2280
25	CTCCAACAAT	ATGCTGCAGT	GCGCTGCAA	GTATGATGGG	CACCGGGTCT	GGCTGCACAA	2340
	CTGCCACACA	GGGAATTTCAT	ACCCAGCCAA	TGCAGAATCT	TCCCTGGAGC	AGGAACAGCG	2400
	TCTCAGGAAC	AACTCTCATC	GAAGCTGTCA	CTGCACATCT	CTAGCTGCTG	CCGATACACC	2460
	AGATACCTCA	GCTTATTGGA	GCCATGCCCT	TCACAGATCT	CCAACTCAGA	GGAAAAGGGC	2520
	CAGTGCCAAG	GGGCACCAAG	AACTGTCTCA	GGAAAGCCTT	TGATGGCAAG	ATCACCACATC	2580
30	CAGATGGTAT	TGCTCCCTCA	GGATGGCTCT	GGGCTTGCCC	CTAAGGGCCT	GTGGCCTATG	2640
	GAATATGTCC	TCCAGGCTTT	GCTCAGCTGA	GCTCCTCTTC	TGTAAGGAAA	CCCACTCATC	2700
	CCTGAATCTT	CCACAGAGGA	TCCGGGATTC	AGGAGCTCTC	AGTTTCTTAG	GGATGGACTA	2760
	TGGCCCACTC	CCCCATCTAA	GTGGTGCTTT	GCAATGTCT	TGGAGGAGTA	TAGGACAGAG	2820
	GACCAAAATA	CACAGCAGGT	AGTGTTAGCT	CTCTGTAGG	AGCTCAAAGC	AACCACACTT	2880
35	GTATCAAAAT	CACAACTGGC	AGAGAAGCTG	GTGGATCCAA	TCCTTTCTTC	ATCTGTGTGT	2940
	ATTTAGAACT	CACCTCTCAC	ACTCTGTTCT	TAGTGTCTCT	TACCTTTATC	TTACCAACACA	3000
	CATGGGTGTT	TCTATTATCC	TTGGAAGCAC	AGACCTCGGG	CATCCCTTTA	TTGCCTGATG	3060
	GGCCAAACACC	AACAGTTACG	GAGTGTCTGA	GAAAGGGCAA	GTTCACAGA	AATGGCCAGA	3120
	TAGGGCCTTC	CTACAGAGCA	GCAAGAGTAG	GCCAAGCAGA	AAGACTGCTG	AGGTAACAGG	3180
40	GACCCACGCC	CCTGTGAGGG	CCTCTGCCAA	GGAAATAATA	TGGACCATTT	ACCTGGCAGG	3240
	CAGTCTGTCT	TCTCTCAGGA	TCACCAACGA	TCTCAGGATT	GGTCTAAACT	TCAAGTCTCA	3300
	ACCAAGTGTG	TGAAGTGAAC	TTTGCAATTGA	ATAAATTTT	GCCATGGAAA	GAACATCAAA	3360
	CAAGCCACTC	ATCTCTACAG	AGATAAGAAA	ACAAGTTTGG	CAGAGCAAGA	GACAGAAGAC	3420
	CGTGGAGAAA	TCAGAAGGGG	GAACAGTCAG	TTTAGTTAAG	GATGGAACTT	GGGAAAAGGG	3480
45	ACCAATCTCG	CTTGATGGGG	CTCTGATTTC	CTCTGTCTCA	AGTGGAAATA	AACCCCATGG	3540
	TCTTCTTGAC	ATGATTCTTG	ATCTTTTCTC	CACCTGAGACA	CACCTAAGTG	ATGATCCTTA	3600
	CAGGACTGAC	ACCTTAATGC	CAATAAAAGT	TGCTCATTAT	GGACTGCTAC	AAAAAAAAAA	3660
	AAAAA						3665
50	Seq ID NO: 175 DNA Sequence						
	Nucleic Acid Accession #: NM_001798.2						
	Coding sequence: 234..1130						
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	ACGGTACTGG	CCCTGTGTTT	CCCTCTCTCG	CGCCCGGAGA	GCCAGGGTCC	GCTTCTGCA	180
	GGGTTCACAG	CGCCCGCTC	CAGGGCCGGG	CTGACCCGAC	TCGCTGGCGC	TTGATGGAGA	240
60	ACTTCAAAA	GGTGGAAAAG	ATCGGAGAGG	GCACGTACGG	AGTTGTGTAC	AAAGCCAGAA	300
	ACAAAGTTGAC	GGGAGAGGTG	GTGGCGCTTA	AGAAAATCCG	CCTGGACACT	GAGACTGAGG	360
	GTGTGCCAGT	TACTGCCATC	CGAGAGATCT	CTCTGCTTAA	GGAGCTTAAC	CATCCTAATA	420
	TTGTCAAGCT	GCTGGATGTC	ATTACACAG	AAAATAAACT	CTACCTGGTT	TTTGAATTTT	480
	TGCACCAAGA	TCTCAAGAAA	TTGATGGATG	CCTCTGCTCT	CACTGGCAAT	CCTCTTCCCC	540
65	TCATCAAGAG	CTATCTGTTT	CAGCTGTCTC	AGGGCCTAGC	TTTCTGCCAT	TCTCATCGGG	600
	TCCTCCACCG	AGACCTTAAA	CCTCAGAAATC	TGCTTATTAA	CACAGAGGGG	GCCATCAAGC	660
	TAGCAGACTT	TGGACTAGCC	AGAGCTTTTG	GAGTCCCTGT	TCGTACTTAC	ACCCATGAGG	720
	TGGTGACCTT	GTGGTACCGA	GCTCCTGAAA	TCCTCTGGG	CTGCAAAAT	TATTCCACAG	780
	CTGTGGACAT	CTGAGGCTG	GGCTGCATCT	TTGCTGAGAT	GGTACTCGC	CGGGCCCTAT	840
	TCCTGGGAGA	TTCTGAGATT	GACCACTCT	TCCGGATCTT	TCGGACTCTG	GGGACCCAG	900
70	ATGAGGTGGT	GTGGCCAGGA	GTTACTTCTA	TGCTTGATTA	CAAGCCAAGT	TTCCCAAGT	960
	GGGCCCCGCA	AGATTTTAGT	AAAGTTGTAT	CTCCCTGGA	TGAAGATGGA	CGGAGCTTGT	1020
	TATCGCAAA	GCTGCACTAC	GACCCCTAAC	AGCGGATTTT	GGCCAAGGCA	GCCCTGGCTC	1080
	ACCCCTTTCT	CCAGGATGTG	ACCAAGCCAG	TACCCCATCT	TCGACTCTGA	TAGCCTTCTT	1140
	GAAGCCCCCA	GCCTTAATCT	CACCTCTCTC	TCCAGTGTGG	GCTTGACCAG	GCTTGGCCTT	1200
75	GGGCTATTGT	GACTCAGGTG	GGCCCTCTGA	ACTTGCTTTA	AACTACTACC	TTCTAGTCTT	1260
	GGCCAGCCAA	CTCTGGGAAT	ACAGGGGTGA	AAGGGGGGAA	CCAGTGAATA	TGAAGGAAG	1320
	TTTCAGTATT	AGATGCACCT	AGTTAGCTCT	CCACCACTCT	TTCCCTCTTC	TCTTAGTTAT	1380
	TGCTGAAGAG	GTTTGGTATA	AAAATAATTT	TAAAAAAGCC	TTCTTACAG	TTAGATTGTC	1440
80	CGTACCAATC	TCTGAATGCC	CCATAATATT	TATTTCCAGT	GTTTGGGATG	ACCAGGATCC	1500
	CAAGCCTCCT	GCTGCCACAA	TGTTTATAAA	GGCCAAATGA	TAGCGGGGGC	TAAGTTGGTG	1560
	CTTTTGAGAA	CCAAGTAAAA	CAAAACCACT	GGGAGGAGTC	TATTTTAAAG	AATTCGGTTG	1620
	AAAAAATAGA	TCCAATCAGT	TTATACCTTA	GTTAGTGTTT	TGCCTCACCT	AATAGGCTGG	1680
	GAGACTGAAG	ACTCAGCCCG	GGTGGGGCTG	CAGAAAAATG	ATTGGCCCCA	GTCCCTTGT	1740
	TTGTCCCTTC	TACAGGCATG	AGGAATCTGG	GAGGCCCTGA	GACAGGGATT	GTGCTTCATT	1800

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CCAATCTATT GCTTCACCAT GGCCTTATGA GGCAGGTGAG AGATGTTTGA ATTTTCTCT 1860
TCCTTTTAGT ATTCTTAGTT GTTCAGTTGC CAAGGATCCC TGATCCCATT TCCTCTGAC 1920
GTCCACCTCC TACCCCATAG GAGTTAGAAG TTAGGTTTGA GGATCATTTT TGAGAATGCT 1980
GACACTTTTT CAGGGCTGTG ATTGAGTGTG GGCATGGGTA AAAATATTTC TTTAAAAGAA 2040
GGATGAACAA TTATATTAT ATTTGAGTT ATATCCAATA GTAGAGTTGG CTTTTTTTTT 2100
TTTTTTTTTG GTCATAGTGG GTGGATTGTG TGCCATGTGC ACCTTGGGGT TTTGTAATGA 2160
CAGTGCTAAA AAAAAAAAAA CATTTTTTTT TATGATTGT CTCTGTACCC CTTGTCTTGT 2220
AGTGCTCTTG CTATTAACGT TATTGTGAAT TTAGTTTGTG GCTCATTAAG AAAATGTGCC 2280
TAGTTTTATA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2328

Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: NM_052827.1
Coding sequence: 234..1028

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Seq ID NO: 177 DNA Sequence
Nucleic Acid Accession #: NM_032738.1
Coding sequence: 118..1197

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1440
1500

5 TCTCAACTGG GGGCAATTTT GGGGGGATGGT GGGATGTGTG TGCTACTGGC ATCCAGTAAA 1560
 GTCATTATAC TTGGGGGGTT GGGGGATGGT GGGATGTGTG TGCTACTGGC ATCCAGTAAA 1620
 TAGAAGCCAG GGGTGCCGCT AAACATCCTA TAATGCACAG GGCAGTACCC CACAACGAAA 1680
 AATAATCTGG CCCAAAATGT CAGTTGTACT GAGTTTGAGA AACCCAGCC TAATGAAACC 1740
 CTAGGTGTGG GGCTCTGGAA TGGGACTTTG TCCCTTCTAA TTATTATCTC TTTCAGCCT 1800
 CATTGAGCTA TTCTTACTGA CATACCACTG TTTAGCTGGT GCTATGGTCT GTTCTTTAGT 1860
 TCTAGTTTGT ATCCCTTCAA AAGCCATTAT GTTGAAATCC TAATCCCCAA GGTGATGGCA 1920
 TTAAGAAGTG GGCCTTTGGG AAGTGATTAG ATCAGGAGTG CAGAGCCCTC ATGATTAGGA 1980
 10 TTAGTGCCCT TATTTAAAAA GGCCCCAGAG AGCTAACTCA CCCTTCCACC ATATGAGGAC 2040
 GTGGCAAGAA GATGACATGT ATGAGAACCA AAAAAAGCT GTGCGCAAAC ACCGACTCTG 2100
 TCGTTGCTT GATCTGAAC TTCAGCCTC CAGAACTATG AGAAATAAAA TTCTGTTGTT 2160
 TGTAAAAAAA AAAAAAAA A 2181

Seq ID NO: 178 DNA Sequence

Nucleic Acid Accession #: NM_002346.1

Coding sequence: 136..531

15 1 11 21 31 41 51
 20 GCTCCGCCCA GCGCGGCTCC AGAGCGCGCG AGGTTCCGGG AGCTCCGCCA GGCTGCTGGT 60
 ACCTGCGTCC GCGCGGCGAG CAGGACAGGC TGCTTTGGTT TGTGACCTCC AGGCAGGACG 120
 GCCATCTCTT CCAGAAATGAA GATCTTCTTG CCAGTGCTGC TGGCTGCCCT TCTGGGTGTG 180
 GAGCGAGCCA GCTCGCTGAT GTGCTTCTCC TGCTTGAACC AGAAGAGCAA TCTGTACTGC 240
 CTGAAGCCGA CCATCTGCTC CGACCAGGAC AACTACTGCG TGACTGTGTC TGCTAGTGCC 300
 25 GGCATTGGGA ATCTCGTGAC ATTTGGCCAC AGCCTGAGCA AGACCTGTTT CCGGCTGCTG 360
 CCCATCCAG AAGGGCTCAA TGTTGGTGTG GCTTCCATGG GCATCAGCTG CTGCCAGAGC 420
 TTTCTGTGCA ATTTCACTGC GGCCTGAGGC GGGCTGCGGG CAAGCGTCA CTTGCTGGGT 480
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 CCCTGTGCCC CGATCCCCCA GCTCAGGAAG GAAAGCCAG CCCTTTCTGG ATCCACAGT 600
 30 GTATGGGAGC CCTTGACTCC TCACGTGCTT GATCTGTGCC CTTGGTCCCA GGTGAGGCC 660
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 GGAGTCTTAC GGTCCAACAT CAGACCAAGT CCGATGGACA TGCTGACAGG TCCCCAGGG 840
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 35 GCACGTGGCG GCTTCTGGGG GCCATGTTTG GGGAGGGAGG TGTGCCAGCA GCGTGAGAG 960
 CTTAGTCTCC TGTAGCCCCC TGCCCTGGCA CAGCTGCATG CACTTCAAGC GCAGCCTTTG 1020
 GGGGTGTGGG TTTCTGCCAC TTCGGGCTT AGGCCCTGCC CAAATCCAGC CAGTCTCTCC 1080
 CCAGCCACC CCCACATTGG AGCCCTCCTG CTGCTTTGGT GCCTCAATA AATACAGATG 1140
 TCCCC 1145

Seq ID NO: 179 DNA Sequence

Nucleic Acid Accession #: XM_113526.2

Coding sequence: 253..2409

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 GAGCAGCACT CCAAGCTCGC CGGCCTTTGG TCTCCAGGAC TTGTCCAGC AGCCCTCGA 120
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 CTGCCAGGCT TCCAGGGCTC CAACTTGACG ACGGCTGTT GTGGGACAGT CTCTGTAATC 240
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 55 TTGAACAAT TCATCTCTCA GCGTGTGGAG GGAGGCTCTG GACTGGATAT TTCTACTCG 360
 GCGCCAGGTT CTCTGCAGAT GCAGTACCAG CAGAGCATGC AGCTGGAGGA AAGAGCAGAG 420
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 AGTCACAAGA GGGCTCGAGT GGAGCTGGAG AGAGCAGCCA GCACCACTGC CAGGAACCTAC 540
 GAGCGTGAGG TCGACCGCAA CCAGGAGCTC CTGACCGGCA TCCGGCAGCT TCAGGAGCGG 600
 60 GAGGCGCGGG CGGAGGAGAA GATGCAAGAG CAGCTGGAGC GCAACAGGCA GTGTGAGCAG 660
 AACTTGGATG CTGCCAGCAA GAGGCTGCGT GAGAAAGAGG ACAGTCTGGC CCAGGCTGGC 720
 GAGACATCA ACGCACTGAA GGGGAGGATC TCGGAATGCG AGTGAGCGT GATGGACAG 780
 GAGATGCGGG TGAAGCGCCT GGAGTGGAG AAGCAGGAGC TGCAAGGAGCA GCTGGACCTG 840
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 65 GCAAGAGCAG ACCACGAGCA GCAGATTAAG GATCTGGAGC AGAAGCTGTC CTTGCAAGAG 960
 CAGGATGCAG CGATTGTGAA GAACATGAAG TCTGAGCTGG TACGGCTCCC TAGGCTGGAA 1020
 CGGAGCTGA AGCAGCTGCG GGAGGAGAGC GCGCACCTGC GGGAGATGAG AGAGACCAAC 1080
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 70 TGGGAGAGCT TGGACCAAGC CATGGGCTTG AGCATCAGGA CTCCAGAAAG CTTTCCAGA 1260
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 CTCAGAAAC GGGTCTGCT GCTCACAAG GAGCGGAGCG GTATGCGGGC CATCTGGGG 1500
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 80 GAGGAAAAG GGAATGCTGA GGCACAGCTG GAGCGGCGAG CTCTGACAGG TGACTATGAC 1860
 CAGAGCAGGA CCAAAGTGCT GCACATGAGC CTGAACCCCA CAGTGTGGC CAGGAGCGC 1920
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5 GTGGCGTAGC CTGCAGGCTC GGGGGCATAG CCGGAGCCAC TCTGCTTGGC CTGACCTGCA 2460
 GGTCCCCCTGC CCGGCCAGCC ACAGGCTGGG TGCAGTCTCT GCCTCTCCAG CCCACAGGG 2520
 CAGCAGCATG ACTGACAGAC ACCTGCGGAC CTACGTCGGG CTTCCTGCTG GGGCGGCCAG 2580
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 AGCCTGGGTT CCTCACCTTG TGAATAAAAA TCTTCTCCCC TAG 2683

Seq ID NO: 180 DNA Sequence

Nucleic Acid Accession #: NM_000273.1

Coding sequence: 1..1275

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 15 TTGGCGCTGG GCCTTCTGCA GCTGCTGCCG GGCCTCGGCG CCGCGGGCCC CGGGTCCCCC 240
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 GGCTGCTCGG GTATGGTGAT CCGGTCCACC GTGTGGTTAG GATTCCCAAA TTTTGTGTGAC 360
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 ATGTGGATCC AGCTGTGTGA CAGTGCCTGC TTCTGGTGGC TGTTTTGCTA TGCACTGGAT 480
 20 GCTTATCTGG TGATCCGGAG ATCGGCAGGA CTGAGCAGCA TCCTGCTGTA TCACATCATG 540
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 25 GTGATCAAGA TCCGATTTTT CAAAATCATG CTGGTTTTAA TTATTTGTGT GTTGTGGAAT 840
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 30 CACCCATCCC CACTGATGCC CCATGAAAC CCTGCTCCG GGAAGGTGTC TCAAGTGGGT 1140
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 CATGAGAGCC TATGAAGGGG ATGTGCTGGG GGTCCAGACC CCATATTCTC CAGACTCAAC 1320
 35 AATTCTTGT CTTTAGAACT GTTTCTCAC CTTCCTCAACA CTGCACTGCC GAAGTGTAGC 1380
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Seq ID NO: 181 DNA Sequence

Nucleic Acid Accession #: NM_139317.1

Coding sequence: 174..1070

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 60 AGGCCACAGG GCGGTGGTGG GTTCTTGAGC CCCAGGAGC CAGGAGTGTG GAGGCGCAGC 900
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Seq ID NO: 182 DNA Sequence

Nucleic Acid Accession #: NM_022161.2

Coding sequence: 174..1016

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Seq ID NO: 183 DNA Sequence

Nucleic Acid Accession #: NM_021020.1

Coding sequence: 112..1902

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Seq ID NO: 184 DNA Sequence
Nucleic Acid Accession #: AF265577
Coding sequence: 1..2193

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Seq ID NO: 185 DNA Sequence
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Coding sequence: 65..1132

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Seq ID NO: 187 DNA Sequence
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CACGCTGCCC CCTCATTCTT CTCTCCAATC TGGAACTCTG ACATTGAACC CAGTTGCTCA 1320
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Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006272.1
Coding sequence: 73..351

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GCAGCCAAAC CTTTCTCTGA ACAGAGACGG TCATGCAAGA AAGCAGACAG CAAGGGCTTG 420
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Seq ID NO: 193 DNA Sequence
Nucleic Acid Accession #: NM_006157.1
Coding sequence: 103..2535

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Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_016180.1
Coding sequence: 26..1618
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GGCAGCGTAT GTGACCCGAG TCCTGCTCAG CGTAGGCTG CCCAGCAGCC TGTACAGCAT 240
TGTGTGGTTC CTCAGCCCCA TCCTGGGATT CCTGCTGCAG CCCGTGCTCG GATCGGCCAG 300
CGACCACTGC CGGTCCAGGT GGGGCCGCGG GAGACCCCTAC ATCCTCACCC TGGGAGTCAT 360
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GAAAAGTTAAA AATGGTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAAA 900
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Seq ID NO: 195 DNA Sequence
Nucleic Acid Accession #: NM_012400.2
Coding sequence: 18..455

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Seq ID NO: 196 DNA Sequence
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Coding sequence: 80..2041

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5	CACCTACACC	ATGTCTCGAA	TCAACTTGGC	GATCCGGGAG	CAGCTTTTCT	CCTCCCTGCT	780
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10	AGCCGTTGGA	GGCGTGCAGA	CCGTTGCGAG	TTTGGGGGCC	GAGGAGCATG	AAGTCTGTGG	1140
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	CAAACCATAC	AAAAATTCCT	TTTCCCGAAG	GAAAAGGGCT	TTCTCAATAA	GCCTCAGCTT	1860
	TCTAAGATCT	AACAAGATAG	CCACCGAGAT	CCTTATCGAA	ACTCATTTTA	GGCAATATG	1920
	AGTTTTATTG	TCCGTTTACT	TGTTTCAGAG	TTTGTATTGT	GATTATCAAT	TACCACACCA	1980
	TCTCCCATGA	AGAAAGGGAA	CGGTGAAGTA	CTAAGCGCTA	GAGGAAGCAG	CAAGTCGGT	2040
	TAGTGGAAAG	ATGATTGGTG	CCCAGTTAGC	CTCTGCAGGA	TGTGGAAACC	TCCTTCCAGG	2100
75	GGAGGTTCTG	TGAATTGTGT	AGGAGAGGTT	GTCTGTGGCC	AGAATTTAAA	CCTATACTCA	2160
	CTTTCCCAAA	TTGAATCACT	GCTCACACTG	CTGATGATT	AGAGTGCTGT	CCGGTGAGGA	2220
	TCCCAACCGA	AGGTCTTATC	TAATCATGAA	ACTCCCTAGT	TCCTTCATGT	AACTTCCCTG	2280
	AAAAATCTAA	GTGTTTCTAT	AATTGAGAG	TCTGTGACCC	ACTTACCTGT	CATCTCACAG	2340
	GTAGACAGTA	TATAACTAAC	AACCAAGAC	TACATATTGT	CACTGACACA	CACGTTATAA	2400
80	TCATTTATCA	TATATATACA	TACATGCATA	CACCTCAAA	GCAATAAATT	TTTCACTTCA	2460
	AAACAGTATT	GACTTGTATA	CCTTGTAAAT	TGAAATATTT	TCTTTGTATA	AATAGATATG	2520
	TATCAATAAA	TAGACCATTA	ATCAG				
	Seq ID NO: 198 DNA Sequence						

Nucleic Acid Accession #: NM_006533.1

Coding sequence: 72..467

1 11 21 31 41 51
 5 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCAGCACC CCCTTGCTCA CTCTCTTGCT 60
 CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCT 120
 TCTCCGACC TGGTGTGAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
 CGGACCAGCA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
 10 CCGACTGCCG ATTCTTGACC ATTCACCGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
 AGGGCCGTCG GCGGCTCTTC TGGGGAGGCA GCGTTCAGG AGATTACTAT GGAGATCTGG 360
 CTGCTCGCCT GGGCTATTTT CCAAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420
 GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CAGGTGAGCT CAGCTACCG 480
 CTGGCCCTCG CGTTTCCCCT CCTTGGGTTT ATGCAATATC AATCAGCCCA GTGCAAAC 538

Seq ID NO: 199 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
 20 MHSFPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOQPGP IGGDAHFDEE ERWTFNFREY NLHRVAAHEL GHSGLSLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 25 FYMRTNPFYP EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVHLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWR DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDAVF MKDGFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

Seq ID NO: 200 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
 30 MHSFPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 35 YTPDLPRADV DHAIEKAPQL WSNVPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOQPGP IGGDAHFDEE ERWTFNFREY NLHRVAAHEL GHSGLSLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVHLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWR DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDAVF MKDGFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

Seq ID NO: 201 Protein sequence

Protein Accession #: NP_002413

1 11 21 31 41 51
 45 MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLEKDVQK FVRRKDSGPV 60
 VKKIREMQKF LGLLEVMRKP SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIEN 120
 YTPDLPRADV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYFPGDGPV 180
 LAHAAYAPGP INGDHAFDD EOWTKDTTGT NLFLVAAHEI GHSGLGFHSA NTEALMYPST 240
 50 HSLTDLTRFS LSLDDINGIQ SLYGPPDPS ETPLVPTPEV PPEPGTPANC DPALSFDAS 300
 TLRGELILFK DRHFWRKSLR KLEPELHLIS SFWSPLPSGV DAAYEVTSKD LVFIFKGNQF 360
 WAIRGNEVRA GYPRGIHTLG FPPTVRKIDA AISDKENKNT YFFVEDKYWR FDEKRNSEMP 420
 GPPKQIAEDF GPIDSKIDAV FEEFGFFYFF TGSSQLEFDP NAKKVTHTLK SNSWLNC

Seq ID NO: 202 Protein Sequence

Protein Accession #: NP_001845

1 11 21 31 41 51
 55 MEPWSSRWKT KRWLWDFTVT TLALTFLFQA REVRGAAPVD VLKALDFHNS PEGISKTTGF 60
 CTNRKNSKGS DTAYRVSKQA QLSAPTKQLF PGFTFPEDFS ILFTVKPKKG IQSFLLSIYN 120
 60 EHGIIQIIGVE VGRSEVFLFE DHTGKPAED YPLFRVTNIA DGKWHRAIS VEKKTVTMIV 180
 DCKKKTTPKL DRSERAIVDT NGITVFGTTRI LDEEVFEGDI QOFLITGDPK AAYDYCEHYS 240
 PDCDSSAPKA AQAQEPQIDE YAPEDIIEYD YEYGEAEYKE AESVTGPTV TEETIAQTEA 300
 NIVDDPFQYIN YGTMESYQTE APRHVSQTNE PNPVEEIPTE EYLTGEDYDS QRKNSDLY 360
 65 ENKEIDGRFS DLLVDGLGE YDFYKEYE DKPTSPPNEE FPGVPAAETD ITETSINGHG 420
 AYGEKGQKGE PAVVEPGLMV EGPPGPAGPA GIMGPPGLQG PTGPPGDPGD RGPGRPGPLP 480
 GADGLPFPFG TMLMLPFRYG GDGSKGPTIS AQEAQAQAIL QQARIALRGP PGPMGLTGRP 540
 GPVGGPGSSG AKGESGDPG QGPRGVQCPP GPTGKPGKRG RPDGAGGRGM PGEPAKGRD 600
 GFDGLPLPLG DKHGRGERGP QGPPGPPGDD GMRGEGEIG PRGLPGEAGP RGLLGPRTGP 660
 GAPGQPGMAG VDGPPGPKGN MGPQGERGPP GQGNPPGPGQ LPGPOGPIGP PGEKGPQKGP 720
 70 GLAGLPAGAD PPGHPGKEGQ SGEKALCPP GPQGPIGXPG PRGVKGADGV RGLKSGKGEK 780
 GEDGFPFGFK DMGLKGDGE VQIGPRGXD GPEGPKGRAG PTGDPGPGSQ AGEKGLGVP 840
 GLPGYPRGPG PKGSTGPFPG PGANGKGRG GVAGKPGPRG QRGPTGPRGS RGARGPTGKP 900
 GPKGTSGGDD PPGPPGERGP QGPQGPVGF PPKPPGPPPG RMGCPGHPGQ RGETGPGKGT 960
 75 GPPGPGVVG POGPTGTEGT IGERGYGPP GPPGEQGLPG AAGKEGAKGD PGPOGISGKD 1020
 GPAGLRGFP ERGLPCAQGA PGLKGGEGPQ GPPGVPVSGP ERGSAGTAGP IGLRGRPGPQ 1080
 GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPPGKGSK 1140
 GKGEGNPPG PGLQGPFVGA PGIAGDGEPP GPRGQQGMFG QKGEDEARGF PGPPGPIGLQ 1200
 GLPGPPGEGK ENGDDVGMGP PGPPGPRGPQ GPNAGDGPQG PPGSVGSGVG VGEKGEPEGA 1260
 80 GNPGPPEAGE VGGPPGERGE KGEAGPPGAA GPPGAKGPPG DDGPKGNRGP VGFPGDPGPP 1320
 GELGPAQDQ VGGDKGEDGD PQQPGPPGPS GEAGPPGPPG KRGPAGAAGA EGRQSEKGA 1380
 GEAGAEGPPG KTGVPVGP GPAGKPPGGLR GIPGVPGEQG LPGAAGQDGP PGPMGPPGLP 1440
 GLKGDGSGK EKHGHLGLL IGPGEQGEK GDRGLPGTQG SPGAKGDGGI PGPAGLPGFP 1500
 GPPGLPGPQG PKGNKSGTGP AQKGDGSLP GPPGPPGPPG EVIQPLPILS SKKTRRHTG 1560
 MQADADDNIL DYSDMGEIEF GSLNLSKQDI EHMKPPMGTP TNPARTCKDL QLSHPDFPDG 1620

EYWDPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPKEKPGS WPSEFKRGKL 1680
 LSYLDVEGNS INMVMTFLK LLTASARQNF TYHCHQSAAM YDVSSGSYDK ALRFLGSNDE 1740
 EMSYDNNFFI KTLYDGCTSR KGYEKTIVIEI NTPKIDQVPI VDVMSIDFGD QNQKFGFEVG 1800
 PVCFLG

Seq ID NO: 203 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
 MRPGQPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGGSPG ANGIPGTGPI PGDRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ 180
 GSPENSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK

Seq ID NO: 204 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MPGTLKTRTG APADYRVILK TSQEDELDPV DDISVRVMSS QSVLVSVDLP VLEKQKKVVA 60
 SRQYTVRYRE KGLARWYK QIANRRVLIE NLIPDTVYEF AVRIQGERD GKWSTSVFQR 120
 TPESAPTTAP ENLNWVPNG KPTVVAASWD ALPETEGVKV VCLLDGTGLFS VSSFQPSAKS 180
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTTPKPSL 240
 SLQCCQECST QKDFCLAYL IDIQTQVMK DPQLEGSVFG PCFLFYFLTF MLDIGGFSFI 300
 MCYEDPVSSL TGNLSKSVAA SKADVQNTTE DNGKPEKPEP SSPSPRAPAS SQHPSVPASP 360
 QGRNAKLLLL DLKNKILANG GAPRKPQLRA KKAEELEDLQS TEITGEEELG SREDSPPMSFS 420
 DTQDQKRTLR PPSRHHGSHV APGRTAVRAR MPALPRREGV DKPGFSLATQ PRPGAPPSAS 480
 ASPAHASTQT GTSRHSPLPA SLNDNDLVDS DEDERAVGSL HPGGAFAQPR PALSPSRQSP 540
 SSVLRDRSSV HPGAKPASPA RRTPHSGAAE EDSSASAPPS RLSPPHGGSS RLLPTQPHLS 600
 SPLSKGGKDG EDAPATNSNA PSRSTMSSSV SSSLSSRTQV SEGAESDGE SHGDGDRDGD 660
 GRQAETAATQ LRARPASGHF HLLRHKPFAA NGRSPSRFSI GRGPRLPQSS SPQSTVPSRA 720
 HPRVPSHSDS HPKLSSGSHG DEEDEKPLPA TVVNDHVPSS SRQPISRGWE DLRRSPQRGA 780
 SLHKEPIPE NPKSTGADTH PQGKYSSLAS KAQDVQQSTD ADTEGHSKPA QPGSTDRHAS 840
 PARPPAARSQ QHPSVPRMT PGRAPEQPPP PVVATSQHHP GPQSRDAGRS PSQPRLSLTQ 900
 AGRPRPTSQG RSHSSSDPYT ASSRGMPLTA LQNDQEDAGG SYDDDDSTEVE AQDVRAPAMA 960
 ARAKEAASL PKHQVQESPT GAGAGGDHRS QRGHAASPAR PSRPGGPQSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQSHVSA EDEEEEDAGF FKGGKEDLLS SSVPKWPSSS TPRGGKDADG 1080
 SLAKEEREPA IALAPRGGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFSTTPMLS LRQMMHARF RNPLSRQPAR PSYRQYNGR PNVEGKVLPG 1200
 SNGKPMGQRI INGPQGTQWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLG GDRITVDLEG 1260
 TPVVSDELPL LFGQGRHGTG LANAQDKPIL SLGGKPLVLG EVIKKTTTHP TTTMQPTTTT 1320
 TPLPTTTTTR PTTATTMQPT TTTTLPPTTT PRPTTATTRR TTTTRPTTTT RTTTRTTTTT 1380
 TPKPTTPIPT CPPTGLERHD DDGNLIMSSN GIPECYAEED EFGSLETDTA VPTEAYVIY 1440
 DEDYEFETSR PPTTTEPSTT ATTPRVIPEE GAISFFPEEE FDLAGRKRKF APYVTYLNKD 1500
 PSAPCSLTDL LDHFDQVDSL EIIIPNDLKS DLPPQHAPRN ITVVAVEGCH SFIVVDWDKA 1560
 TPGDLVTGYL VYSASYEDI RNKFSTQASS VTHLPIENLK PNTRYFKVQ AQNPFGYGI 1620
 SPSVSFVTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 205 Protein Sequence
 Protein Accession #: NP_055059

1 11 21 31 41 51
 MDPPAGAARR LLCFALLLLL LLLPPPLLP PPANARLA AAADPPGGPL GHGAERILAV 60
 PVRTAQGRRL VSHVVAATS RAGVRARRAA PVRTSPSPGG NEEEPGSHLF YNVTVFGRDL 120
 HLRLRNARL VAPGATMEHQ GEKCTTRVEP LLGSLCYLVG VAGLAESSV ALSNCDGLAG 180
 LIRMEEEFF IEPLEKGLAA QEAQGRVHV VYRRPPTSP LGGPQALDTG ASLDSLDSLS 240
 RALGVLEHA NSSRRARRH AADDYNIIEV LLGVDDSVVQ FHGKEHVQKY LLTLMNIVNE 300
 IYHDESLGAH INVVLVRIIL LSYGKSMSLI EIGNPSQSL NVCRWAYLQQ KPDTHGDEYH 360
 DHAIFLTRQD FGSPGMQGYA PVTGMCHPVR SCTLNHEDGF SSAPVVAHET GHVLGMEHDG 420
 QGNRCGDEVR LGSIMAPLVQ AAFHRFHWRS CSQQELSRYL HSYDCLLDLP FAHDWPAIPQ 480
 LPGLHYSMNE QCRDFGLGY MMCTAFRTFD PCKQLWCSHP DNPYFCKTKK GPPLDGTMCA 540
 PGKHCYKGC IWLTPDILKR DGSWGAWSPP GSCSRTCTGT VKFRTRQCDN PHPANGGRTC 600
 SGLAYDFQLC SRQDCPDLSA DFREEQCRQW DLYFEHDAQ HHWLPHEHRD AKERCHLYCE 660
 SRETGEVVS M KRMVHDGTRC SYKDAFSLCV RGDCKRVGCD GVIGSSKQED KCGVCGGDNS 720
 HCKVVKGTFT RSPKKGHYK MFEIPAGARH LLIQEV DATS HHLAVKNLET GKFI LNEEND 780
 VDASSKTFIA MGVWEYERDE DGRETQTMG PLHGTITVLV IPVGDTRVSL TYKMIHEDS 840
 LNVDDNNVLE EDSVVYEWAL KKWSPCKSKP GGGSQFTKYG CRRRLDHKMV HRGFCAALSK 900
 PKAIRACNP QECSQPVVWT GEWEPCSQTC GRTGMQVRSV RCIQPLHNT TRSVHAKHCN 960
 DARPESRRAC SRELCPGRWR AGPWSQCSVT CGNGTQERP PV PCRTADDSFG ICQEERPETA 1020
 RTCLRGCPR NISDPKSKSY VVQWLSRPDP DSPIRKISSK GHCQGDKSIF CRMEVLSRYC 1080
 SIPGYNKLSK KSCNLYNNLT NVEGRIEPPP GKHNDIDVFM PTLPVPTVAM EVRPSSTPL 1140
 EVPLNASSTN ATEHPETNA VDEPKIHGL EDEVQPNLI PRRPSPYEKT RNQRIQELID 1200
 EMRKKEMLGK F 1211

Seq ID NO: 206 Protein sequence
 Protein Accession #: NP_076927

1 11 21 31 41 51
 MGENDPPAVE APFSPRSLFG LDDLKISPVA PDADAVAAQI LSLPLKFFP IIVIGIALI 60
 LALAIGLGH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVVRV GGQNAVQLVF 120
 TAASWKTMC S DDWKGHYANV ACAQLGFPY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHSHVYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQMPW QASLQFGYH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLDN PAPSHLVEKI VYHSHYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360

VPLISNKICN HRDVYGGIIS PSMCLCAGYLT GGVDSCQGDG GGPLVCQERR LWKLVGATSF 420
GIGCAEVNKP GYVTRVTSFL DWIHEQMERD LKT

Seq ID NO: 207 Protein Sequence
Protein Accession #: CAC03433.2

1 11 21 31 41 51
1 MSSTDTFTA SWELVVRVDH PNEEQQKDVLT LRVSGDLHVG GVMLKLVEQI NISQDWSDF 60
10 LWHEQKHCHL LKTHWTLDKY GVQADAKLLP TPQHKMLRLR LPNLKMLRLR VSFSAVVFKA 120
VSDICKILNI RRSEELSLK PSGDYFKKKK KDKNNKEPI IEDILNLESS PTASGSSVSP 180
GLYSKTMPTI YDPIINGTPAS STMTWFSDSP LTEQNCILA FSQPPQSPEA LADMYQPRSL 240
VDKAKLNAGW LDSSRSLEMQ GIQEDQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300
LLEEIDCTEE EMLIFAAALQY HISKLSLSAE TQDFAGESEV DEIEAALSNI EVTLEGGKAD 360
15 SLLEDITDIP KLADNLKLFK PKKLLPKAFK QYWFIFKDTI IAYFNKELE QGEPELKLNL 420
RGCEVVPDVM VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKGMTMADS 480
SYQPEVLNLI SFLRMKNRNS ASQVASSLEN MDMNPECFVS PRCAKHKSK QLAARILEAH 540
QNVAQMPLVE AKLRFIQAWQ SLPEFGLTYY LVRFKSGSKD DILGVSYNRL IKIDAATGIP 600
VTTWRFTNKK QWNVNMETRQ WVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660
20 NETLDEDLFH KLTGGQD 677

Seq ID NO: 208 Protein Sequence
Protein Accession #: NP_114433.1

1 11 21 31 41 51
25 MASRSMRLLL LLSCLAKTGV LGDIIMRPSK APGWFYHKSQ CYGYFRKLNR WSDAELECCS 60
YGNAGHLASI LSLKEASTIA EYISGVQRSQ PIWIGLEDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP 158

Seq ID NO: 209 Protein Sequence
Protein Accession #: XP_051860.2

1 11 21 31 41 51
30 MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPNWPGH DQDHHVHIGQ 60
GKTLILLTSSA TVYSIHISEG GKLVKDHDE PIVLRTRHIL IDNGGELHAG SALCPFGGNF 120
35 TIILYGRADE GIQDPDYYGL KYIGVGKGA LELHGQKKLS WTFLNKLTHP GGMAEGGYFF 180
ERSWGHGRVI VHIIDPKSGT VIHSDRFDY RSKKESERLV QYLNAVDPGR ILSVAVNDEG 240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTUVKGNPSS SVEDHIEYHG HRGSAARVF 300
KLFQTEHGEY FNVLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
40 IQATTMDGVN LSTEVYKKG QDYRFACYDR GRACRSYRVR FLCKGKVRPK LTVTIDTNVN 420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPGR SCAPNQVKA GKPMYHLIGE 480
EIDGVDMAE VGLLSRNIIV MGEMEDKCYR YRNHICNFFD FDTFGGHIFK ALGFKAAHLE 540
GTELKHMGOQ LVGQYPIHFH LAGDVDERGG YDPPTYIRD LSIHHTFSRCV TVHGSNGLLI 600
KDVVGYNLSG HCFPTEDGPE ERNTFDHCLG LLVKSGLTLLP SDRDSKMKM ITEDSYPGYI 660
45 PKPRQDCNAV STFWMANFNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720
LGKFNYNRAH SNYRAGMIID NGVKITEASA KDKRPFLSII SARYSPHQA DPLKPREPAI 780
IRHFIAKQK DHGAWLRGGD VWLDSRCFAD NGIGLTLASG GTFFPYDDGSK QEIKNSLFVG 840
ESGNVGTMM DNRIWPGGL DHSGRTLPIG QNPPIRGIQL YDGPINQNC TFRKFVALEG 900
RHTSALAFRL NNAMQSCPHN NVTGIAFEDV PITSRVFFGE PGWPNQLDM DGDKTSVFHD 960
50 VDGVSSEYPG SYLTNDNWL VRHPDCINVP DWRGAIKSGC YAQMYIAYK TSNLRMKIIL 1020
NDPFSHPHLYL EGALTRSTHY QYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV 1080
GLCYPRGTF SILSDVHNL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDSGLLFL 1140
KLKAQNEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKTERAV VDVPMKKLF 1200
GSQKTKDHF LEVMESSQK HFFHLWDFIA YIEVDGKYP SSEDGIQVVV IDGNQGRVVS 1260
55 HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE 1320
QMAFVGFKGS FRPIVWTLDT EDHKAKIFQV VPIPVVKKK L 1361

Seq ID NO: 210 Protein Sequence
Protein Accession #: NP_036244.1

1 11 21 31 41 51
60 MSQVKSYSY DAPSDFINFS SLDEGDTQN IDSWFEKAN LENKLLGKNG TGGLFQGKTP 60
LRKANLQAI VTLPLKVDNT YYKEAEKENL VEQSIPSNAC SSLEVEAAS RTKFAQPORR 120
SLRLSAQKDL EQKEKHVMK KAKRCATPVI IDEILPSKKM KVSNNKKKE EESAHQDTA 180
65 EKNASSPEKA KGRHTVPCMP PAKQKFLKST EEQELESKM MQQEVVEMRK KNEEFKLLAL 240
AGIGQPVKKS VSQVTSVDF HFRTERIKQ HPKNQEEYKE VNFTELRKH PSSPARVTKG 300
CTIVKPFNLG QGKKRTFDET VSTYVPLAQ VEDFHKRTFN RYHLRSKKDD INLLPSKSSV 360
TKICRDPQTP VLQTKHARA VTCKSTAELE AEELEKLQY KFKARELDR ILEGGPILPK 420
KPPVPPTPEP IGFDLEIEKR IQERESKKKT EDEHFEPHSR PCPTKILEDV VGVPEKKVLP 480
70 ITVPKSPAPA LKNRIRMPK EDEEEDPVV IKAQPVPHYG VPFKQIPEA RTVEICPFSF 540
DSRDKERQLQ KEKKIKELQK GEVPKFKALP LPHFTINLP EKKVKNVTQI EPFCLETDRR 600
GALKAQTMWK QLEELRQKQ EAACFKARP TVISQEPFVP KKEKSAVAG LSGSLVQEPF 660
QLATEKRAKE RQLEKRMKE VEAQKAQQL EEARLQEEQK KEELARLRRE LVHKANPIRK 720
YQGLEIKSSD QPLTVPVSPK FSTRFHC 747

Seq ID NO: 211 Protein Sequence
Protein Accession #: NP_065169.1

1 11 21 31 41 51
80 MSRRKQAKPO HINSEEDQGE QOPOQQTPEF ADAAPAAPAA GELGAPVNHG GNDEVASEDE 60
ATVKRLAREE THVCEKCCAE FFSISEFLEH KIONCTKNPV LIMNDEGPV PSEDFSGAVL 120
SHQPTSPGSK DCHRENGGSS EDMKEKPDAE SVVYLKTETA LPPTQDISY LAKGKVANTN 180
VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQQLQIQI LTEQIRIQVN 240
MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP 300
SATSSLSPLG APFTLKPDTG RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK 360

5 GKPPNISAVD VKPKDEAALY KHKCKYCSKV FCTDSSLQIH LRSHTGERPF VCSVCGHRT 420
TKGNLKVHFM RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSPVLVT 480
TSVGLPQNLK SGTNPDKLTG GSLPGDLQPG PSPSEGGPT LPGVGNPNYS PRAGGFQSGG 540
TPEPGSETLK LQQLVENIDK ATTDPNELI CHRVLSCQSS LKMHYRTHGT ERPFQCKICG 600
RAFSTKGNLK THLGVHRTNT SIKTQHSCEI CQKKFTNAVM LQQHIRMGMG QQIPNTPLPE 660
NPCDPTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP 720
TLGFAMMASL DAPGKVGAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL 780
ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPSTFI RAPPTYVKVE 840
VPGTFVGPST LSPGMTPLLA AOPRRQAKQH GCTRCGNFIS SASALQIHER THTGEKPFVC 900
10 NIGGRAFTTK GNLLKVMYTH GANNNSARRG RKLAIENMA LLGTDGKRVS EIFPKEILAP 960
SVNVDPVVMN QYTSMLNGGL AVKTNESIVI QSGGVPTLPV SLGATSVVMN ATVSKMDGSG 1020
SGISADVEKP SATDGVPKHQ FPHFLEENKI AVS 1053

15 Seq ID NO: 212 Protein Sequence
Protein Accession #: NP_005092
1 11 21 31 41 51
| | | | |
MGWDLTVKML AGNEFQVSL SSMVSVELKA QITQKIGVHA PQQLLAVHPS GVALQDRVPL 60
ASQGLGPGST VLLVVDKCE PLSILVRNNK GRSTYEVRL TQTVHLKQQ VSGLEGVQDD 120
20 LFWLTPEGPK LEDQLPLGEY GLKPLSTVFM NLRLRGGGTE PGGRS 165

Seq ID NO: 213 Protein sequence
Protein Accession #: Eos sequence
1 11 21 31 41 51
| | | | |
25 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCXPGKTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSY DVHGFVGRYC GDELPPDDIIS TGNVMTLKFL SDASVTAGGF 240
30 QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSL

Seq ID NO: 214 Protein sequence
Protein Accession #: NP_009046.1
1 11 21 31 41 51
| | | | |
35 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCXPGKTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
DLEDDPGCLA DYVEIYDSY DVHGFVGRYC GDELPPDDIIS TGNVMTLKFL SDASVTAGGF 240
40 QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSL

Seq ID NO: 215 Protein Sequence
Protein Accession #: NP_006389.1
1 11 21 31 41 51
| | | | |
45 MAPNASCLCV HVRSEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
RSLSSYGIKQ EKTIIHLTKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
TKTGIIPETQ IVTCNGKRLD DGMKMDYGI RKGNLLFLAS YCIGG 165

50 Seq ID NO: 216 Protein Sequence
Protein Accession #: NP_002349.1
1 11 21 31 41 51
| | | | |
55 MALQLSREQG ITLRGSAEIV AEFFSFGINS ILYQRGIYPS ETFTRVQKYG LTLVTTDL 60
LILYLNWVE QLKDWLYKCS VQKLWVVISN IESGEVLERN QFDIECDKTA KDDAPREKS 120
QKAIQDEIRS VIRQITATVT FLPILLEVSCS FDLIYTDDK LVVPEKWEES GPQFITNSE 180
VRLRSFTTTI HKVNSMVAYK IPVND 205

60 Seq ID NO: 217 Protein sequence
Protein Accession #: NP_001889.1
1 11 21 31 41 51
| | | | |
65 MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQALHF AISEYNKATK 60
DDYYRRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKQLCSF 120
EIEYEVWENR RSLVKSRCQE S

70 Seq ID NO: 218 Protein sequence
Protein Accession #: NP_009162.1
1 11 21 31 41 51
| | | | |
MDKLKCPSPF KCREKEKVA SSENPHVGEN DENQDRGNWS KKS DYLLSMI GYAVGLGNV 60
RFPYLYSNG GGAFLIPYAI MLALACLPLF FLECSLQQA SLGPVSVWRI LPLFGVGIT 120
MVLISIFVTI YYNVIAIYSL YYMFASFQSE LPWKNCSWS DKNCRSPIV THCNVSTVNK 180
GIQEIIMNK SWDINNFTC INGSEIYQPG QLPSEYWNK VALQRSSGMN ETGVIWVYLA 240
LCLLLAWLIV GAALFKGKIS SGKVYFTAL FPYVLLILL VRGATLEGAS KGISYYIGA 300
SNFTKLKEAE VWKDAATQIF YSLVAVGGL VALSSYNKFK NNCPSDAIVV CLTNCLTSVF 360
AGFAIFSILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPFWSI LFFFMLLTG 420
LDSQPASIEI ITTTIQDLFP KVMKMRVPI TLGCCLVFL LGLVCVTQAG IYVWHLIDHF 480
CAGWGLIAA ILELVGIWI YGGRNFIEDT EMMIGAKRWI FWLWWRACWF VITPILLIAI 540
80 FIWSLVQFHR PNYGAIPYD WGVALGWCHI VFCIIWIPIM AIIKIIQAKG NIFQRLISCC 600
RPASNWGPYL BQHRGERYKD MVDPKKADH EIPTVSGSRK PE

Seq ID NO: 219 Protein sequence
Protein Accession #: NP_006389.1

1 11 21 31 41 51
 MAPNASCLCV HVRSEEDWLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
 RSLSSYGIDK EKTITLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
 TKTGIIPEQT IVTCNGKRLE DGKMMADYGI RKGNNLFLAS YCIGG

Seq ID NO: 220 Protein sequence
 Protein Accession #: XP_094741.1

1 11 21 31 41 51
 MKANYSAEER FLLLGPSDWP SLQPVLFALV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60
 FLCHLALVDA GETTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAVMALD 120
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLLDHFICEL 180
 PALLKLACGG DGDITTENQMF AARVVILLPL FAVILASYGA VARAVCCMRF SGRRRRAVGT 240
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFTYV VTPALNPLIY TLRNKKVKG 300
 ARRLRLSLGR GQAGQ

Seq ID NO: 221 Protein Sequence
 Protein Accession #: NP_061155.1

1 11 21 31 41 51
 MDPFTEKLE RTRARRENLO RMAERPTAA PRSMTHAKRA RQPLSEASNQ QPLSGGEEKS 60
 CTKPSPSKKR CSDNTEVEVS NLENKQPVES TSAKSCSPSP VSPQVQQA DTISDSVAVP 120
 ASLLGMRRLG NSRLLEATAAS SVKTRMQKLA EQRRRWNDND MTDDIPESL FSPMPSEEKA 180
 ASPPKPLLNS ASATPVGRRG RLANLAATIC SWEDDVNHSF AKQNSVQEQP GTACLKSFSS 240
 ASGASARINS SSVKQEAATFC SQRDGDASLN KALSSSADDA SLVNASISS VKATSPVKST 300
 TSITDAKSCE QQNPPELLPKT PISPLKTGVS KPIVKSTLSQ TVPSKGELSR EICLQSQSKD 360
 KSTTPGGGTI KPFLERFGER CQESKESPA RSTPHRTPII TPNTKAIQER LFKQDTSSST 420
 THLAQLKQGE RQKELACLGR RFDKGNWSA EKGNSKSKQ LETKQETHCQ STPLKKHQGV 480
 SKTQSLFVTE KVTENQIPAK NSSTEPKGF ECEMTKSSPL KITLFLEEDK SLKVTSDPKV 540
 EQKIEVIREI EMSVDDDDIN SSKVINDLFS DVLEEGELDM EKSQEEMDQA LAESSEEQED 600
 ALNISSMSLL APLAQTVGVV SPESLVSTPR LELKDTSRSD ESPKPGKFQR TRVPRAESGD 660
 SLGSEDRDLL YSIDAYRSQR FKETERPSIK QVIVRKEDVT SKLDEKNNAF PCQVNIKQKM 720
 QELANNEINMO QTVIYQASQA LNCCVDEEHG KGSLEEAEAE RLLLIATGKR TLLIDELNKL 780
 KNEGPRKKNK ASPOSEFMPS KGSVTLSEIR LPLKADFVCS TVQKPDAAHY YYLIIILKAGA 840
 ENMVATPLAS TSNSLNGDAL TFTTFTLQD VSNDFEINIE VYSLVQKKDP SGLDKKKKTS 900
 KSKAITPKRL LTSITTKSNI HSSVMASPGG LSAVRTSNFA LVGSYTLISL SVGNTEFVLD 960
 KVPFLSSLEG HIYLIKIKQV NSSVEERGFL TIFEDVSGFG AWHRRWCVLG GNCISYNTYP 1020
 DDEKRNPIG RINLANCTSR QIEPANREFC ARRTNFELIT VRPQREDDRE TLVSQCRDTL 1080
 CVTKNWLSD TKEERDLWMO KLNQVLVDIR LWQPDACYKP IGKP 1124

Seq ID NO: 222 Protein Sequence
 Protein Accession #: Q9H8V3

1 11 21 31 41 51
 MAENSVLTST TGRSLADSS IFDSKVTEIS KENLLIGSTS YVEEEMPQIE TRVILVQEAG 60
 KQEELTKALK DIKGVGVKME SVEEFGELDS PEFENVFVVT DFQDSVFNLD YKADCRVIGP 120
 PVVLNCSQKG EPLPFSCRPL YCTSMNNLVL CFTGFRKKEE LVRLVTLVHH MGGVIRKDFN 180
 SKVTHLVANC TQGEKFRVAV SLGTPIMKPE WIYKAHERRN EQDFYAAVDD FRNEFKVPFP 240
 QDCIFSLFGF SDEEKTNME MTEMQGGKYL PLGDERCTHL VVEENIVKDL PFEPESKLYV 300
 VKQEWFWGSI QMDARAGETM YLYEKANTPE LKKSVMLSL NTPNSNRKRR RLKETLAQLS 360
 RDTDVSPFPF RRRPSAEHSL SIGSLDISN TPESSINYGD TPKSCTKSSK SSTPVPSKQS 420
 ARWQVAKELY QTESNYVNL ATIIQLFQVP LEEEGQRGGP ILAPEEIKTI FGSIPIDFDV 480
 HTKIKDDLED LIVNDESKS IGDIFLKYSK DLVKTYPPFV NFFEMSKETI IKCEKQKPRF 540
 KEVMTIHED KRKTEAQKI FVVVEVDGC PANLLSSHRS LVORVETISL GEHPCDRGEQ 600
 HAFLLKINQAK PECGRQSLVE LLIRPVQRLP SVALLNLNKL KHTADENPDK STLEKAIGSL 660
 KEVMTIHED KRKTEAQKI FVVVEVDGC PANLLSSHRS LVORVETISL GEHPCDRGEQ 660
 VTLFLFNCLC EIARKRHKVI GTFRSPHGQT RPPASLKHIH LMPLSQIKKV LDIRETECH 720
 NAFALLVRPP TEQANVLLSF QMTSDELPKE NWLKMCRHV ANTICKADAE NLIYTADPES 780
 FEVNTKMDMS TLSRASRAIK KTSKKVTRAF SFSKTPKRAL RRALMTSHGS VEGRSPSSND 840
 KHVMSRLSST SSLAGIPSPS LVSLPSFFER RSHTLSRSTT HLI 883

Seq ID NO: 223 Protein Sequence
 Protein Accession #: NP_002488.1

1 11 21 31 41 51
 MPSRAEDYEV LYTIGTGSYG RCQKIRKSD GKILVMKELD YGSMTEAEQ MLVSEVNLLR 60
 ELKHPNIVRY YDRIIDRTNT TLYIVMEYCE GGDLASVITK GTKERQYLDE EFVLRVMTQL 120
 TLALKCHERR SDGHTVTLHR DLKPANVFLD GKQNVKLGDF GLARILNHDT SFAKTAVGTP 180
 YYMSPEQMR MSYNEKSDIW SLGCLLYELC ALMPPTAFS QKELAGKIRE GKFRPIPYRY 240
 SDELNEIIR MLNLKDYHRP SVEEILENPL IADLVADEQR RNLERRGRQL GEPEKSDQSS 300
 PVSELKLKE IQLQERERL KAREERLEQK EQELCVRELR AEDKLARAEN LLKNYSLLKE 360
 RKFLSLASNP ELLNLPSVSI KKKVHFSGES KENIMRSNS ESQLTSSKSC KDLKKRLHAA 420
 QLRAQALSDI EKNYQLKSQ ILGMR 445

Seq ID NO: 224 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 DISYENENYN SSWIPGSHIV SPSLLNLNN GQLLPLOLQG PLNSWIPFSS GILQOQQQAQ 60
 IPGLSQFSLD ALDQFAGLLP NQIPLTGEAS FAQGAQAGQV DPLQLQTPPQ TQPGSHVMP 120
 YVFSFKMPQE QQMFQYYPV YMVLPWEQPP QTVPRSPQQT RQQQYEEQIP FYAQPGYIPQ 180
 LAEPAISGGQ QQLAFDPQLG TAPEIAVMST GEEIPYLQKE AINFRHDSAG VFMPSTSPKP 240
 STTNVFTSAV DQTIITPELPE EKDKTDSIRE P 271

Seq ID NO: 225 Protein Sequence
Protein Accession #: eos sequence

5
1 11 21 31 41 51
| | | | |
RQKEHRSRMV QIFLFRSRK IYHTMKIII LLGFLGATLS APLIPQRLMS ASNSNELLN 60
LNNGQLLPQ LQGLNLSWIP PFSGLQQQQ QAQIPGLSQF SLSALDQFAG LLPNQIPLTG 120
EASFAQGAQA QGVDPQLQQT PPQTQPGPSH VMPYVFSFKM PQEQGQMFQY YPVYMLPWE 180
10 QPQQTVPSP LRTRQQQYEE QIPFYAQGY IPQLAEPAS GQQQLAFDP QLGTAPETAV 240
MSTGEEIPYL QKEAIFNRHD SAGVFMPSST PKPSTTNVFT SAVDQITITPE LPEEKDKTDS 300
LREP 304

Seq ID NO: 226 Protein Sequence
Protein Accession #: NP_003970.1

15
1 11 21 31 41 51
| | | | |
MATTVPDGR NGLSKYYRL CDKAEAWGIV LETVATAGVV TSVAFMLTL ILVCKVQDSN 60
RRKMLPQFL FLGLVLGIFG LTFAPIIGLD GSTGPTRFLL FGILFSICFS CLLAHAVSLT 120
KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTNRT NVNVFSELSA PRNRNDFVLL 180
20 LTYVLFMLAL TFLMSSFTFC GSFTGWRHG AHYILTMLS IAIWVANITL LMLPDFDRRW 240
DDTILSSALA ANGWVFLLAY VSPFVLLTK QRNPMQYVPE DAFCKPQLVK KSYGVENRAY 300
SQEETQCFE ETGDTLYAPY STHFQLQNQP PQKEFSIPRA HAWPSYKDY EVKKEGS 357

Seq ID NO: 227 Protein Sequence
Protein Accession #: NP_116575.1

25
1 11 21 31 41 51
| | | | |
MPKIVLNGVT VDFPFQPYKC QQEYMTKVLE CLQKQVNGIL ESPTGTGKTL CLLCTTLAWR 60
EHLRDGISAR KIAERAQGL FPDRLSSWG NAAAAAGDPI ACYTDIPKII YASRTHSOLT 120
30 QVINELRNTS YRPKVCVLGS REQLCIHPEV KQESNHLQI HLCKKVASR SCHFYNNVEE 180
KSLEQELASP ILDIEDLVKS GSKHRVCPYY LSRNLKQAD IIFMPYNYLL DAKSRRAHNI 240
DLKGTVVIFD EAHNVKMCCE ESASFOLDTPH DLASGLDVID QVLEEQTKAA QQGEHPPEFS 300
ADSPSPGLNM ELEDIAKLKM ILLRLEGAID AVELPGDDSG VTKPGSYIFE LFAEAQITFQ 360
TKGCILDSLD QIIQHLAGRA GVFTNTAGLQ KLADIIQIVF SVDPSGSPG SPAGLGALQS 420
35 YKVHIHPDAG HRRTAQRSDA WSTTAARKRG KVLSYWCFSP GHSMHLEVRQ GVRSLILTSG 480
TLAPVSSPAL EMQIPFPVCL ENPHIIDKHQ IWGVVPRGP DGAQLSSAFD RRFSEECSS 540
LGKALGNIR VVPYGLLIFF PSYPVMEKSL EFWARDLAR KMEALKPLFV EPRSKGSFSE 600
TISAYARVA APGSTGATFL AVCRGKASEG LDFSDTNGRG VIIVTGLPYPP RMDPRVVLKM 660
QFLDEMKGQ GAGGQFLSGQ EYRQASRA VNQAIGRVIR HRQDYGAVFL CDHRFAFADA 720
40 RAQLPSWVRP HVRVYDNFGH VIRDAQFFR VAERTMPAPA PRATAPSVRG EDAVSEAKSP 780
GPFFSTRKAK SLDLHVPSLK QRSSGSPAAG DPESLCEVEY EQEPVPARQR PRGLLAALFH 840
SEQRAGSPGE EAHNSCSTLS LLSKRPAAE PRGGRKKIRL VSHPEEPVAG AQTDRAKLFM 900
VAVKQELSQA NFATFTQALQ DYKGSDDFAA LAACLGPLFA EDPKKNLLQ GFYQFVRPHH 960
KQQFEVCIC LTGRGCGYRP EHSIPRRQRA QVLDPTGRT APDPKLTVST AAAQQLDPQE 1020
45 HLNQGRPHLS PRPPPTGDPG SQPQWGSVP RAGKQGHAV SAYLADARRA LGSAGCSQLL 1080
AALTAYKQDD DLDKVLAVLA ALTTAKPEDF PLLHRFSMFV RPHHKQRFQ TCTDLTGRPY 1140
PGMEPPGPQE ERLAVPPVLT HRAVPPGPSR SEKTGKTQSK ISSFLRQRP GTVGAGGEDA 1200
GPSQSSGPPH GPAASEWGEH HGRDIAGQQA TCAPGGPLSA GCVCQCGGAE DVVPFQCPAC 1260
50 DFQRCQACW RHLQASRMCP ACHTASRKQS VMQVFWPEPH KDHEGAGGAR PVAAPVGUGA 1320
ACPAAGAGCT RSGRNTLPL AGRRDRGAAG VCPVPPRHLC AAAPVPRQPH DVMPVSTAPL 1380
HAVLELPGAL PLLQPLRGA 1400

Seq ID NO: 228 Protein Sequence
Protein Accession #: NP_057518.1

55
1 11 21 31 41 51
| | | | |
MPKIVLNGVT VDFPFQPYKC QQEYMTKVLE CLQKQVNGIL ESPTGTGKTL CLLCTTLAWR 60
EHLRDGISAR KIAERAQGL FPDRLSSWG NAAAAAGDPI ACYTDIPKII YASRTHSOLT 120
60 QVINELRNTS YRPKVCVLGS REQLCIHPEV KQESNHLQI HLCKKVASR SCHFYNNVEE 180
KSLEQELASP ILDIEDLVKS GSKHRVCPYY LSRNLKQAD IIFMPYNYLL DAKSRRAHNI 240
DLKGTVVIFD EAHNVKMCCE ESASFOLDTPH DLASGLDVID QVLEEQTKAA QQGEHPPEFS 300
ADSPSPGLNM ELEDIAKLKM ILLRLEGAID AVELPGDDSG VTKPGSYIFE LFAEAQITFQ 360
TKGCILDSLD QIIQHLAGRA GVFTNTAGLQ KLADIIQIVF SVDPSGSPG SPAGLGALQS 420
35 YKVHIHPDAG HRRTAQRSDA WSTTAARKRG KVLSYWCFSP GHSMHLEVRQ GVRSLILTSG 480
TLAPVSSPAL EMQIPFPVCL ENPHIIDKHQ IWGVVPRGP DGAQLSSAFD RRFSEECSS 540
LGKALGNIR VVPYGLLIFF PSYPVMEKSL EFWARDLAR KMEALKPLFV EPRSKGSFSE 600
TISAYARVA APGSTGATFL AVCRGKASEG LDFSDTNGRG VIIVTGLPYPP RMDPRVVLKM 660
QFLDEMKGQ GAGGQFLSGQ EYRQASRA VNQAIGRVIR HRQDYGAVFL CDHRFAFADA 720
40 RAQLPSWVRP HVRVYDNFGH VIRDAQFFR VAERTMPAPA PRATAPSVRG EDAVSEAKSP 780
GPFFSTRKAK SLDLHVPSLK QRSSGSPAAG DPESLCEVEY EQEPVPARQR PRGLLAALFH 840
SEQRAGSPGE EAHNSCSTLS LLSKRPAAE PRGGRKKIRL VSHPEEPVAG AQTDRAKLFM 900
VAVKQELSQA NFATFTQALQ DYKGSDDFAA LAACLGPLFA EDPKKNLLQ GFYQFVRPHH 960
KQQFEVCIC LTGRGCGYRP EHSIPRRQRA QVLDPTGRT APDPKLTVST AAAQQLDPQE 1020
45 HLNQGRPHLS PRPPPTGDPG SQPQWGSVP RAGKQGHAV SAYLADARRA LGSAGCSQLL 1080
AALTAYKQDD DLDKVLAVLA ALTTAKPEDF PLLHRFSMFV RPHHKQRFQ TCTDLTGRPY 1140
PGMEPPGPQE ERLAVPPVLT HRAVPPGPSR SEKTGKTQSK ISSFLRQRP GTVGAGGEDA 1200
GPSQSSGPPH GPAASEWGL 1219

Seq ID NO: 229 Protein Sequence
Protein Accession #: NP_056462.1

80
1 11 21 31 41 51
| | | | |
MPAPAPRATA PSVRGEDAVS EAKSPGPFPS TRKAKSLDLH VPSLKQRSSG SPAAGDPSS 60
LCVEYEQEPV PARQPRGLL AALEHSEORA GSPGEEQAH CSTLSLLSEK RPAEEPRGGR 120

5
 KKIRLVSHPE EPVAGAQTDR AKLFMVAVKQ ELSQANFATF TQALQDYKGS DDFAALAACL 180
 GPLFAEDPKK HNLQGFYQF VRPHKQKFE EVCIQLTGRG CGYRPEHSIP RRQRAQPVLD 240
 PTGRTAPDFK LTVSTAAAOQ LDPQEHNLQG RPHLSRPPPP TGDPGSQPQW GSGVPRAQKQ 300
 QHAVASAYLA DARRALGSAG CSQLLAALTA YKQDDLDKV LAVLAALTTA KPEDFPLLHR 360
 FSMFVRPHHK QRSQTCTDL TGRPYPGMEP PGQOEERLAV PPVLTHRAPO PGPSRSEKTK 420
 KTQSKISSLF RQRPAQTGVA GGEDAGPSQS SGPPHGPAAS EWGEPHGRDI AGQATGAPC 480
 GPLSAGSCVQ GCGAEDVVPF QCPACDFQRC QACWQRHLQA SRMCPACHTA SRKQSVMQVF 540
 WPEPQ 545

10
 Seq ID NO: 230 Protein Sequence
 Protein Accession #: NP_003814.1
 1 11 21 31 41 51
 | | | | |
 15
 MRALEGPGLS LLCLVLALPA LLPVPAVRGV AETPTYPRWD AETGERLVCA QCPPGTFVQR 60
 PCRDSPTTC GPCPPRHYTQ FWNLYERCRY CNVLCGEREE EARACHATHN RACRCRTGFF 120
 AHAGFCLEHA SCPPGAGVIA PGTPSQNTQC QCPPGTFSFA SSSSSEQCQP HRNCTALGLA 180
 LNVPGSSSHD TLCTSTCTGFP LSTRVPGAEE CERAVIDFVA PQDISIKRLQ RLLQALEAPE 240
 GWGPTPRAGR AALQKLRRR LTELGAQDG ALLVRLQLAL RVARMPGLER SVRERFLPVH 300

20
 Seq ID NO: 231 Protein Sequence
 Protein Accession #: NP_116563.1
 1 11 21 31 41 51
 | | | | |
 25
 MRALEGPGLS LLCLVLALPA LLPVPAVRGV AETPTYPRWD AETGERLVCA QCPPGTFVQR 60
 PCRDSPTTC GPCPPRHYTQ FWNLYERCRY CNVLCGEREE EARACHATHN RACRCRTGFF 120
 AHAGFCLEHA SCPPGAGVIA PGTPSQNTQC QCPPGTFSFA SSSSSEQCQP HRNCTALGLA 180
 LNVPGSSSHD TLCTSTCTGFP LSTRVPGAEE CERAVIDFVA PQDISIKRLQ RLLQALEAPE 240
 GWGPTPRAGR AALQKLRRR LTELGAQDG ALLVRLQLAL RVARMPGLER SVRERFLPVH 300

30
 Seq ID NO: 232 Protein Sequence
 Protein Accession #: NP_000584.2
 1 11 21 31 41 51
 | | | | |
 35
 MAELLASAGS ACSWDFPRAP PSFPPPAASR GGLGGTRSFH PHRGAESPRP GRDRDGVVRP 60
 MASSRCAPAP GCRCLPGASL AWLGTIVLLL ADMVLLRTAL PRIFSLLVET ALPLLVRVAV 120
 GLSRWAVLWL GACGLVRATV GSKSENAGAQ GWLAALKPLA AALGLALPGL ALFRELISWG 180
 APGSADSTRL LHMGSHTAF VVSYAAALPA AALWHKLGSL WVPGGQGGSG NPVRRLLGCL 240
 GSETRRLSLF LVLVLLSLG EMAIPFTTGR LTDWILQDGS ADTFTRNLT LMSILTIASAV 300
 LEFVGQGYLN NTMGHVHSHL QGEVFGAVLR QETEFQOQNG TGNIMSRVTE DTSTLSDLSL 360
 40
 ENLSLFLWYL VRGLCLLIGM LMGSVSLTMV TLITLPLLEF LPKKVKGWYQ LLEVQVRESL 420
 AKSSQVAIEA LSAMPTVRSP ANEEGEAQKF REKIQEIKTL NQKEAVAYAV NSWTTISISM 480
 LLKVGLIYIG GQLVTSAGVS SGNLVTFLVY QMQFTQAVEV LLSIYPRVQK AVGSSEKIFE 540
 YLDRTPRCPP SGLLTPLHLE GLVQFQDVSE AYPNRPDVLV LQGLTFTLRP GEVTALVGNP 600
 45
 GSGKSTVAAL LQNLVQFTGG QLLDGKPLP QYEHRYLHRQ VAAVGQEPQV FGRSLQENIA 660
 YGLTQKPTME EITAAAVKSG AHSFISGLPQ GYDTEVDEAG SOLSGGQORQ VALARALIRK 720
 PCVLILDDAT SALDANSQIQ VEQLLYESPE RYSRSVLLIT QHLSLVEQAD HILFLEGGAI 780
 REGGTHQQLM EKKGCTWAMV QAPADAPE 808

50
 Seq ID NO: 233 Protein Sequence
 Protein Accession #: NP_002414.1
 1 11 21 31 41 51
 | | | | |
 55
 MRLTVLCAVC LLPGSLALPL PQEAGGMSSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK 60
 EMQKFGELPI IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
 PHITVDRLVS KALNMWKEI PLHFRKVWVG TADIMIGFAR GAHGDSYFPD GPGNTLAHAF 180
 APGTGLGDDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMHGSSDPNA VMYPTYGNGD 240
 PQNFKLSQDD IKGIQKLYGK RNSNRKK 267

60
 Seq ID NO: 234 Protein Sequence
 Protein Accession #: NP_061144
 1 11 21 31 41 51
 | | | | |
 65
 MPPIEVCKIK FAEEDAKPKE KEAGDEQSL L GAVAPGAAPR DLATFASTST LHGLGRACGP 60
 GPHGLRRTLW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAPAPVA GFPAVTLQNI 120
 NFRHSAISLD ADIFHLANLT GLPPKDRDGH RAAGLRYPEP DMVDILNRTG HQADMLKSC 180
 NFSGHHCAS NFSVYTRYG KCYTFNADPR SSLPSRAGGH GSGLEIMLDI QQEYLPINR 240
 ETNETSFEG IRVQIHSQEE PPYIHQLGFG VSPGFQTFVS CQEQLRTYLP QPWGNCRAES 300
 ELREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY IECADHTLDS 360
 LGGGPEGPCF CPTPCNLTRY GKEISMVRIP NRGSAARYLAR KYNRNETYIR ENFLVDVFF 420
 70
 EALTSEAMEQ RAAYGLSALL GDLGGQMGFL ICASILTLE ILDYIYEVSW DRLLKRVWRRP 480
 KTPLRTSTGG ISTLGLQELK EQSPCPSLGR AEGGGVSSLL PNHHHPHGPP GGLFEDFAC 539

75
 Seq ID NO: 235 Protein Sequence
 Protein Accession #: BAC03567
 1 11 21 31 41 51
 | | | | |
 80
 MEVSSPSPAQ RLRRKKRPMV QGPAGCQVFQ PSPSGGTAGD PGGLSDPFYP PRSGSLALGD 60
 PSSDPACSQS GPMEAEEDSL PEQPEDSAQL QQEKPSLYIG VRGTVVRSMQ EVLWTRLREL 120
 PDPVLSEEVV EGIAAGIEAA LWDLTQGTNG RYKTKYRSL L FNLDRPNRLD LFLKVHVGDD 180
 TPYDLVRMSS MQLAPQELAR WRDQEEKRGL NIIEQQQKEP CRLPASKMTH KGEVEIQORDM 240
 DQTLTLEDLV GPQMFMDSCP QALPIASEDT TGQHDHFFLD PNCHICKDWE PSNELLGSFE 300
 AAKSGDNIF QKALSQTPMP APEMPKTREL SPTEPQDRVP PSGHLVPAAP TKALPLPPW 360
 EGVLDMSFIK RFRARAQLVS GHSCRLVQAL PTVIRSAGCI PSNIVMDLLA SICPAKAKDV 420
 CVVRLCPHGA RDTQNCRLLY SYLNDQRHGH LASVEHMGWV LLPLPAFQPL PTRLRPLGGP 480

		GLEVTHSSLL	LAVLLPKEGL	PDTAGSSPWL	GKVQKMVSFN	SKVEKRYYP	DDRRPNVPLK	540
		GTPPPGGAWQ	QSQGRGSIAP	RGISAWQRP	RGRGRWLWPE	ENWQHPRGQ	WPPEPGLRQS	600
		QHPVSVAPAG	HGFGRGQHFH	RDSCPHQALL	RHLESLATMS	HQLQALLCPQ	TKSSIPRPLQ	660
		RLSSALAAPE	PPGPARDSSL	GPTDEAGSEC	PFPRKA			696
5		Seq ID NO: 236 Protein Sequence						
		Protein Accession #: NP_005282						
		1	11	21	31	41	51	
10		MSKRWWAGS	RKPPREMLKL	SGSDSSQSMN	GLEVAPPGLI	TNFSLATAEQ	CGOETPLENM	60
		LFASFYLLDF	ILALVGNLTA	LWLFIRDHKS	GTPANVFLMH	LAVADLSCVL	VLPTRLVYHF	120
		SGNHWPFGEI	ACRLTGFLPY	LNMYASIFYL	TCISADRFLA	IVHPVKSLLK	RRPLYAHLAC	180
		AFLLVVVAVA	MAPLLVSPQT	VQTNHTVVCL	QLYREKASHH	ALVSLAVAPT	FPFITVTCTY	240
		LLIIRSLROG	LRVEKRLKTK	AVRMIAIVLA	IFLVCFVPYH	VNRSVYVLHY	RSHGASCATQ	300
15		RILALANRIT	SCLTSLNGAL	DPIMYFFVAE	KFRHALCNLL	CGKRLKGPPP	SFEGKTNESS	360
		LSAKSEL						367
		Seq ID NO: 237 Protein Sequence						
		Protein Accession #: NP_061113						
		1	11	21	31	41	51	
20		MRKTRLWGLL	WMLFVSELRA	ATKLTEEKYE	LKEGQTLQVK	CDYLEKFAF	SQKAWQIIRD	60
		GEMPTLACT	ERPSKNSHPV	QVGRILEEDY	HDHGLLRVRM	VNLQVEDSGL	YQCVIYQPPK	120
		EPHMLFDRIR	LVTYKGFSTQ	PGSNENSTQN	VYKIPPTTK	ALCELYTSPR	TVTQAPPKST	180
25		ADVSTPDSEI	NLTNVTDIIR	VPVFNIVILL	AGGFLSKSLV	FSVLFAVTLR	SFVP	234
		Seq ID NO: 238 Protein Sequence						
		Protein Accession #: NP_003458						
		1	11	21	31	41	51	
30		MEGISIYTS	NYTEEMSGSD	YDSMKEPCFR	EENANFNKIF	LPTIYSIIFL	TGIVGNGLVI	60
		LVMGYQKKLR	SMTDKYRLHL	SVADLLFVIT	LPFWAVDAVA	NWYFGNFLCK	AVHVIYTVNL	120
		YSSVLILAFI	SLDRYLAIVH	ATNSQRPRKL	LAEKVVYVGV	WIPALLLTIP	DFIFANVSEA	180
		DDRYICDRFY	PNDLWVVVFQ	FOHIMVGLIL	PGIVILSCYC	IIISKLSHMK	GHQKRKALKT	240
35		TVILILAFFA	CWLPYYIGIS	IDSFILLEII	KQGCDEFNTV	HKWISITEAL	APFFHCLNPI	300
		LYAFILGAFK	TSQAHALTSV	SRGSSSLKILS	KGRGGHSSV	STESSESSFH	SS	352
		Seq ID NO: 239 Protein Sequence						
		Protein Accession #: NP_036338.1						
		1	11	21	31	41	51	
40		MHPQVILSL	ILHLADSVAG	SVKVGGEAGP	SVTLPCHYSG	AVTSMCWNRG	SCSLFTQONG	60
		IVMTNGTHVT	YRKDTRYKLL	GDLSRRDVS	TIENTAVSDS	GVYCCRVEHR	GWFNMDKITV	120
		SLBIVFPKRY	TTPIVTTVPT	VTTVRTSTTV	PTTTTVPTTT	VPTTMSIPTT	TTVPTTMTVS	180
45		TTTSVPTTTS	ITPTTSVPVT	TTVSTFVPPM	PLPRQNHPEV	ATSPSSSQPA	ETHPTTLQGA	240
		IRREPTSSPL	YSYTTDGNIT	VTSSDGLWN	NNQTQLFLEH	SLLTANTTKG	IYAGVCISVL	300
		VLLALGLVII	AKKYFFKKEV	QQLSVSFSSL	QIKALQNAVE	KEVQAEDNIY	IENSLYATD	359
		Seq ID NO: 240 Protein Sequence						
		Protein Accession #: NP_004923.1						
		1	11	21	31	41	51	
50		MRTYRYFLLL	FWVGQPYPTL	STPLSKRTSG	FPAKKRALEL	SGNSKNELNR	SKRSWMWNOF	60
		FLLEEYTGSD	YQYVGKLHSD	QDRGDGSLKY	ILSGDGAGDL	FIINENTGDI	QATKRLDREE	120
55		KPVYILRAQA	INRRTGRPVE	PESEFIIKIH	DINDNEPIFT	KEYVTATVPE	MSDVGTFFVQ	180
		VTATADDDPT	YGNSAKVVS	ILQGQPYFSV	ESETGIIKTA	LLNMDRENRE	QYQVVIQAKD	240
		MGGQMGGLSG	TTTVNITLTD	VNDNPPRFPO	STYQFKTPES	SPPGTPIGRI	KASDADVGEN	300
		AETEYSITDG	EGLDMFDVIT	DQETQEGIIT	VKKLLDFEKK	KVYTLKVEAS	NPYVEPRFLY	360
60		LGPFKDSATV	RIVVEDVDEP	PVFSKLAYIL	QIREDAQINT	TIGSVTAQDP	DAARNPVKYS	420
		VDRHTDMORI	FNIDSGNGSI	FTSKLLDRET	LLWHNITVIA	TEINNPQKSS	RVPLYIKVLD	480
		VNDNAPEFAE	FYETFVCEKA	KADQLIQLTH	AVDKDDPYSG	HQFSFSLAPE	AASGSNFTIQ	540
		DNKDNTAGIL	TRKNGYNRHE	MSTYLLPVVI	SDNDYPVQSS	TGTVTVRVCA	CDHHGNMQSC	600
		HAEALHTPTG	LSTGALVAIL	LCIVILLVTV	VLFAALRRQR	KKEPLIISKE	DIRDNIYSYN	660
65		DEGGGEDTQ	AFDIGTLRNP	EAIEDNKLRR	DIVPEALFLP	RRTPTARDNT	DVRDFINQRL	720
		KENDTDPTAP	PYDSLATYAY	EGTGSVADSL	SSLESVTDA	DQDYDYLSDW	GPRFKKLADM	780
		YGGVDSDDKS						790
		Seq ID NO: 241 Protein Sequence						
		Protein Accession #: BAB14227.1						
		1	11	21	31	41	51	
70		MRLTRLRLVL	PVFGVLWITV	LLFFWVTKRK	LEVPTGPEVO	TPKVMSLFFK	VAGMSPHAPQ	60
		VPVSPTPPYQ	RGLHPTGGHL	AVCHFPCLLQ	EAQPHLOTQV	FLQVRCTLLV	YCTDLPTPTSI	120
		IITFNHARS	TLLRTIRSVL	NRTPTHLIRE	IILVDDFSND	PDDCKQLIKL	PKVKCLRNNE	180
75		RQGLVRSRIR	GADIAQGTTL	TFLDSHCEVN	RDWLQPLLHR	VKEDYTRVVC	PVIDIINLDT	240
		FTYIESASEL	RGGFDSWLSHF	QWEQLSPEQK	ARRLDPTPEI	RTPIIAGGLF	VIDKAWFDYL	300
		GKYDMDMDIW	GGENFEISFR	VWMCSSLEI	VPCSRVGHVF	RKXHPYVFPD	GNANTYIKNT	360
		KRTAEVWMDK	YKQYAAARP	FALERPPGNV	ESRLDLRKNL	RCQSFKWYLE	NIYPELSIPK	420
		ESSIQKGNIR	QRQKLESQR	QNNQETPNLK	LSPCAKVKEG	DAKSQVWAPT	YTQILQEEL	480
80		CLSVITLFPQ	APVVVLCLNK	GDDRQQWTKT	GSHIEHIAH	LCLDITDMFGD	GTENGKEIVV	540
		NPCSSLSMSQ	HWMVSS					557
		Seq ID NO: 242 Protein Sequence						
		Protein Accession #: AAH10659						

	1	11	21	31	41	51	
	MRLRLRLVL	PVFGVLWITV	LLFFWVTKRK	LEVPTGPEVQ	TPKPSDADWD	DLWDQFDERR	60
5	YLNAAKWRVG	DDPYKLYAFN	QRESERISSN	RAIPDTRHLR	CTLVYCTDL	PPTSIIITFH	120
	NEARSTLLRT	IRSVLNRTP	HLIREIILVD	DFSNDPDDCK	QLIKLPKVKC	LRNNERQGLV	180
	RSRIRGADIA	QGTTLTFLDS	RCEVNRDWLQ	PLLHRVKEDY	TRVVCVIDI	INLDTFTYIE	240
	SASELRGGFD	WSLHFQWEQL	SPEQKARRLD	PTEPIRTPII	AGGLFVIDKA	WFDYLGKYDM	300
	DMDIINGENF	EISFRVWMC	GSLEIVPCSR	VGHVFRKKHP	YVFPDGNANT	YIKNTKRTAE	360
10	VWMDYKQYY	YAARPFALER	PFGNVESRLD	LRKNLRCSQF	KWYLENIYPE	LSIPKESSIQ	420
	KGNIRQRQKC	LESQRQNNQE	TPNLKLSPCA	KVKGEDAKSQ	VWAFYTYQOI	LQEEELQSVI	480
	TLFPAGPVVL	LSKNGDDRRQ	QWTKTGSHE	HIASHLCLDT	DMFGDGTENG	KEIVVNPCE	540
	SLMSQHWDMV	SS					552
15	Seq ID NO: 243 Protein Sequence Protein Accession #: AAH10659.1						
	1	11	21	31	41	51	
	MRLRLRLVL	PVFGVLWITV	LLFFWVTKRK	LEVPTGPEVQ	TPKPSDADWD	DLWDQFDERR	60
20	YLNAAKWRVG	DDPYKLYAFN	QRESERISSN	RAIPDTRHLR	VLNRTPTHLI	REIILVDDFS	120
	NDPDDCKQLI	KLPKVKCLRN	NERQGLVRSR	IRGADIAQGT	TLTFLDSHCE	VNRDWLQPLL	180
	HRVKEDYTRV	VCPVIDIINL	DTFTYIESAS	ELRGGFDWSL	HFQWEQLSPE	QKARRLDOTE	240
	PIRTPIIAGG	LFVIDKAWFD	YLGKYDMDMD	IWGGENFEIS	FRVWMCSSGL	EIVPCSRVGH	300
	VFRKHPPYVF	PDGNANTYIK	NTKRTAEVWM	DEYKRYYYAA	RPFALERPF	NVESRLDLRK	360
	NLRQCSFKWY	LENIYPELSI	PKESSIQKGN	IRQRQKCLCS	QRQNNQETPN	LKLSPCAQVK	420
25	GEDAKSQVWA	FTYTYQQLQE	ELCLSVITLF	PGAPVVLVLC	KNGDDRQQWT	KTGSHIEHIA	480
	SHLCLDTDMF	GDGTENGKEI	VVNPCESSLM	SQHWDMVSS			519
30	Seq ID NO: 244 Protein Sequence Protein Accession #: NP_078848.1						
	1	11	21	31	41	51	
	MNGKVMSPGP	FGALTSAPRAH	SDFLDHCEV	NRDWLQPLLH	RVKEDYTRVV	CPVIDIINLD	60
	TFTYIESASE	LRGGFDWSLH	FQWEQLSPEQ	KARRLDPTPE	IRTPIIAGGL	FVIDKAWFDY	120
35	LGKYDMDMDI	WGGENFEISF	RVWMCSSGLE	IVPCSRVGHV	FRKKHPYVFP	DGNANTYIKN	180
	TKRTAEVWMD	EYKQYVYAAR	PFALERPFGN	VESRLDLRKN	LRCQSFKNYL	ENIYPELSIP	240
	KESSIQKGN	RQRQKCLCSQ	RQNNQETPNL	KLSPCAKVKG	EDAKSQVWAF	TYTYQQLQEE	300
	LCLSVITLFP	GAPVVLVLC	NGDDRQQWTK	TGSHIEHIA	HLCLDTDMFG	DGTENGKEIV	360
	VNPCESSLMS	QHWDMVSS					378
40	Seq ID NO: 245 Protein Sequence Protein Accession #: NP_001209.1						
	1	11	21	31	41	51	
	MRRSLHAAA	VLLLVILKEQ	PSSPAPVNGS	KWTFYFGPDGE	NSWSKKYPSC	GGLLQSPIDL	60
45	HSDILQYDAS	LTPLEFGQYN	LSANKQFLLT	NNGHSVKLNL	PSDMHIQGLQ	SRYSATQLHL	120
	HWGNPNDPHG	SEHTVSGQHF	AAELHIVHYN	SDLYPDASTA	SNKSEGLAVL	AVLIEMGSFN	180
	PSYDKIFSHL	QHVYKQGEA	FVPGFNIEEL	LPERTAAYYR	YRGLTTPPC	NPTVLWTVFR	240
	NPVQISQEQ	LALLETALYCT	HMDDPSPREM	INNFRQVQKF	DERLVYTSFS	QVQVCTAAGL	300
50	SLGIILSLAL	AGILGICIVV	VVSINLFRRK	SIKKGDNKGV	IYKPKATMET	EAAH	354
55	Seq ID NO: 246 Protein Sequence Protein Accession #: BC000278						
	1	11	21	31	41	51	
	MRRSLHAAA	VLLLVILKEQ	PSSPAPVNGS	KWTFYFGPDGE	NSWSKKYPSC	GGLLQSPIDL	60
	HSDILQYDAS	LTPLEFGQYN	LSANKQFLLT	NNGHSVKLNL	PSDMHIQGLQ	SRYSATQLHL	120
	HWGNPNDPHG	SEHTVSGQHF	AAELHIVHYN	SDLYPDASTA	SNKSEGLAVL	AVLIEMGSFN	180
	PSYDKIFSHL	QHVYKQGEA	FVPGFNIEEL	LPERTAAYYR	YRGLTTPPC	NPTVLWTVFR	240
60	NPVQISQEQ	LALLETALYCT	HMDDPSPREM	INNFRQVQKF	DERLVYTSFS	QGIILSLALA	300
	GILGICIVVV	VVSINLFRRK	IKKGDNGKVI	YKPKATMETE	AHA		343
65	Seq ID NO: 247 Protein Sequence Protein Accession #: NP_006623.1						
	1	11	21	31	41	51	
	MQVDETLP	KGPSLCSARY	GIALVLHFCN	FTTIAQNVIM	NITMAMVNS	TSPQSQNLDS	60
	SEVLVDSFG	GLSKAPKSLP	AKSSILGGQF	AIWEKWPPO	ERSRLCSIAL	SGMLLCCTA	120
	ILIGGFIS	LGWPFVYFIF	GGVGCVCCLL	WVVIYDDPF	SYPWISTSEK	EYIISLKKQ	180
	VGSSKQPLP	KAMLRSLPIW	SICLCGFSHQ	WLVTMVVYI	PTYISSVYHV	NIRDNGLLSA	240
70	LPFIVAMVIG	MVGGYLAFL	LTKKFRITV	RKIATILGSL	PSSALIVSLP	YLNAGYITAT	300
	ALLTLSCGLS	TLCQSGIYIN	VLDIAPRYSS	FLMGASRGFS	SIAPVIVPTV	SGFLLSQDPE	360
	FGWRNVFFLL	FAVNLGLLLF	YLIFGEADVQ	EWAKERKLTR	L		401
75	Seq ID NO: 248 Protein Sequence Protein Accession #: NP_003049.1						
	1	11	21	31	41	51	
	MPTTVDDVLE	HGGEFHFQK	QMFFLLALLS	ATFAPYVGI	VFLGFTPDHR	CRSPGVAELS	60
	LRCGWSPAE	LNVTVPQGP	AGEASPRQCR	RYEVDWNQST	FDCVDPLASL	DTNRSRLPLG	120
80	PCRDGWVYET	PGSSIVTEFN	LVCANSWMLD	LFQSSVNVGF	FIGSMSIGYI	ADRFGRKLCL	180
	LTTVLINAAA	GVLMAISPTY	TWMLIFRLIQ	GLVSKAGWLI	GYILITEFVG	RRYRTTVGIF	240
	YQVATYGLL	VLAVAYALP	HWRWLQFTVA	LPNFFFLYY	WCIPESPRWL	ISQNKNAEAM	300
	RIIKHIAKKN	GKSLPASLQR	LRLEEETGKK	LNPSFLDLVR	TPQIRKHTMI	LMYNWFTSSV	360
	LYQGLIMHMG	LADGNIYLD	FYSALVEFPA	AFMIILTIDR	IGRRYPWAAS	NMVAGAACLA	420

SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
 TPFLVYRLTN IWLEPLMVF GVLGLVAGGL VLLLPETGK ALPETIEEAE NMQRPRKNKE 540
 KMIYLVQQL DIPLN 555

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Seq ID NO: 249 Protein Sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MQPAIQVWFG	EDLPLSPRSP	LTPRHGPGLA	NVCQYDEWIA	VRHEATLLPM	QEDLSIWLSG	60
LLGIKVKAEK	LLEELDNGVL	LCQLIDVLQN	MVKTCSNEES	GNFPMRKVPC	KKDAASGSFF	120
ARDNTANFLH	WCRDYGVDET	YLFSEGLVL	HKDPRQVYLC	LLEIGRIVSR	YGVPEPVLVK	180
LEKEIELEET	LLNTSGPEDS	ISIPKSCCRH	EELHEAVKHI	AEDPPCSCSH	RFSIEYLSG	240
RYRLGDKILF	IRMLHGKHMV	VRVGGGWDTL	QGFLLYDPC	RILQFATLEQ	KILAFQKGV	300
NESVPSDPA	TPQPPENPL	SAVNMFOKQN	SKPSVPVSIP	KSKEQGRPP	GALVPASSLK	360
GGNLGMSVR	SKLPNSPAAS	SHPKLKSSKG	ITKKPQAPSN	NASSSLASLN	PVGKNTSSPA	420
LPRTAPCISE	SPRKCISSPN	TPKAKVIPAQ	NSADLPSTL	LPNKCSGKTQ	PKYLKHNHIS	480
SRDNAVSHLA	AHSNSSSKCP	KLPKANIPVR	PKPSFQSSAK	MTKTSSTKIA	TGLGTQSQPS	540
DGAPQAKPVP	AQKLKSAALN	NQPVSVSVSV	PVKATQKSKD	KNIVSATKKQ	PQNKSAFQKT	600
GPSSLKSPGR	TPLSIVSLPQ	SSTKTQTAPK	SAQTAKSQH	STKGPPRSRG	TPASIRKPPS	660
SVKADDSGDK	KPTAKKEDD	DHYFVMTGSK	KPRK			694

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Seq ID NO: 250 Protein Sequence
 Protein Accession #: NP_001035.1

1	11	21	31	41	51	
MSKSKCSVGL	MSSVVAPAKE	PNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVEAQR	60
ETWKKIDFL	LSVIGFAVDL	ANVWRFPLYC	YKNGGGAFLV	PYLLPMVIAG	MPLFYMELAL	120
QQFNREGAAG	VWKICPILKG	VGPTVILISL	YVGFYVNVII	AWALHYLFSS	FTTELPWIHC	180
MNSWNPNCS	DAHGGSSSGD	SSGLNDTFGT	TPAAEYFERG	VLHLHQSHGI	DDLGPWRWL	240
TACLVLVIVL	LYFSLWKGVK	TSGKVVWITA	TPYVVLTLAL	LLRGVTLPGA	IDGIRAYLSV	300
DFYRLCEASV	WIDAAQVCF	SLGVGFGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
GFVVSFLIGY	MAQKHSVPIG	DVAKDGPGLI	FIYYPEAIAT	LPLSSAWAVV	FFIMLLTLGI	420
DSAMGGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHFAA	480
GTSILFGLVI	EAIGVAVFYG	VGQFSDDIQQ	MTGQRPSLYW	RLCKWLVSPP	FLLFVVVVSI	540
VTFRPPHYGA	YIFPDWANAL	GWVIATSSMA	MPPIYAAYKF	CSLPGSFREK	LAYAIAPKED	600
RELVDREGEVR	QFTLRHWLKV					620

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Seq ID NO: 251 Protein Sequence
 Protein Accession #: NP_071356.1

1	11	21	31	41	51	
MPLGHIMRLD	LEKIALEYIV	PCLHEVGFCY	LDNFLGEVVG	DCVLERVKQL	HCTGALRDGQ	60
LAGPRAGVSK	RHLRGDQITW	IGGNEEGCEA	ISFLLSLIDR	LVLYCGSRLG	KYYVKERSKA	120
MVACYPNGNT	GYVRHVDNPN	GDGRICITCIY	YLNKNWDAKL	HGGILRIFFE	GKSFIADEVF	180
IFDRLLFFWS	DRRNPHVEQP	SYATRYAMTV	WYFDAEERAE	AKKKFRNLTR	KTESALTED	239

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Seq ID NO: 252 Protein Sequence
 Protein Accession #: NP_647475.1

1	11	21	31	41	51	
MSGAPTAGAA	LMCAATAVL	LSAQGGPVQS	KSPRFASWDE	MVFLAHGLLQ	LGQGLREHAE	60
RTRSQLSALE	RRLSACGSAC	QGTGGSTDL	LAPESRDVPE	VLHSLQTQLK	AQNSRIQQLF	120
HKVAQQQRHL	EKQHLRIQHL	QSQFGLLDHK	HLDEHAKPA	RRKRLPEMAQ	PVDPAHNVSR	180
LHRLPRDCQE	LFQVGERQSG	LFETIQPGSP	PFLVNCMKTS	DGQWTVIQRR	HDSGVDFNRP	240
WEAYKAGFGD	PHGEFWLGL	KVHSITGDRN	SRLAVQLRDW	DGNAELLQFS	VHLGGEDTAY	300
SLQLTAPVAG	QLGATTVPSP	GLSVFFSTWD	QDHDLRRDKN	CAKSLSGGWN	FGTCSHSLNL	360
GQYFRSIPQQ	RQKLKKGIFW	KTRWGRYYPL	QATTMLIQPM	AAEAAS		406

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Seq ID NO: 253 Protein Sequence
 Protein Accession #: NP_001207.1

1	11	21	31	41	51	
MAPLCPSPL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMQEDSPLG	GGSSGEDDPL	60
GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPEVKP	KSEEBGSLKL	EDLPTVEAPG	120
DPQEPQNAH	RDKEGDDQSH	WRYGGDPPWP	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
ELLGFLPPL	PELRLRMNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
VEGHRFPAEI	HVVHLSTAF	RVDEALGRPG	GLAVLAAFL	EGPEENSAYE	QLLSRLEEIA	300
EEGSETQVPG	LDISALLPSD	FSRYFYQEGS	LTPPCAQGV	IWTVFNQTM	LSAKQLHTLS	360
DTLWPGDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	420
GLLFAVTSVA	FLVMQRQRH	RGTGKGVSYR	PAEVAETGA			459

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Seq ID NO: 254 Protein Sequence
 Protein Accession #: NP_003030.1

1	11	21	31	41	51	
MEQQDQSMKE	GRLTLVLALA	TLIAAFGSSF	OYGVNVAAVN	SPALLMQQFY	NETYYGRTGE	60
FMEDFPLTL	WSVTVMFPF	GGFIGSLLVG	PLVNFGRKGC	ALLFNNIFSI	VPAILMGCSR	120
VATSFELIII	SRLLVGICAG	VSSNVVPMYL	GELAPKNLRG	ALGVVPQLFI	TVGILVAQIF	180
GLRNLALND	GWPILLGLTG	VPAALQLLLL	PPFPESPRYL	LIQKKDEAAA	KKALQTLRGW	240
DSVDREVAEI	RQDEAEAKAA	GFISVLKLF	MRSRLRWOLLS	IIVLMGGQQL	SGVNAIYYA	300
DQIYLSAGVP	EEHVQYVTAG	TGAVNVMTF	CAVFWVELLG	RRLLLLLGFS	ICLIACCVLT	360
AALALQDTS	WMPYISIVCV	ISYVIGHALG	PSPIPALLIT	EIFLQSSRPS	AFMVGSGVHW	420
LSNFTVGLIF	PFIQEGGLPY	SFIVFAVICL	LTTIYIFLIV	PETKARTFIE	INQIFTMKNK	480
VSEVYPEKEE	LKELPPVTSE	Q				501

Seq ID NO: 255 Protein Sequence	
Protein Accession #: NP_001243.1	
5	1 11 21 31 41 51 MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60 QLNHTGPOOD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMHQIV TLAICSSSTA 120 SRHHPTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN 180 TDETFPGVQW VRP 193
Seq ID NO: 256 Protein Sequence	
Protein Accession #: NP_060562.2	
15	1 11 21 31 41 51 MLFTSFVEQK KKAGVFQBIT KTHGTIIGIT SGIVLVLLII SILVQVQPR KKMVACKTAP 60 NKTGFQEVFD PPHYELFSLR DKEISADLAD LSEELDNYQR MRRSSTASRC IHDHHCQSQA 120 SSVKQSRTNL SSMELPLRND FAQPQPMKTF NSTFKKSSYT FKQGHECPQE ALEDRVMEEI 180 PCEIYVRGRE DSAQASISID F 201
Seq ID NO: 257 Protein Sequence	
Protein Accession #: Eos sequence	
20	1 11 21 31 41 51 IIAATINNAS MTSPIDNAGL AADDFKMNAS LQTQISTDAE AVSSAKSEIM ELKQVLQSLQ 60 HELQSVLAMQ SSPBGTLADT EAGYVAQLSE IKMYISILEE QICQIRGETE YQNTTEYAQLQ 120 DIKTRLEVEI ETYHRLGGE GGSEAREAES KG 152
Seq ID NO: 258 Protein Sequence	
Protein Accession #: NP_003256.1	
30	1 11 21 31 41 51 MRQTLPCIFY WGGLLPFGML CASSTTKCTV SHEVADCSHL KLTQVPDDL P TNITVLNLTH 60 NQLRRLPAAN PTRYSQLTSL DVGFTNTISK ELPCQKLP M LKVLNLQHNE LSQLSDKTFA 120 FCTNLTELHL MSNSIQIKI NPFVVKQKLI TLDLSHNGLS STKLGTVQL ENLQELLN 180 NKIQALKSEE LDFANSSSL KLELSSNQIK EFSPGCFHAI GRLFGFLNN VQLGPSLTEK 240 LCLELANTSI RNLSLSNSQL STTSNTTFLG LKWTNLTM LD LSYNNLNVVG NDSFAWLPOL 300 EYFLEYNNI QHLSHSLHG LFNVRVNLK RSFTKQSISL ASLPKIDDFS FQWLKCLEHL 360 NMEDNDIPGI KSNMFTGLIN LKYLSSNSF TSLRTLNET FVSLAHSPLH ILNLTKNKIS 420 KIESDAFSWL GHLEVLDLGL NEIGQELTQ EMRGLENI FE IYLSYNKYQL LTRNSFALVP 480 SLQRLMLRRV ALKNVDSSPS PFQPLRNLT I LDLSNNNIAN INDDMLEGLE KLEILDLOHN 540 NLARLWKHAN PGPIIYFLKG LSHLHILNLE SNGFDEIPVE VFKDLFLKI IDLGLNLT 600 LPASVFNNQV SLKSLNLQKN LITSVEKKVF GPAFRNLTEL DMRFNPFDCI CESIAWFWNW 660 INETHNIPE LSSHYLCNTP PHYHGFPVRL FDTSSCKDSA PFELFFMINT SILLIFIFIV 720 LLIHFEGRRI SFYWNVSVHR VLGFKEIDRQ TEQFEYAAYI IHAYKDKDW WEHFSMEKE 780 DQSLKFCLEE RDEAGVFEL EAVNSIKRS RKIIFVITHH LKDPPLCKRF KVHHAQQAI 840 EQNLDSIILV FLEETPDYKL NHALCLRRGM FKSHCILNWP VQKERIGAFR HKLQVALGSK 900 NSVH 904
Seq ID NO: 259 Protein Sequence	
Protein Accession #: NP_000570.1	
50	1 11 21 31 41 51 MDYQVSSPIY DINYYTSEPC QKINVQIAA RLLPPLYSLV FIFGFVGNML VILILINCKR 60 LKSMTDIYLL NLAISDLFFL LTVPFWAHYA AAQWDFGNTM COLLTGLYFI GFFSGIFFII 120 LLTIDRYLAV VHAFVALKAR TVTFGVVTSV ITWVAVFAS LPGIIFTRSQ KEGLHYTCSS 180 HFPYSQYQFW KMFQTLKIVI LGLVPLLV M VICYSGLIKT LLRCRNEKKR HRAVRLIFTI 240 MIVYFLFWAP YNIVYLLNTF QEPPGLNCS SSNRDQAMQ VTETLGMTHC CINPIIYAFV 300 GEKFRNYLLV FQKHIAKRF CKCCSIFQOE APERASSVYT RSTGEQEISV GL 352
Seq ID NO: 260 Protein Sequence	
Protein Accession #: Eos sequence	
60	1 11 21 31 41 51 PQPPPGPGI PGAKGELGLP GAPGIDGEG PKGQKGDPE PGPAGLKGEA GEMGLSGLPG 60 ADGLKGEKE SASDSLQESL AQLIVERGPP GPPGPPGPMG LQGIQGPGL DGAKGEKGAS 120 GERGPSGLPG PVGPPLIGL PGTKGEKGRP GEPGLDGPFG PRGEKGRDSE RGEKGERGVP 180 GRKGVKGQKQ EPGPPGLDQ CPVGPDGLPV PGCWHK 216
Seq ID NO: 261 Protein Sequence	
Protein Accession #: NP_004852.1	
70	1 11 21 31 41 51 MLPPQKKPWE SMAKGLVLGA LFTSFLLLVY SYAVPPLHAG LASTTPEAAA SCSPPALEPE 60 AVIRANGSAG EQQPRRNVF LKTHKTASST LLNILFRFG KHRLKFAFPN GRNDFDYPTF 120 FARSLVQDYR PGACFNII CN HMRPHYDEV R GLVPTNAIFI TVLRDPAFL ESSPHYFGPV 180 VPLTWKLSAG DKLETFIQDP DRYYPDPGNF AHYLRNLFF DLGYDNSLDP SSPQVQEHIL 240 EVERRPHLV LQEYFDESIV LKDLCCWEL EDVLYFKLNA RRDSPVRLS GELYGRATAW 300 NMLDSHYLRH FNASFWRKVE AFGRRMARE VAALRHANER MRTICIDGGH AVDAAAIQDE 360 AMQPWQLGT KSILGYNLKK SIGQRHAQLC RRMLTPEIQY LMDLGANLWV TKLWKFIRDF 420 LRW 423
Seq ID NO: 262 Protein Sequence	
Protein Accession #: NP_061130.1	
80	1 11 21 31 41 51

	MASVLSRRRLG	KRSLLGARVL	GPSASEGPSA	APPSEPLLEG	AAPQPFITSD	DTPCQEQPKE	60
	VLKAPSTSGL	QQVAFQPGQK	VYVWYGGQEC	TGLVEQHSWM	EGQVTWVLE	QKLQVCCRVE	120
	EVWLAEELQGP	CQAPPLEPG	AQALAYRFVS	RNIDVPKRKS	DAVEMDEMA	AMVLTSLSCS	180
5	PVVQSPPGTE	ANFSASRAAC	DPWKESGDIS	DSGSSTTSGH	WSGSSGVSTP	SPPHQASPK	240
	YLGDAGFSQ	TDHFETDPD	PFLDEPAPR	KRKNVSVKMY	KCLWPNCKV	LRSIVGKRH	300
	VKALHLGDTV	DSQFKREED	FYYTEVLKE	ESAAAAAAA	AGTPVPGTPT	SEPAPTPSMT	360
	GLPLSALPPP	LHKAQSSGPE	HPGPSSSLPS	GALSKSAPGS	FWHIQADHAY	QALPSFIQIV	420
	SPHIYTSVSW	AAAPSAACSL	SPVRSRSLSP	SEPQQAPAPM	KSHLIVTSP	RAQSGARKAR	480
10	GEAKKCRKVY	GIEHRDQWCT	ACRWKKACQR	FLD			513

Seq ID NO: 263 Protein Sequence
Protein Accession #: AB058765.2

	1	11	21	31	41	51	
15	MRENYETLVS	VGTAELLPLS	AFLSPSEPGR	AVGGGSHADE	GQEPAGCGDP	QGGQPRHSLH	60
	LTALVLQVKE	IPEFLFGEVK	GAMDSPESES	RGASLDGERA	SPEAAAAAREP	CPLRGLLSCL	120
	PDGPTSQPHL	ATTPTDSSCS	SGPTGDGVQ	SPLPIKTADK	PWPTRKEGPG	ALGGEPSPT	180
	HSPSRKRSR	QGERGTSEAG	ISPGNSPLQG	LINCLKEILV	PGPRHPETSP	SFLPPLPSLG	240
20	TSRLTRADLG	PGSPPMVAVKT	EAVSGDCPLQ	GLLHCLKELP	EAQDRHPSPS	GVGNRRILQEN	300
	PGAWKRGSG	PGYLLTPPPH	PDLGAGGLLS	VKMENSWQVS	PPGPASCQPG	RQPLSPSATG	360
	DTRGVQPSW	GPEAQASAS	SSPLEALEAC	LKGIPFNGSS	PSQLFPTSCS	QNPQPGDSRS	420
	QKPELQPHRS	HSEATREPV	LPLGLQSCVR	DGFSRPLAPR	GTFTSFSSSS	STDWDLDFGS	480
	PVGNQGGHP	KGSPPGSSPL	QGLENCLEKI	FVPVLRPAWP	CSSAADRGPR	RAEPRNWTAD	540
25	KEGLRAEACE	SARLGGQGRGE	APTRSLHLVS	PQVFTSSCPV	ACHQRGFKDP	GATRPGVWRW	600
	LPEGSAFKPS	PLHCLSEALR	GILPVRPLRP	ACVGGPSPSP	SPGSSSSFSG	SEGEDPRPEP	660
	ELWKPLPQER	DLPLSCKPPV	PLSPCPGGTP	AGSSGGSPGE	DPRTTEPRYC	SGLGAGTAQD	720
	PCVVSQLEKR	PRVSEASRGL	ELGHGRPRVA	AKTHERLLPQ	GPPELPSESP	PPELPPPEAA	780
	PPVLPASSLQ	PPCHCGKPLQ	QELHSLGAAL	AEKLDRLATA	LAGLAQEVAT	MRTQVNRRLR	840
30	RPQGGPGMGE	ASMMWTLPRG	PRWAHGPGHR	HLPYWRQKGP	TRPKPKILRG	QGESCRAQDL	900
	QGLSRGTARR	ARLPPDAPF	AEPPLGHCSS	SQQLLSSTPS	CHAAFPAPHL	LAHTGGHQSP	960
	LPLVPAALP	LQASPPAAS	ADADVPTSGV	APDGIPEPRK	EPSSLLGGVQ	RALQEELWGG	1020
	EHRDPRWGAH						1030

Seq ID NO: 264 Protein Sequence
Protein Accession #: AL831935.1

	1	11	21	31	41	51	
40	PAGCGDPOGG	QPRHSLHLTA	LVQLVKEIPE	FLFGEVKGAM	DSPESESARGA	SLDGERASPE	60
	AAAREPCPLR	GLLSCLPDGP	TSQPHLATTP	TDSSCSSGPT	GDGVQGSPLP	IKTADKPWPT	120
	RKEGPGALGG	EPSPTTSPSP	RRKSHRGQER	GTSEAGISPG	NSPLQGLINC	LKEILVPGPR	180
	HPETSPPSLF	PLPSLGTSLR	TRADLGPGSP	PWAVKTEAVS	GDCPLQGLLH	CLKELPEAQD	240
	RHPSPSGVGN	RRLQENPGAW	KRGSGGPGYL	LTPPPHDLG	AGLLSVKME	NSWVQSPPGP	300
	ASQCPGRQPL	SPSATGDTRG	VQPSWGPPEA	QAASASSSPL	EALACLKGI	PPNGSSPSQL	360
45	PPTSCSQNPQ	PGDSRSQKPE	LQPHRSHEE	ATREPVPLIG	LQSCVRDGPS	RPLAPRGTFP	420
	SFSSSSSTDW	DLDFGSPVGN	QGHHPGKGGP	PGSSPLQGLE	NCLKEIPVPV	LRFAPWCSSA	480
	ADRGPRRAEP	RNWTADKEGS	APKPSPLHCL	ESALRGILPV	RPLRFACVGG	PSPSPSGSSS	540
	SSFGSGEGED	PRPEPDLWKP	LQERDRLPS	CKPPVPLSPC	PGGTPAGSSG	GSPGEDPRRT	600
50	EPRYCSGLGA	GEFGVS					616

Seq ID NO: 265 Protein Sequence
Protein Accession #: AAH29071.1

	1	11	21	31	41	51	
55	RTRGRTRGRL	RSGVMMPLAE	AGALAQGGGP	SATEWACILR	RKTPRHKQPT	LLMVRASRRS	60
	GKTSVAILKAG	RQSVSGRKNS	TSKDLVTLGA	SSLREERGHP	LHPRHRKAVH	LRTRGRTRGW	120
	VQTLARMSRR	TRGVVERAAA	AAAAAAGGDA	GHAPFPFPPA	ADGARAPRSP	QVTPRGLRL	180
	RLPRRESLLR	GLCRPLRPLL	GFRESDSAKP	ASLRLQLHTP	SARRNYRIAG	ARLMRSNYPP	240
60	PLSSAALRGA	GPTRRN					256

Seq ID NO: 266 Protein Sequence
Protein Accession #: NP_002095.1

	1	11	21	31	41	51	
65	MTKFSSFSLF	FLIVGAYMTH	VCFNMEIIGG	KEVSPHSRPF	MASIQYGGHH	VCGGVLDIDPO	60
	WVLTAAHCQY	RFTKGQSPTV	VLGAHSLSKN	EASKQLEIK	KFIPFSRVTS	DQSNIDIMLV	120
	KLQTAALKNK	HVKMLHIRSK	TSLSRGTCKK	VTGWGATDPD	SLRPSDTLRE	VTVTVLSRKL	180
	CNSQSYNGD	PFITKDMVCA	GDAKGQKQDSC	KGDSGGPLIC	KGVFHAIVSG	GHECGVATKP	240
70	GIYTLTKKY	QTWKSNLVP	PHTN				264

Seq ID NO: 267 Protein Sequence
Protein Accession #: NP_443179.1

	1	11	21	31	41	51	
75	MQVNTLFETS	QVPDWSPPQ	VQVQETVRET	ISCSQMPAFS	EPAGEESPFT	GTTTISFSNL	60
	GGVHKENASL	AQHSEVKPCT	CGPQEEKQD	RDGNIPDNFR	EDLKYEQSIS	EANDETMSPG	120
	VFSRHLPKDA	RADFREPVAV	SVASPEPTDT	ALTLENVCDE	PRDREAVCAM	ECFEASDQGT	180
	CFDTIDSLVG	TPVDNYSPPQ	ICSDVTELA	GQNKVSDLCS	SNDKTLEVFF	QTQVSETSVS	240
	TKSSKDGNS	VMSPLFISTF	TLNISHTASE	GATGENLAKV	EKSTYPLAST	VHAGQEQPSP	300
80	SNSGGLDETQ	LLSSENNPLV	QFKEGGDKSP	SPSAADTTAT	PASYSISVSF	PWEKPTTLTA	360
	NNECFQATRE	TVTITATEVHP	AKYLAVSIPE	DKHAGGTEER	FPRASHEKVS	QFSPQVOVDH	420
	ILSGATIKST	KELLCRAPSV	PGVPHVLQL	PEGEGFCNSN	PLQVDNLSGD	KSQTVDRADF	480
	RSYEENFQER	GSETKQGVQ	QSLSQGSL	APDFQQLSPT	TSAAQEERNL	VPTAPSPASS	540
	REGAGQRSGW	GTRVSVVAET	AGEEDSQALS	NVPSLSLILL	EESKEYRPGN	WEAGNKLKII	600

5
10
15

TLEASASEIW PPRQLTNSSE KASDGGLIIP DKVWAVPDSL KADAVVPELA PSEIAALAH 660
 PEDAESALAD SRESHKGEET TISVHWRLS SRGFSQPRLL ESSVDPVDEK ELSVTDLSLA 720
 ASETGGKENV NNVSQDQEEK QLMMDHTAFF KFLTCPKIL ESSVDPIDEI SVIEYTRAGK 780
 PEPSETTPQG AREGGQSNMG NMGHEAEIQS AILQVPCLOQ TILSENRISS SQEGSMKQEA 840
 EQIQPEEAKT AIWQVLQPSG GGERIPSGCS IGQIQESSDG SLGEAEQSKK DKAELISPTS 900
 PLSSCLPIMT HSSLGVDTHN STGQIHDVPE NDIVEPRKRQ YVFPVSQKRG TIENERGKPL 960
 PSSPDLTRFP CTSSPEGNVT DFLISHKMEE PKIEVLQIGE TKPPSSSSSS AKTLAFISGE 1020
 RELEKAPKLL QDPCQKGTIG CAKSREREK SLEARAGKSP GTLTAVTGSE EVKRKPEAPG 1080
 SGHLAEGVKK KILSRVAALR LKLEKENIR KNSAFLKKMP KLETSLSHTE EKQDPKKPSC 1140
 KREGRAVLL KKIQAEMFPE HSGNVKLSQO FAEIHEDSTI CWTKDSKSLA QVQASAGDNS 1200
 TVSFAIVQAS PKDQGLYYCC IKNSYGVKTA EFNLTAEVLK QLSRQDTKG CEEIEFSQLI 1260
 FKEDFLHDSY FGRLRGQIA TEELHFGEGV HRKAFRSTVM HGLMPVFKPG HACVLKVHNA 1320
 IAYGTRNDE LIQRNYKLAA QECYVQNTAR YYAKIYAAEA QPLEGFGVEP EIIPFIPIHR 1380
 PENNIPYATV EEELIGEFVK YSIRDGKEIN FLRRESEAGQ KCCTFQHWVY QKTSGCLLV 1440
 DMQGVGMKLT DVGIATLAKG YKFGKNCMSM TFIDQFKALH QCNKYCKMLG LKSLQNNNQK 1500
 KQGPSIGKSK VQNSMTVKK AGPETPGEKK T 1531

20

Seq ID NO: 268 Protein Sequence
Protein Accession #: NP_602293.1

1 11 21 31 41 51
 | | | | |
 MGKQNSKLRP EVLQDLRENT EFTDHELQEW YKGLKDCPT GHITVDEFKK IYANFFPYGD 60
 ASKFAEHVFR TFDITNGDGTI DFREFIIALS VTSRGKLEQK LKWAFSMYDL DNGYISRSR 120
 MLEIVQAIYK MVSSVMKMP DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV 180
 RLLQCDPSSA SQF 193

25

Seq ID NO: 269 Protein Sequence
Protein Accession #: NP_002140.2

1 11 21 31 41 51
 | | | | |
 MGKQNSKLRP EVLQDLRENT EFTDHELQEW YKGLKDCPT GHITVDEFKK IYANFFPYGD 60
 ASKFAEHVFR TFDITNGDGTI DFREFIIALS VTSRGKLEQK LKWAFSMYDL DNGYISRSR 120
 MLEIVQAIYK MVSSVMKMP DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV 180
 RLLQCDPSSA SQF 193

30

Seq ID NO: 270 Protein Sequence
Protein Accession #: NP_003937.1

1 11 21 31 41 51
 | | | | |
 MGNAQERPE TIDRERKRLV ETLQADSGLL LDALLARGVL TGPEYEALDA LPDAERRVRR 60
 LLLLVQKGKE AACQELLRCA QRTAGAPDPA WDWQHVGPY RDRSYDPPCP GHWTPEAPGS 120
 GTTCPLPRA SDPDEAGGPE GSEAVQSGTP EEPEPELEAE ASKEAPEPE PEPEPEPEAE 180
 AEPEPELEPE PDPEPEPDFE ERDESEDS 208

35

Seq ID NO: 271 Protein Sequence
Protein Accession #: NP_004198.1

1 11 21 31 41 51
 | | | | |
 MGAUVDEGP TGVKAPDGGW GMAVLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSDT 60
 AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGLGFASL GMVAASFCSR IIQVLTITGV 120
 ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPILQLL QDRYGNRGGF 180
 LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLLDL SVFRDRGFVL YAVAASVMVL 240
 GLFVPPVFVV SYAKDLGVDP TKAALLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
 SMFFNGLADL AGSTAGDYG LVVFCIFFGI SYGMVGLQF EVLMAIVGTH KFSSAIGLVL 360
 LMEAVAVLVC PPSGGKLLDA THVMYVFIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
 VAAAEELKLV KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

40

Seq ID NO: 272 Protein Sequence
Protein Accession #: NP_060705.1

1 11 21 31 41 51
 | | | | |
 MAALTTLFKY IDENQDRYIK KLAKWVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE 60
 LVDIGKQKLP DGSEIPLPPI LLGRLGSDPQ KKTVCIIYGH L DVQPAALDGD WDSEPTLVE 120
 RDGKLYGRGS TDDKGPVAGV INALEAYQKT GOEIPVNVRF CLEGMEESGS EGLDELIFAR 180
 KDTFFKDVYD VCISDNYWLG KKKPCITYGL RGICYFFIEV ECSNKDLHSG VYGGSVHEAM 240
 TDLILLMGS L VDKRGNILIP GINEAVAAVT EEEHKLDDI DFDIEEFAKD VQAQILLHSH 300
 KQDILMHRWR YPSLSLHGIE GAFSGSGAKT VIPRKVVGKF SIRLVPMNTP EVVGEQVTSY 360
 LTKKFAELRS PNEFKVYMGH GKGKPVSDFS HPHYLGRRA MKTVFVGEVD LTREGGSIPV 420
 TLTFQATGK NVMLLPVGSA DDGAHSQNEK LNRNYNIEGT KMLAAYLYEV SQLKD 475

45

Seq ID NO: 273 Protein Sequence
Protein Accession #: AF258592.1

1 11 21 31 41 51
 | | | | |
 MAALTTLFKY IDENQDRYIK KLAKWVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE 60
 LVDIGKQKEI PNVNRFCLG MEESGSEGLD ELIFARKDTF FKDVYVCIS DNYWLKGGKP 120
 CITYGLRGIC YFFIEVECSN KDLHSGVYGG SVHEAMTDLI LLMGSLVDKR GNILIPGINE 180
 AVAAVTEEEH KLYDDIDFDI EEFKDVGAQ ILLHSHKKDI LMHRWRYPSP SLHGIEGAFS 240
 GSGAKTVIPR KVVGKFSIRL VPMNTEPVVG EQVTSYLTAK PAELRSPNEF KVYMGHGGKP 300
 WVSDFSHPHY LAGRRAMKT VGVPEDLTRE GGSIPVTLTF QEATGKQVML LPVGSADDGA 360
 HSQNEKLNRY NYIEGTKMLA AYLVEVSQK D 391

70

Seq ID NO: 274 Protein Sequence
Protein Accession #: NP_060871.1

	1	11	21	31	41	51	
	MGGNHSHKPP	VFDENEENF	DHFQILRAIG	KGSFGKVCIV	QKRDTKKMYA	MKYMNKQKCI	60
	ERDEVNVPFR	ELQIMOGLEH	PFLVNLWYSF	QDEEDMFVW	DLGLGGDLRY	HLQONVHFTF	120
5	GTVKLYICEL	ALALEYLQRY	HHHRDIKPD	NILLDEHGHV	HITDFNIATV	VKGAERASSM	180
	AGTKPYMAPE	VFOVYMDRGP	GYSYPVDWMS	LGITAYELLR	GWRPYEIHVS	TPIDEILNMF	240
	KVERVHYSST	WCKGMVALLR	KLLTKDPESR	VSSLHDIQSV	PYLADMNWDA	VFKKALMPGF	300
	VPNKGRLLNCD	PTFELEEMIL	ESKPLHKKKK	RLAKNRSRDG	TKDSCPLNGH	LQHCLLETVRE	360
10	EFIIIFNREKL	RRQGGGSQL	LDTDSRGGGQ	AQSKLQDGCN	NNLLTHTCTR	GCSS	414
	Seq ID NO: 275 Protein Sequence						
	Protein Accession #: NP_004198.1						
	1	11	21	31	41	51	
	MGGAVVDEGP	TGVKAPDGGW	GWAVLPGCFV	ITGFSYAFPK	AVSVFFKELI	QEFIGIGYSDT	60
15	AWISSILLAM	LYGTGPLCSV	CVNRFGCRPV	MLVGGLFASL	GMVAASFCRS	IIQVYLTTGV	120
	ITGLGLALNF	QPSLIMLNRY	FSKRRPMANG	LAAAGSPVFL	CALSPGLQLL	QDRYGRWGFF	180
	LILGGLLLNC	CVCAALMRPL	VVTAQPGSGP	PRPSRRLDL	SVFRDRGFVL	YAAVAAVMVL	240
	GLFVPPVVFV	SYAKDLGVDP	TKAFLTLTIL	GFIDIFARPA	AGFVAGLGKV	RPYSVYLFSF	300
20	SMFFNGLADL	AGSTAGDYGG	LVVFCIPFGI	SYGMVAGALQ	EVLMAIVGTH	KFSSAIGLVL	360
	LMEAVAVLVG	PPSGGKLLDA	THVYMYVFI	AGAELVTSSL	ILLGNFFCCI	RKKPKPEQPE	420
	VAAAEELKLH	KPPADSGVDL	REVEHFLKAE	PEKNGEVVHT	PETSV		465
	Seq ID NO: 276 Protein Sequence						
	Protein Accession #: NP_006589.1						
	1	11	21	31	41	51	
	MPTNFTVVV	EAHADGGGDE	TAERTEAPGT	PEGPEPERPS	PGDGNPRENS	PFLNNVEVEQ	60
	ESFFEGKQMA	LFEEEMDSNP	MVSSLLNKLA	NYTNLSQGVV	EHEEDEESRR	REAKAPRMGT	120
30	FIGVYLPCLQ	NILGVILFLR	LTWIVGVAGV	LESFLIVAMC	CTCTMLTAIS	MSAIATNGVV	180
	PAGGSYYMIS	RSLGPEFGVA	VGLCFYLGTT	FAGAMYILGT	IEIFLTYISP	GAAIFQAEAA	240
	GGEEAAMLNH	MRVYGTCTLV	LMALVVVFVG	KYVNKLALVF	LACVLSILA	IYAGVIKSAF	300
	DPDPIPVCLL	GNRTLRRRSF	DACVKAYGIH	NNSATSALWG	LFCNGSQPSA	ACDEYFIQNN	360
	VTEIQIGPGA	ASGVFLENLW	STYAHAGAPV	EKKGVSPSPV	AEESRSTLDP	VYVLTIDIAAF	420
35	TLVGIYFPPS	VTGIMAGSNR	SGDLKDAQKS	IPTGTILAIV	TTSFIYLSCL	VLFACIEGV	480
	VLRDKFGEAL	QGNLVIGMLA	WPSPWVIVIG	SFFSTCGAGL	QTLTGAPRL	QAIARDGIVP	540
	PLQVFGHGKA	NGEPTWALL	TVLICETGIL	IASLDSVAPI	LSMFFLMCYL	FVNLACAVQT	600
	LLRTPNWRPR	KFKYHWTLSF	LGMSLCLALM	FICSMYYALS	AMLIAGCIYK	YIEYRGAEKE	660
	WGDGIRGLSL	NAARYALLRV	EHGPPHTKNW	RPOVLVLMNL	DAEQAVKHPR	LLSFTSQLKA	720
40	GKGLTIVGSV	LEGTYLDKHM	EAQRAENIR	SLMSTKTKG	FCQLVVSSSL	RDGMSHLIQS	780
	AGLGGLKHN	VLMAMPASWK	QEDNPFWSKN	FVDTVRDTTA	AHQALLVAKN	VDSFPQNQER	840
	FGGGHIDVNW	IVHDGGMMLL	LPFLLRQHKV	WRKCRMRIFT	VAQVDDNSIQ	MKKDLQMFY	900
	HLRISAEVEV	VMVENDISA	PTYERTLMME	QRSQMLKQMQ	LSKNEQEREA	QLIHDRNTAS	960
45	HTAAAARTQA	PPTPDVKQMT	WTREKLIAEK	YRSRDTLSLG	FKDLFSMKPD	QSNVRRMHTA	1020
	VKLANGVVLNK	SQDAQVLLN	MPGPPKNRQG	DENYMEFLEV	LTEGLNRVLL	VRGGGREVIT	1080
	IYS						1083
	Seq ID NO: 277 Protein Sequence						
	Protein Accession #: NP_004576.1						
	1	11	21	31	41	51	
	MASPHQEPKP	GDLEIFIRLG	YEHWALYIGD	GYVIHLAPPS	EYPGAGSSSV	FSVLSNSAEV	60
	KRGRLDVDVG	GCCYRVNNSL	DHEYQPRPVE	VIISAKEMV	QQKMKYSIVS	RNCEHFVAQL	120
55	RYGKSRCQKV	EKAKEVEGVA	TALGILVVAG	CSFAIRRYQK	KATA		164
	Seq ID NO: 278 Protein Sequence						
	Protein Accession #: NP_004687.1						
	1	11	21	31	41	51	
	MLKREGKVQP	YTKTLDGGWG	WMIVIHFFLV	NVFMVMTKT	FAIFFVVFQE	EFEGTSEQIG	60
60	WIGSIMSSLR	FCAGPLVAII	CDILGEKTTT	ILGAFVVTGG	YLISSWATSI	PFLCVTMGLL	120
	PGLGSFLYQP	VAAVVTYKYP	KKRLALSTAI	ARSGMGLTFL	LAPFTKFLID	LYDWTGALIL	180
	FGAIALNLVP	SSMLLRPIHI	KSENNSGIKD	KGSSLSAHGP	EAHATETHCH	ETEESTIKDS	240
	TTQKAGLPSK	NLTVSQNSE	EFYNGPNRNR	LLKSDSEED	KVISWCKQL	FDISLFRNPF	300
65	FYIFTWSFLL	SQLAYFIPTF	HLVARAKTLG	IDIMDASYLV	SVAGILETVS	QIISGWVADQ	360
	NWIKKYHYHK	SYLILCGITN	LLAPLATTFP	LLMTYTICFA	IFAGGYLALI	LPVLVDLCRN	420
	STVNRFLGLA	SFFAGMAVLS	GPPIAGMLYD	YTQTYNGSFY	FSGICYLLSS	VSFFVPLAE	480
	RWKNSLT						487
70	Seq ID NO: 279 Protein Sequence						
	Protein Accession #: NP_000349.1						
	1	11	21	31	41	51	
	MALEFVRLAL	ALALALGPAA	TLAGPAKSPY	QLVLQHSRLR	GRQHGPNVCA	VQKVIGTNRK	60
75	YFTNCKWYQ	RKICGKSTVI	SYECCPGYEK	VPGERGCPAA	LPLSNLYETL	GVVGTITQL	120
	YTDRETEKLR	EMEGPGSFTI	FAPSNEAWAS	LPAEVLDSL	SNVNIELNLA	LRHYMVGRRV	180
	LTDELKHGNT	LTSYMQNSNI	QIHHPYNGIV	TVNCAARLLK	DHHAATNGVH	LIDKIVSTIT	240
	NNIQIIEIE	DTFETLRAAV	AASGLNTMLE	GNGQYTLAP	TNEAFKIPIS	ETLNRILGDP	300
80	EALRDLLNNH	ILKSAMCAEA	IVAGLSVETL	EGTTLEVGC	GDMLTINGKA	IISNKDILAT	360
	NGVIHYDEL	LIPDSAKTLF	ELAAESDVST	AIDLFRQAGL	GNHLSGGERL	TLAPLANSVF	420
	KDGTTPPIDAH	TRNLRLRNHII	KDQLASKYLY	HGQTLLETGG	KKLRVVFVYRN	SLCIENS CIA	480
	AHDKRGRYGT	LFTMDRVLT	PMGTVMVVLK	GDNRFSMLVA	AIQSAGLTET	LNREGVYTVF	540
	APTNEAFRL	PPRERSRLLG	DAKELANILK	YHIGDEILVS	GGIGALVRLK	SLQGDKLEVS	600
	LQNVVSVN	EPVAEPDIMA	TNGVVHVITN	VLQPPANRPQ	ERGDELADSA	LEIFKQASAF	660

SRASQSVRL APVYQKLLER MKH

683

Seq ID NO: 280 Protein Sequence

Protein Accession #: NP_663623

5
1 11 21 31 41 51
MEGSGGGAGE RAPLLGARRA AAAAAAGAP AGRRACGAV LLETLLERAA FYGITSNLVL 60
FLNGAPFCWE GAQASEALLL FMGLTYLGSP FCGWLADARL GRARAILLSL ALYLLQMLAF 120
10 PLLAAPATRA ALCGSARLLN CTAPGPDAAA RCCSPATFAG LVLVGLGVAT VKANITPFGA 180
DQVKDRGPEA TRRFNWFYV SINLGAILSL GGIAYIQQNV SFVTGYAIPT VCVGLAFVVF 240
LGGQSVFITK PPDGSAFTDM FKILTYSCCS QKRSGERQSN GEGIGVFQOS SKQSLFDSCK 300
MSHGGPFTTE KVEDVKALVK IVPVFLALIP YNTVYFQMT TYVLQSLHLR IPEISNITTT 360
PHTLPAWLT MFDVALLILL IPLKDKLVDP ILRRHGLLPS SLKRIAVGMP FVMCSAFAAG 420
15 ILESKRLNLV KEKTINQITG NVVYHAADLS LWWQVPQYLL IGISEIFASI AGLEFAYSAA 480
PKSMQSAIMG LFFFFSGVGS FVGSGLLALV SIKAIQWMSS HTDFGNINGC YLNYFFFLLA 540
AIQGATLLLF LIISVKYDHH RDHQSRANG VPTSRAA 577

Seq ID NO: 281 Protein Sequence

Protein Accession #: NP_001241.1

20
1 11 21 31 41 51
MYRLPLQCVL WGCCLTAVHP EPPTACREKQ YLINSQCCSL CQPGQKLVSD CTEFTETECLE 60
PGGESEFLDT WNRETHCHQH KYCDPNLGLR VQQKGTSETD TICTCEGWH CTSEACESCV 120
LHRSCSPGFG VKQIATGVSD TICEPCPVGP FSNVSSAFK CHPTWSCETK DLVVFQAGTN 180
25 KTDVVCGPQD RLRLVVIPI IFGILFAILL VLVFIKKVAK KPTNKAPHEK QEPQEIFFPD 240
DLPGSNTAAP VQETLHGQCP VTQEDGKESR ISVQERQ 277

Seq ID NO: 282 Protein Sequence

Protein Accession #: NP_003833.3

30
1 11 21 31 41 51
MEQRQGNAPA ASGARKRHGP GPREARGARP GLRVPKTLVL VVAAVLLLVV AESALITQQD 60
LAPQQRAPQ QKRSSPSEGL CPPGHHSIED GRDCISCKYG QDYSTHWNLD LFCLRCTCD 120
35 SGEVELSPT TTRNTVCQCE EGTFREEDSP EMCRCRTGC PRGMVKVGDG TPWSDIECVH 180
KESGTHSGE APAAEETVTS SPGTSPASPCS LSGIIGVTV AAVVLIVAVF VCKSLWKKV 240
LPYLKIGCSG GGGDPERVDR SSQRPGEADN VLNEIVSILQ PTQVPEQEME VQEPAEPTGV 300
NMLSPGESEH LLEPAEAERS QRRRLVPAN EGDPTETLRQ CFDDFADLVF FDSWEPLMRK 360
LGLMDNEIKV AKAEAAGHRD TLYTMLIKWV NKTGRDASVH TLDALETGL ERLAKQKIED 420
40 HLLSSGKPMY LEGNADAMS 440

Seq ID NO: 283 Protein Sequence

Protein Accession #: NP_671716.1

45
1 11 21 31 41 51
MEQRQGNAPA ASGARKRHGP GPREARGARP GLRVPKTLVL VVAAVLLLVV AESALITQQD 60
LAPQQRAPQ QKRSSPSEGL CPPGHHSIED GRDCISCKYG QDYSTHWNLD LFCLRCTCD 120
SGEVELSPT TTRNTVCQCE EGTFREEDSP EMCRCRTGC PRGMVKVGDG TPWSDIECVH 180
KESGTHSGE VAAVVLIVAV FVCKSLWKKV VLPYLKIGCS GGGDPERVDR RSSQRPGEAD 240
50 NVLNEIVSIL QPTQVPEQEM EVQEPAEPTG VNMLSPGESE HLEPAEAERS SQRRRLVPA 300
NEGDPETELR QCFDDFADLV PFDSWEPLMR KLGLMDNEIK VAKAEAAGHR DTLTYTMLIKW 360
VNKTGRDASV HTLDALETGL GERLAKQKIE DHLSSGKPM YLEGNADAMS S 411

Seq ID NO: 284 Protein Sequence

Protein Accession #: NP_002002.2

55
1 11 21 31 41 51
MRLLALLGV LLSVPGPPVL SLEASEEVEL EPCLAPSLEQ QEQLTVALG QPVRLCCGRA 60
ERGGHMYKEG SRLAPAGRVR GWRGRLEIAS FLPEDAGRYL CLARGSMIVL QNLTITGDS 120
60 LTSSNDDDDP KSHRDLNHRH SYPQAPYWT HPQRMKKLH AVPAGNTVKF RCPAAGNPTP 180
TIRWLKDGQA FHGENRIGGI RLRHQHWSLV MESVVPDRG TYTCLVENAV GSIRYNYLLD 240
VLERSPHRPI LQAGLPANTT AVVGSDEVLL CKVYSDAQPH IQWLKHIVIN GSSFGADGFP 300
YVQVLKTADI NSSEVEVLYL RNVSADAGE YTCLAGNSIG LSYSQSAWLV LPEEDPTWTA 360
AAPEARYTDI ILYASGSLAL AVLLLAGLY RGQALHGRHP RPPATVQKLS RFPLARQFSL 420
65 ESGSSGKSSS SLVRGVRLSS SGPALLAGLV SLDPLDPLW EFPRDRLVLG KPLGEGCFGQ 480
VVRAEAFGMD PARPDQASTV AVKMLKONAS DKDLADLVSE MEVMKLIGRH KNIINLLGVC 540
TOEGPLYVIV ECAAKGNLRE FLRARRPPGP DLSPDGPRSS EGPLSFPVLV SCAYQVARGH 600
QYLESRKCIH RDLAARNVLV TEDNVMKIAD FGLARGVHHI DYYKTSNGR LPVKWMAPEA 660
LFDVRVYTHS DVMSFGILLW EIFTGGSPY PGIPVEELFS LLREGHRMDR PPHCPPELYG 720
70 LMRECWHAAP SQRPFTFKQLV EALDKVLLAV SEEYLDRLT FGPYSPSGGD ASSTCSSDS 780
VFSHDLPLG SSSFPFGSGV QT 802

Seq ID NO: 285 Protein Sequence

Protein Accession #: NP_075252.1

75
1 11 21 31 41 51
MRLLALLGV LLSVPGPPVL SLEASEEVEL EPCLAPSLEQ QEQLTVALG QPVRLCCGRA 60
ERGGHMYKEG SRLAPAGRVR GWRGRLEIAS FLPEDAGRYL CLARGSMIVL QNLTITGDS 120
LTSSNDDDDP KSHRDLNHRH SYPQAPYWT HPQRMKKLH AVPAGNTVKF RCPAAGNPTP 180
TIRWLKDGQA FHGENRIGGI RLRHQHWSLV MESVVPDRG TYTCLVENAV GSIRYNYLLD 240
80 VLERSPHRPI LQAGLPANTT AVVGSDEVLL CKVYSDAQPH IQWLKHIVIN GSSFGADGFP 300
YVQVLKTADI NSSEVEVLYL RNVSADAGE YTCLAGNSIG LSYSQSAWLV LPGTGRIPHL 360
TCDLTPAGR TKSPTLQFSL ESGSSGKSSS SLVRGVRLSS SGPALLAGLV SLDPLDPLW 420
EFPRDRLVLG KPLGEGCFGQ VVRAEAFGMD PARPDQASTV AVKMLKONAS DKDLADLVSE 480
MEVMKLIGRH KNIINLLGVC TOEGPLYVIV ECAAKGNLRE FLRARRPPGP DLSPDGPRSS 540

	EGPLSFPVLV	SCAYQVARGM	QYLESRKCIH	RDLAARNVLV	TEDNMVKIAD	FGLARGVHHI	600
	DYYKTSNGR	LPVKMAPEA	LFDRVYTHQS	DVWSFGILLW	EIFTLGGSFY	PGIPVEELFS	660
	LLRBGHRMDR	PPHCPPELYG	LMRECWAAP	SQRPTFKQLV	EALDKVLLAV	SEEYLDLRLT	720
5	FGPYSPSGGD	ASSTCSSSDS	VFSHDLPLG	SSSFPPGSGV	QT		762
	Seq ID NO: 286 Protein Sequence						
	Protein Accession #: NP_002836.2						
	1	11	21	31	41	51	
10	MRGLGTCLAT	LAGLLLTAA	ETPSGGCLFD	EPYSTCGYSQ	SEGDDFNWEQ	VNTLTKPTSD	60
	PWMPSSGLML	VNASGRPEGQ	RAHLLLPQLK	ENDTHCIDFH	YFVSSKSNP	PGLLNYYVKV	120
	NNGLGNPIW	NISGDPTRTW	NRAELAISTF	WPNFYQVIFE	VITSGHQGYL	AIDEVKVLGH	180
	PCTRTPHFLR	IQNVEVNAQ	FATPQCSAIG	RTVAGDRLWL	QGIDVRDAPL	KEIKVTSSRR	240
	FIASFNVNT	TKRDAGKYRC	MIRTEGGVGI	SNYAEVLVKE	PPVPIAPPQL	ASVGATYLMW	300
15	QLNANSING	GPIVAREVEY	CTASGWNDR	QPVDSYSYKI	GHLDPDTEYE	ISVLLTRPCE	360
	GGTGSPPGAL	RTRTKCADPM	RGRPKLEVVE	VKSQITIRW	EPFGYNVTRC	HSYNLTVHYC	420
	YQVGGQEQVR	EEVSDNTENS	HPQHTITNLS	PYTNVSVKLI	LMNPEGRKES	QELIVQTDED	480
	LPGAVPTESI	QGSTFEKIF	LQWREPTQTY	GVITLYEITY	KAVSSFDPEI	DLSNQSGRVS	540
	KLGNETHFLF	FGLYPGTTYS	FTIRASTAGK	FGPPATNQPT	TKISAPSMFA	YELETPLNQ	600
20	DNTVTMLKP	AHSRGAQVSV	YQIVVEEERP	RRTKKTTEIL	KCYPVPIHFQ	NASLLNSQY	660
	FAAEFPADSL	QAAQPTTIGD	NKTYNGYWNT	PLLKYKSYRI	YFQAASRANG	ETKIDCVQVA	720
	TKGAATPKPV	PEPEKOTDHT	VKIAGVIAGI	LLEFVIIFLGV	VLVMKKRKLK	KRKETMSST	780
	RQEMTMVMS	MDKSYAEQGT	NCDEAFSPMD	THNLNGRSVS	SPSSPTMTKN	TLSTSVFNSY	840
	YPDETHMAS	DTSSLVQSHT	YKREPADVP	YQTGQLHPAI	RVADLLQHIT	QMKCAEGYGF	900
25	KEEYESPFEG	QSAFVDSAKK	DENRMKNRYG	NIIAYDHSRV	RLQTIQEDTN	SDYINGNYID	960
	GYHRPNHYIA	TQGPQETIY	DFWRMVWHEN	TASIMVTNL	VEVGRVKCKC	YWPDDTEIYK	1020
	LKIVTLIETE	LLAEVIRTFT	AVEKRGVHEI	REIRQFHFTG	WPDHGVPIYA	TGLLGFVRQV	1080
	KSKSPPSAGP	LUVHCSAGAG	RTGCFIVIDI	MLDMAEREGV	VDIYNCVREL	RSRRVNMVQT	1140
	EEQYVFIHDA	ILEACLGGDT	SVPASQVRS	YYDMNKLDQ	TNSSQIKEEF	RTLNMVTPTL	1200
30	RVEDCSIAL	PRNHKKNRCM	DILPPDRCLP	FLITIDGESS	NYINAALMDS	YKQPSAFIVT	1260
	QHPLPNTVKD	FWRVLVDYHC	TSVVMNLNDV	PAQLCPQYWP	ENGVRHRGPI	QVEFVSADLE	1320
	EDIISRIFRI	YNAARPDQGY	RMVQFQFLG	WPMYRDTVPS	KRSFLKLIRQ	VDKQVEEYNG	1380
	GEGPTVVHCL	NGGGRSGTFC	AISIVCEMLR	HQRTVDVFHA	VKTLRNNKPN	MVDLLDQYKF	1440
35	CYEVALEYLN	SG					1452
	Seq ID NO: 287 Protein Sequence						
	Protein Accession #: NP_057635.1						
	1	11	21	31	41	51	
40	MGFLQLLVVA	VLASEHRVAG	AAEVFGNSSE	GLIEFSVGKF	RYFELNRPPF	EEAILHDISS	60
	NVTFLFIQIH	SQYQNTTVSF	SPILLNSNSE	TGTASGLVFI	LRPEQSTCTW	YLGTSIGIQPV	120
	QNMALLSYS	ERDPVPGCGN	LEFDLIDIPN	IYLEYNFFET	TIKFAPANLG	YARGVDPPPC	180
	DAGTDQDSRW	RLQYDVYQYF	LPENDLTEEM	LLKHLQRMVS	VPQVKASALK	VVTLTANDKT	240
	SVSFSSLPQ	GVYINVIWMD	PFLNTSAAYI	PAHTYACSPF	AGEGSCASLG	RVSSKVFFTL	300
45	FALLGFFICF	FGHRFWKTEL	FFIGFIIMGF	FFYILITRLT	PIKYDVNLIL	TAVTGSVGGM	360
	FLVAVMWRFG	ILSICMLCVG	LVLGFLISSV	TFFTPLGNLK	IFHDDGVFWV	TFSCIAILIP	420
	VVFMGCLRLI	NILTCGVIGS	YSVVLADISY	WSTSLSYITL	NVLKRALNKD	FHRAFTNVPP	480
	QTNDFIILAV	WGMLAVSGIT	LQIRRRERGR	FFPPHYPKLV	KQERERRVTN	ILDPSYHIPP	540
50	LRERLYGRIT	QIKGLFQKEQ	PAGERTPLLL				570
	Seq ID NO: 288 Protein Sequence						
	Protein Accession #: NP_003811.1						
	1	11	21	31	41	51	
55	MEPPGDWGP	PWRSTPTD	LRLVLYLTF	GAPCYAPALP	SCKEDEYVPG	SECCPKCSPG	60
	YRVKEACGEL	TGTVCEPCPP	GTIAHLNGL	SKCLQCMCD	PAMGLRASRN	CSRTENAVCG	120
	CSPGHFCIVQ	DGDHCAACRA	YATSSPGQRV	QKGTESQDT	LCQNCPPGTF	SPNGTLEECQ	180
	HQTKCSWLVT	KAGAGTSSSH	WWWFLSGSL	VIVIVCSTVG	LIIICVRRRP	RGDVVKVIVS	240
60	VQRKRQEAEG	EATVIEALQA	PPDVTTVAVE	ETIPSFTGRS	PNH		283
	Seq ID NO: 289 Protein Sequence						
	Protein Accession #: NP_000943.1						
	1	11	21	31	41	51	
65	MEPHDSSHMD	SEFRYTLFPI	VYSIIFVLGV	IANGYVLWVF	ARLYPCKKFN	EIKIFMVNLT	60
	MADMLFLITL	PLMIVYYQNO	GNWILPKFLC	NVAGCLFFIN	TYCSVAFGLV	ITYNRFOAVT	120
	RPKTAQANT	RKRGISLSLV	IWVAIVGAAS	YFLILDSTNT	VPDSAGSGNV	TRCFEHYEKG	180
	SVPLIIHIF	IVSFLLVFL	IILFCNLVII	RTLLMQPVQ	QRNAEVKRRR	LWMVCTVLAV	240
	FIICFVPHHV	VQLFWTLAEL	GFQDSKFHQA	INDAHQVTL	LLSTNCVLD	VIYCFLTKKF	300
70	RKHLTEKFYS	MRSRKRCSRA	TTDTVTEVVV	PFNQIPGNSL	KN		342
	Seq ID NO: 290 Protein Sequence						
	Protein Accession #: NP_003262.1						
	1	11	21	31	41	51	
75	GCLGAIKENK	CLLLTFLLLL	LLVFLLEATI	AILFFAYTDK	IDRYAQDQDK	KGLHLYGTQG	60
	NVGLTNAWSI	IQTDPRCCGV	SNYTDWEVY	NATRVDPSCC	LEFSESCGLH	APGTWKKAPC	120
	YETVKVHLQE	NLLAVGIFGL	CTALVQILGL	TFAMTMYCQV	VKADTYCA		168
80	Seq ID NO: 291 Protein Sequence						
	Protein Accession #: NP_005620.1						
	1	11	21	31	41	51	
	MAKKSANGI	YSVSGDEKKG	PLIAPGPDGA	PAKGDGPVGL	GTPGGR LAVP	PRETWTRQMD	60

	FIMSCVGFV	GLGNVVRFPY	LCYKNGGGVF	LIPYVLIALV	GGIPIFFLEI	SLGQFMKAGS	120
	INWVNICPLF	KGLGYASPMV	VFYCNYYIM	VLWGFYYLV	KSFTTTLPPA	TCGHTWNTPD	180
	CVEIFRHEDC	ANASLANLTC	DQLADRRSPV	IEFWENKVL	LSGGLEVPGA	LWVEVTLCLL	240
5	ACHVLVYFCV	WKGVKSTGKI	VYFTATFPYV	VLVLLVRGV	LLPGALDGI	YYLKPDMWSL	300
	GSPOVWIDAG	TQIFFSYAIG	LGALTALGYS	NRFNNNCYKD	AIILALINS	TSFFAGFVVF	360
	SILGFMAAEQ	GVHISKVAES	GPGLAFIAYP	RAVTLMPVAP	LWAALFFFML	LLGLDSQFV	420
	GVEGFTITGL	DLSPASYFR	FQREISVALC	CALCFVIDLS	MVTDGGMYVF	QLFDYYSASG	480
	TLLWQAFWE	CVVAVVYGA	DRFMDDIACM	IGYRPPCPMK	WCWSFPTPLV	CMGIFIFNVV	540
10	YYEPLVYNN	TVYPWVGEM	GWAFALSSML	CVPLHLGLCL	LRAKGTMAER	WQHLTQPIWG	600
	LHHLEYTRAQD	ADVRGLTTLT	PVSESSKVVV	VESVM			635
	Seq ID NO: 292 Protein Sequence						
	Protein Accession #: NP_037464.1						
15	1	11	21	31	41	51	
	MKHVLNLYLL	GVVLTLLSIF	VRVMSLEGL	LESPPSGTSM	TTRSQLANTE	PTKGLPDHPS	60
	RSM						63
	Seq ID NO: 293 Protein Sequence						
	Protein Accession #: NP_064527.1						
20	1	11	21	31	41	51	
	MAGASLGARF	YRQIKRHPGI	IPMIGLICLG	MGSAAALYLLR	LALRSPDVCW	DRKNNPEPMN	60
25	RLSPNDQYKF	LAVSTDYKKL	KKDRPDF				87
	Seq ID NO: 294 Protein Sequence						
	Protein Accession #: NP_002195.1						
30	1	11	21	31	41	51	
	MGPGPSRAPR	APRLMLCALA	LMVAAGGCVV	SAFNLDTRFL	VVKEAGNPGS	LFGYSVALHR	60
	QTERQQRILL	LAPAGRELAV	PDGYTNRTGA	VYLCPLTAHK	DDCERMNITV	KNDPGHHIE	120
	DMWLGTVVAS	QGPAGRVLC	AHRYTQVLWS	GSEDQRRMVG	KCYVRGNLDE	LDSSDDWQTY	180
	HNEMCNSNTD	YLETGMQCLG	TSGGFTQNTV	YFGAPGAYNW	KGNSYMIQK	EWDLSEYSYK	240
35	DPEDQGNLYI	GYTMQVGSFI	LHPKNITIVT	GAPRRHRMGA	VFLLSQEAGG	DLRRRQVLEG	300
	SQVGAYFGSA	IADLADLNDG	WQDLLVGAPY	YFERKEEVGG	AIYVFMNQAG	TSFPAHPSLL	360
	LHGPGSGAFG	LSVASIGDIN	QDGFQDIAVG	APFEGLGKVV	IYHSSSKGLL	RQPOQVIHGE	420
	KLGLPGLATF	GYSLSGQMDV	DENFYDILLV	GSLSHDIVLL	RARPVINIVH	KTLPVPRPAVL	480
	DPALCTATSC	VQVELCFAYN	QSAGNPYR	NITLAYTLEA	DRDRPPRLR	FAGESAVFH	540
40	GFFSMPEMRC	QKLELLMDN	LRDKLRPIII	SMNYSPLRM	PDRPRLGLRS	LDAYPILNQA	600
	QALENHTEVQ	FQKECGPDNK	CESNLQMRRA	FVSEQQQKLS	RLQYSRDVRK	LLLSINVTNT	660
	RTSERSGEDA	HEALLTLVVP	PALLLSSVRP	PGACQANETI	FCELGNPFFK	NORMELLIAF	720
	EVIQVTLHTR	DLQVQLQST	SSHQDNLWPM	ILTLVDYTL	QTSLSMVNHR	LQSPFGGTVM	780
	GESGMKTVED	VGSPLKYEFQ	VGPMGEGLVG	LGLTLVLGLEW	PYEVSNQKWL	LYPTEITVHG	840
45	NGSWPCRPFG	DLINPLNLTL	SDPGDRPSSP	QRRRRQLDPG	GGQPPPPVTL	AAAKKAKSET	900
	VLTCATGRAH	CVWLECPIDP	APVVTNVTVK	ARVMNSTFIE	DYRDFDRVRV	NGWATLFLRT	960
	SIPTINMENK	TTWFSVDIDS	ELVEELPAEI	ELWLVLVAVG	AGLLLLGLII	LLLWKCGFFK	1020
	RARTRALYEA	KRQKAEMSKQ	PSETERLTDD	Y			1051
	Seq ID NO: 295 Protein Sequence						
	Protein Accession #: NP_005492.1						
50	1	11	21	31	41	51	
	MGPGPSRAPR	APRLMLCALA	LMVAAGGCVV	SAFNLDTRFL	VVKEAGNPGS	LFGYSVALHR	60
	QTERQQRILL	LAPAGRELAV	PDGYTNRTGA	VYLCPLTAHK	DDCERMNITV	KNDPGHHIE	120
55	DMWLGTVVAS	QGPAGRVLC	AHRYTQVLWS	GSEDQRRMVG	KCYVRGNLDE	LDSSDDWQTY	180
	HNEMCNSNTD	YLETGMQCLG	TSGGFTQNTV	YFGAPGAYNW	KGNSYMIQK	EWDLSEYSYK	240
	DPEDQGNLYI	GYTMQVGSFI	LHPKNITIVT	GAPRRHRMGA	VFLLSQEAGG	DLRRRQVLEG	300
	SQVGAYFGSA	IADLADLNDG	WQDLLVGAPY	YFERKEEVGG	AIYVFMNQAG	TSFPAHPSLL	360
	LHGPGSGAFG	LSVASIGDIN	QDGFQDIAVG	APFEGLGKVV	IYHSSSKGLL	RQPOQVIHGE	420
60	KLGLPGLATF	GYSLSGQMDV	DENFYDILLV	GSLSHDIVLL	RARPVINIVH	KTLPVPRPAVL	480
	DPALCTATSC	VQVELCFAYN	QSAGNPYR	NITLAYTLEA	DRDRPPRLR	FAGESAVFH	540
	GFFSMPEMRC	QKLELLMDN	LRDKLRPIII	SMNYSPLRM	PDRPRLGLRS	LDAYPILNQA	600
	QALENHTEVQ	FQKECGPDNK	CESNLQMRRA	FVSEQQQKLS	RLQYSRDVRK	LLLSINVTNT	660
	RTSERSGEDA	HEALLTLVVP	PALLLSSVRP	PGACQANETI	FCELGNPFFK	NORMELLIAF	720
65	EVIQVTLHTR	DLQVQLQST	SSHQDNLWPM	ILTLVDYTL	QTSLSMVNHR	LQSPFGGTVM	780
	GESGMKTVED	VGSPLKYEFQ	VGPMGEGLVG	LGLTLVLGLEW	PYEVSNQKWL	LYPTEITVHG	840
	NGSWPCRPFG	DLINPLNLTL	SDPGDRPSSP	QRRRRQLDPG	GGQPPPPVTL	AAAKKAKSET	900
	VLTCATGRAH	CVWLECPIDP	APVVTNVTVK	ARVMNSTFIE	DYRDFDRVRV	NGWATLFLRT	960
	SIPTINMENK	TTWFSVDIDS	ELVEELPAEI	ELWLVLVAVG	AGLLLLGLII	LLLWKCDFFK	1020
70	RTTRYQIMPK	YHAVRIRREE	RYPPPGSTLP	TKKHVWTSWQ	TRDQYY		1066
	Seq ID NO: 296 Protein Sequence						
	Protein Accession #: NP_003777						
75	1	11	21	31	41	51	
	MDALCGSGEL	GSKFWSNLS	VHTENPDLT	CFQNSLLAWV	PCIYLWVALP	CYLLYLRRHC	60
	RGYIILSHLS	KLKMLVGLVL	WCVSWADLFY	SFHGLVHGRA	PAPVFFVTPL	VGVVTMLLAT	120
	LLIQYERLQG	VQSSGVLIIF	WFLCVVCAIV	PFRSKILLAK	ABGEISDPFR	FTTFYIHFAL	180
	VLSALILACF	REKPPFFSAK	NVDPNYPET	SAGFLSRLFF	WMFTKMAIYG	YRHPLEKDL	240
80	WSLKEEDRSQ	MVQQQLLEAW	RKQEKQTARH	KASAAPGKNA	SGDEVLLGA	RPRPKPSFL	300
	KALLATFGSS	FLISACFKLI	QDLSFINPQ	LLSILIRFIS	NPMAPSWMGF	LVAGLMFLCS	360
	MMQSLTLQHY	YHYIFVTGVI	FRTGIMGVII	RKALVITNSV	KRASTVGEIV	NLMSVDAQRF	420
	MDLAPFLNLL	WSAPLQIILA	IYFLWQNLGP	SVLAGVAFMV	LLIPLNGAVA	VKMRAFOVKQ	480
	MKLKDSRIKL	MSEILNGIKV	LKLYAMEPSF	LKQVEGIRQG	ELQLLRTAAY	LHTTTTFTWM	540

	CSPFLVTLIT	LWVYVYVDPN	NVLDAEKAFV	SVSLFNILRL	PLNMLPQLIS	NLTQASVSLK	600
	RIQQFLSQEE	LDQPSVERKT	ISPGYAITIH	SGTFTWAQDL	PPTLHSLDIQ	VPKALVAVV	660
	GPVGGGKSSL	VSALIGEMEK	LEGKVMKGS	VAYVPOQAWI	QNCTLQENVL	FGKALNPKRY	720
5	QQTLEACALL	ADLEMLPGGD	QTEIGKEGIN	LSGGQRQRVS	LARAVYSAD	IFLLDDPLSA	780
	VDSHVAKHIF	DHVGPEGVL	AGKTRVLVTH	GISFLPQTFD	IIVLADGQVS	EMGPYPALLQ	840
	RNGSFANFLC	NYAPDEDQGH	LEDSTWALEG	AEDKEALLIE	DTLSNHTDLT	DNDPVTYVVQ	900
	KQFMRQLSAL	SSDGGGQGRP	VPRRHLPSE	KVQVTEAKAD	GALTQEEKAA	IGTVLSVFW	960
	DYAKAVGLCT	TLAICLLYVG	QSAAMIGANV	WLSAWTNDAM	ADSRQNTSL	RLGVYAALGI	1020
10	LQGLVLMAL	MAMAAGGIA	ARVLHQALLH	NKIRSPQSFF	DTTPSGRIIN	CFSKDIYVVD	1080
	EVLAPVILML	LNSPFAIST	LUVIMASTPL	FTVILPLAV	LYTLVQRFYA	ATSRQLKRL	1140
	SVSRSPYISH	FSETVTGASV	IRAYNRSRDF	EIISDTKVDA	NQRSCYPYII	SNRWLSIGVE	1200
	FVGNVVLFA	ALFAVIGRSS	LNPGLVGLSV	SYSLQVTFAL	NWMIRMSDL	ESNIVAVERV	1260
	KEYSKTETEA	PWVVEGSRPP	EGWPPRGEVE	FRNYSVRYRP	GLDLVLRLDS	LHVHGGEKVG	1320
	IVGRTGAGKS	SMTLCFLFRIL	EAAKGEIRID	GLNVADIGLH	DLRSQTLIIP	QDPILFSGTL	1380
15	RNMLDPFGSY	SEEDINWALE	LHLHTFVSS	QPAGLDQFCS	EGGENLSVQG	RQLVCLARAL	1440
	LRKSRLVLD	EATAIDLET	DNLQIATIRT	QFDTCTVLT	AHRLNTIMDY	TRVLVLDKGV	1500
	VAEFDSPANL	IAARGIFYGM	ARDAGLA				1527
20	Seq ID NO: 297 Protein Sequence Protein Accession #: NP_002692.1						
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	MHEFYRLFLGA	TRRFLNPEWK	GEIDNWCYV	LTSLLPFIQ	SQDIKALQKE	LEQFAKLLKQ	60
25	KRITLGYTQA	DVGLTLGLVF	GKVFSTTIC	RFEALQLSFK	NMCKLRPLLQ	KWVEEADNNE	120
	NLQETCKAET	LQAKRKRRKT	SIENRVRGNL	ENLFLQCPKP	TLQOISHIAQ	QLGLEKDVVR	180
	VWFCNRRQKG	KRSSSDYAQR	EDFEAAGSPF	SGGPVSFPLA	PGPHFGARGY	GSPHFTALYS	240
	SVFPPEGEAF	PPVSVTTLGS	PLHSN				265
30	Seq ID NO: 298 Protein Sequence Protein Accession #: NP_005449.1						
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	MASPRRSQGP	GRPPPPPPPP	ARLLLLLLLP	LLLPLAPGAW	GWARGAPRPP	PSSPPLSIMG	60
35	LMPLTKEVAK	GSIGRGVLP	VELAIEQIRN	ESLLRPYFLD	LRLYDTECDN	AKGLKAFYDA	120
	IKYGNHLMV	FGGVCPSTVS	IIAESLQGMN	LVQLSFAATT	PVLADKKKYP	YFFRTVPSDN	180
	AVNPAILKLL	KHYQWKRVGT	LTQDVQRFSE	VRNDLTGVLY	GEDIEISDTE	SFSNDPCTSV	240
	KKLKGMVRI	ILQGFQDNMA	AKVFCCAYEE	NMYGSKYQWI	IPGWYEPSWW	EQVHTEANSS	300
	RCLRKNLLAA	MEGYIGVDPE	PLSSKQIKTI	SGKTPQYER	EYNNKRSVG	PSKFHGYAYD	360
40	GIWVIAKTLQ	RAMETLHASS	RHQRIQDFNY	TDHTLGRILL	NAMNETNFFG	VTGQVVRFRG	420
	ERMGTIKFTQ	FQDSREVKVG	EYNAVADTLE	IINDTIRPOG	SEPPKDKTII	LEQLRKISLP	480
	LYSILSALTI	LGMIMASAFI	FFNIKNRNQK	LIKMSPPYMN	NLIILGGMLS	YASIFLFGLD	540
	GSEVSEKTFE	TLCTVRTWIL	TVGYTTAFGA	MFAKTWRVHA	IFKNVKKMKK	IKDKQLLVI	600
	VGGMLLIDL	ILICWQAVDP	LRRTEVEKYS	EPDPAGRDIS	IRPLLEHCEN	THMTIWLGI	660
45	YAYKGLMLF	GCFLAWETRN	VSIPALNDSK	YIGMSVYVNG	IMCIIGAASV	FLTRDQPNVQ	720
	FCIVALVLI	CFSTITLCLVF	VPKLITLRTN	PDAATQNRRE	QFTQNKQKED	SKTSTSVTSV	780
	NQASTSRLEG	LQSENHRLRM	KITELDKOLE	EVTMLQLOTP	EKTTYIKQNH	YQELNDILNL	840
	GNFTSTDDG	KAILKMHLDQ	NPQLQWNTTE	PSRTCKOPIE	DINSPEHIQR	RLSLQLFILH	900
	HAYLPSIGGV	DASCVCSPCVS	PTASPRHRHV	PPSFRVMVSG	L		941
50	Seq ID NO: 299 Protein Sequence Protein Accession #: NP_055632						
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	MEARALRL	LVVCGCLALP	PLAEPVCPER	CDQHPQHLL	CTNRGLRVVP	KTSSLPSPHD	60
55	VLTYSLQGNF	ITNITAFDFH	RLGQLRRLLD	QYNQIRSLHP	KTFEKLSRLE	ELYLGNNLLQ	120
	ALAPGTALPL	RKRIRILYANG	NEISRLSRGS	FEGLLESLVL	RLDGNALGAL	PDVAFAPLGN	180
	LLYLHLESNR	IRFLGKNAPA	QIGKLRFLNL	SANELQPSLR	HAATFAPLRS	LSSLILSANS	240
	LQHLGPRIFQ	LPRLGLLSL	RGNQLTHLAP	EAFWGLEALR	ELRLEGNRLS	QLPTALLEPL	300
60	HSLEALDLG	NELSALHLPAT	FGLHRLREL	SLRNALSAL	SGDIFAASPA	LYRLDLGNG	360
	WTCDCRLRLG	KRMWGDWHSQ	GRLLTVFVQC	RHPPALRGKY	LDYLDQOQLQ	NGSCADPSPS	420
	ASLTADRRRQ	PLPTAAGEEM	TPPAGLAEEL	PPQPQLQQQG	RFLAGVAVDG	AARELVGNRS	480
	ALRLSRRPG	LQQPSPSVAA	AAGPAPQSLO	LHKKPQRGRP	TRADPALAEP	TPTASPGSAP	540
	SPAGDPWQRA	TKHRLGTEHQ	ERAAQSDGGA	GLPPLVSDPC	DFNKFILCNL	TVEAVGADSA	600
65	SVRWAVREHR	SPRPLGGARF	RLLFDRFGQQ	PKFHRFVYLP	ESSDSATLRE	LRGDTPYLVC	660
	VEGVLGGRVC	VPAPRDHCAG	LVTLPAGSR	GGVDYQLLTL	ALLTVNALLV	LLALAAMASR	720
	WLRRKLRRAR	KGGAPVHVHR	MYSTRRLRS	MGTGVSADFS	GFQSHRPRTT	VCALSEADLI	780
	EFPCDRFMD	AGGGAGGSLR	REDRLQRFA	D			811
70	Seq ID NO: 300 Protein Sequence Protein Accession #: NP_001783.2						
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	MCRIAGALRT	LLPLLAALIQ	ASVEASGEIA	LCKTGFPEDV	YSAVLSKDVH	EQQPLNVKF	60
75	SNCGKRRKQ	YESSEPADFK	VDEDMVYAV	RSFPLSSEHA	KFLIYAQDKE	TQEKQWVAVK	120
	LSLKPTLTEE	SVKESAEVEE	IVFPQFSKH	SGHLQQRKRD	WVIPPINLPE	NSRGPFPQEL	180
	VRIRSDRDN	LSRLSVTGP	GADQPTGIF	IINPISGQLS	VTKPLDREQI	ARFHLRAHAV	240
	DINGQVENP	IDIVINVIDM	NDNRPEFLHQ	VWNGTVPEGS	KPGTYVMVT	AIDADDPNAL	300
	NGMLRYRIVS	QAPSTPSPNM	FTINNETGDI	ITVAAGLDRE	KVQYQTLIIQ	ATDMEGNPTY	360
80	GLSNTATAVI	TVDVNDNPP	EFTAMTFYGE	VPENRVDIIV	ANLTVTDKQ	PHTPAWNAVY	420
	RISGGDPTGR	FAIGTDPNSN	DGLVTVVKPI	DFETNRMFVL	TVAENQVPL	AKGIQHPPOS	480
	TATVSVTVID	VNENPYFAPN	PKIIRQEEGL	HAGTMLITFT	AQDPDRYMQ	NIRYTKLSDP	540
	ANWLKIDPVN	QOITIAVLD	RESPNVKNNI	YNATFLASDN	GIPPMSTGT	LQIYLLDIND	600
	NAPQVLPQEA	ETCETPDPS	INITALDYDI	DPNAGPFAFD	LPLSPVTIKR	NMTITRLNGD	660
	FAQLNLKIKF	LEAGIYEVPI	IITDSGNPPK	SNISILRVKV	CQCDNSGDC	DVDRIVGAGL	720

GTGATIAILL CIIILLILVL MFVVMKRRD KERQAKQLLI DPEDDVRDNI LKYDEEGGGE 780
 EDQDYDLSQL QQPDVPEPDA IKPVGIIRMD ERPIHAEPQY PVRSAAPHGP DIGDFINEGL 840
 KAANDNDTAP PYDSLIVFDY EGSGSTAGSL SSLNSSSSGG EQDYDYLNDW GPRFKKLADM 900
 YGGGDD 906

5

Seq ID NO: 301 Protein Sequence
 Protein Accession #: NP_058637.1

1 11 21 31 41 51
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 10 MVSPRMSGLL SQTIVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCLRLF 60
 RVCLKPGLSE EAAESPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAMPGTF 120
 SFIIETWREE LGDQIGGPAPW SLARVAGRR RLAAGGPWAR DIQRAGAWEL RFSYRACEP 180
 PAVGTACTRL CRPSAPSRG GPGLRPCAPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL 240
 15 EGWGTPLCTV PVSTSSCLSP RGPSSATTGC LVPGPQPCDG NPCANGGSCS ETPRSFECTC 300
 PRGFYGLRCE VSGVTCADGP CFNGGLCVGG ADPDSAYICH CPPGFGGSCN EKRVDRCSLQ 360
 PCRNGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGCTCVGG GAHRCSCALG 420
 FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP 480
 PGLRPGDPQR YLLPPALGLL VAAGVAGAAAL LLVHVRRRGH SQDAGSRLLA GTPEPSVHAL 540
 20 PDALNNLRTO EGSGDGPFSS VDMNRPEVD PQGIYVISAP SIYAREVATP LFPPLHTGRA 600
 GQRQHLLFPY PSSILSVK 618

Seq ID NO: 302 Protein Sequence
 Protein Accession #: fgenes prediction

1 11 21 31 41 51
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 25 MCQAFLLWVLG TLWLLKNARC LQYPPEHAQ SCLISEAKQG QAQLPLGWVK WPLHLRSSLS 60
 KRLERKYPGL LGEIEAQIC KTSSELEPSC DLVTADGSTV VTISENLPAV GPHICQQQDS 120
 HVEGMVNISK ASSQGM 136

30 Seq ID NO: 303 Protein Sequence
 Protein Accession #: NP_079088.1

1 11 21 31 41 51
 | | | | |
 35 MGCGGSRADA IEPYRYESWT RETESTWLTY TDSADAPSAA APDSGPEAGG LHSGMLEDGL 60
 PSNGVPRSTA PGGIPNPEKK TNCETQCPNP QSLSSGSLTQ KQNGLQTTEA KRDAKRMPEK 120
 EVTINVTDSI QQMDRSRRIT KNCVN 145

Seq ID NO: 304 Protein Sequence
 Protein Accession #: XP_040550.1

1 11 21 31 41 51
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 40 MGADGETVVL KNMLIGINLI LLGSMIKPSE CQLEVTTERV QRQSVEEEGG IANYNTSSKE 60
 QPVVFNHVVN INVPLDNLCS SGLEASAEQE VSAEDETLAE YMQQTSKHES QVTFTIRINF 120
 PKKACPCASS AQLVQELLSR IEMLEREVSV LRDQCNANCC QESAATQQLD YIPHCSGHGN 180
 45 SFESCOCIC NEGFWGKNCB EPYCPLGCSS RGVCDGQCI CDSEYSGDDC SELRCPTDCS 240
 SRGLCVDEEG VCEEPYTGED CRELRCPGDC SGKGRACNGT CLCEEGYVGE DCGQRCLNA 300
 CSGRGQCEEG LCVCEEGYQG PDCSAVAPPE DLRVAGISDR SIELEWDGPM AVTEYVISYQ 360
 PTALGGQLQ QRVPGDWSGV TITELPEGLT YNISVYAVIS NILSLPITAK VATHLSTPQG 420
 50 LQFKTITETT VEVQNEPFSF SFDGWEISFI PKNNEGGVIA QVPSDVTSFN QTGLKPGEEY 480
 IVNVVALKEG ARSPPTSASV STVIDGPTQI LVDRVSDTVA FVEWIPPRAK VDFILLKYGL 540
 VGGEGGRITF RLQPPPLSQYS VQALRPGSRY EVSVSAVRGT NESDSATTQF TTEIDAPKNL 600
 RVGSRATSL DLEWDSAEAE VQEKVYVST LAGEQYHEVL VPRGIGPTTR ATLTLDPVGT 660
 EYGVGISAVM NSQQSVPMAT NARTELDSPR DLMVTASSET SISLIWTKAS GPIDHYRITF 720
 55 TPSSGIASEV TVPKORTSYT LTDLEPGAET IISVTAERGR QQSLESTVDA FTGFRPISHL 780
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 60 ATNITPTEAL LQKAPVGEV ENYVIVLTHF AVAGETILVD GVSEEFRLVD LLPSTHYTAT 1020
 MYATNGPLTS GTISTNFTSL LDPPANLTAS EVTRQSALIS WQPPRAEIEY VYLTYKSTDG 1080
 SRKELIVDAE DTHIRLEGLL ENTDTYVLLQ AAQDTTWSSI TSTAFTTGR VFPHPQDCAQ 1140
 HLMNGDLSG VYPIFLNGEL SQKLQVYCDM TTDGGGWIVF QRRQNGQTFD FRKWADYRVG 1200
 FGNVEDEFWL GLDNIHRITS QGRYELRVDM RDQGEAFAFAS YDRFSVEDSR NLYKLIRIGSY 1260
 65 NGTAGDSLST HQGRPFSTED RDNDAVAVTNC AMSYKGAWNY KNCHRTNLNG KYGESRHSQG 1320
 INWYHWKGHE FSIPFVEMOM RPYNHRLMAG RKRQSLQF 1358

Seq ID NO: 305 Protein Sequence
 Protein Accession #: NP_005874.1

1 11 21 31 41 51
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 70 MASSVAPYEQ LVRQVEALKA ENSHLRQELR DNSSHLKLE TETSGMKEVL KHLQKLEQE 60
 ARVLVSSGQT EVLEQLKALQ MDITSLYNLK FQPPITLGPPE AARTPEGSPV HGSQPSKDSF 120
 GELSRATIRL LEELDRERCF LLNEIEKEEK EKLWYYSQIQ GLSKRLDELP HVETQFSMQM 180
 DLIRQQLFEF AQHISLMEE RFGTSDVMQ RAQIRASRLQ QIDKELLEAQ DRVQOTEPQA 240
 75 LLAVKSVFVD EDPTETVPH PEDGTPOGPN SKVEVFWLL SMLATRDQED TARTLLAMSS 300
 SPESCVAMRR SGCLPLLLQI LHGTEAAAGG RAGAPGAPGA KDARMANAA LHNIVFSQPD 360
 QGLARKEMRV LHVLEQIRAY CETCDWLQIA RDGGPEGGGA GSAPIPIEPQ ICQATCAVMK 420
 LSFDEEYRRA MNEGLGLQAV AELLQVDYEM HKMTRDPLNL ALRRYAGMTL TNLTFGDVAN 480
 KATLCARRGC MEATVAQLAS DSEELHQVVS SILRNLWSRA DINSKKVLRE AGSVTALVQC 540
 80 VLRATKESTL KSVLSALWNL SAHSTENKAA ICQVDGALGF LVSTLTYSKQ SNLSLIIESG 600
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 ELLWDLGAVG MLRNVLHSHK XMIAMGSAAL LRNLAAHRA KHQAAATAVS PGSCVPSLYV 720
 RKQRALEAEL DARHLAQALE HLEKQGPAA EAATKKPLPP LRHLDGLAQD YASDSGCFDD 780
 DDAPSSLAAA AATGEPASPA ALSFLGSPF LQQQALARTP PTRRGKEAE KDTSGEAAVA 840
 AKAKAKLALA VARIDQLVED ISALHTSSDD SFLSSGDPG QEAPREGRAQ SCSPCRGPEG 900

	GRREAGSRAH	PLRLKAHAH	SLSNDSLSNG	SASDGYCPRE	HMLPCPLAAL	ASRREDPRCG	960
	QRPSPRLDLD	LPQCQAEPPA	REATSADARV	RTIKLSPTYQ	HVPLLEGASR	AGAELAGPG	1020
	ISPGARKQAW	LPADHLSKVP	EKLAAAPLSV	ASKALQKLA	QEGPLSLSRC	SSLSSLSSAG	1080
	RPGPSEGGDL	DDSDSSLEGL	EEAGPSEAE	DSTWRAPGAT	SLPVAIPAPR	RNRGRGLGVE	1140
5	DATPSSSEN	YVQETPLVLS	RCSSVSSLGS	FESPSIASSI	PSEPCSQQGS	GTISPSELDP	1200
	SPGQTMPPSR	SKTPPLAPAP	QGPPEATQFS	LQWESYVKRF	LDIADCRERC	RLPSELDAQS	1260
	VRFTVEKDE	NFSCASSLSA	LALHEHYVQQ	DVELRLLPAS	CPERGGGAGG	AGLHFAGHRR	1320
	REEGPAPTS	RPRGAADQEL	ELLRECLGAA	VPARLRKVAS	ALVPGRRALP	VPVYMLVPAP	1380
	APAQEDDSCT	DSAEGETPVNF	SSAASLSDET	LQGPFRDQPG	GPAGRQRPTG	RPTSARQAMG	1440
10	HRHKAGGAGR	SABQSRGAGK	NRAGLEPLG	RPPSAPADKD	GSKPGRTRGD	GALQSLCLTT	1500
	PTEEAVYCFY	GNDSDDEEPPA	AAPTPTTHRT	SAIPRAPTRE	RPQGRKEAPA	PSKAAPAAP	1560
	PARTQPSLIA	DETPPCYSL	SSASSLSEPE	PSEPPAVHPR	GREPAVTKDP	GPGGGRDSSP	1620
	SPRAAEELQ	RCISSALPRR	RPPVSGLRRR	KPRATRLDER	PAEGSRERGE	EAAGSDRASD	1680
	LDSVEMRAIQ	EGANSIVTWL	HQAAAATREA	SSESDSILSF	VSGLSVGSTL	QPPKHKGRQ	1740
15	AEGEMGSARR	PEKRGAAAVK	TSGSPRSPAG	PEKPRGTQKT	TPGVPAVLRG	RTVIYVPSPA	1800
	PRAQPKGTPG	PRATPRKVP	PCLAQPAAPA	KVPSPGQORS	RLHRPAKTS	ELATLSQPPR	1860
	SATPPARLAK	TPSSSSSQTS	PASQPLPRKR	PPVTQAAGAL	PGPGASVPVK	TPARTLLAKQ	1920
	HKTQSPVRI	PFQPRARRG	PPPLARAVPE	PGPRGRAGTE	AGPGARGGRL	GLVRVASALS	1980
	SGSESSDRSG	FRQLTFIKE	SPGLRRRRESE	LSSAESASA	PQGASPRRGR	PALPAVLCS	2040
20	SRCEELRAAP	RQGPAPARQR	PAAARPSPE	RPARRTTSES	PSRLPVRAPA	ARPETVKRYA	2100
	SLPHISVARR	PDGAVPAAPA	SADAARRSSD	GEPRPLPRVA	APGTTWRRIR	DEDVPHILRS	2160
	TLPATALLPR	GSTPEDAPAG	PPRKTSDAV	VQTEEVAAPK	TNSSTSPSLE	TREPPGAPAG	2220
	GQLSLGSDV	DGPSLAKAPI	SAPFVHEGLG	VAVGGFPASR	HGSPSRARSV	PPFNYVPSPM	2280
25	VVAATTDAA	EKAPATASAT	LLE				2303
	Seq ID NO: 306 Protein Sequence						
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30	MFLTEDLITF	NLRNLLFQL	WESSFSPGAG	GFCTTLPPSF	LRVDDRATSS	TTDSSRAPSS	60
	PRPPGSTSHC	GISTRCTERC	LCVLPLRTSQ	VPDVMAPQHD	QEFKFDLAYS	CLGKSFSMSN	120
	QDLGYSTSS	LALGLAWLSW	ETKKQNVHLH	VGLDSL			156
	Seq ID NO: 307 Protein Sequence						
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35	MASTRSIELE	HFEERDKRPR	PGSRRGAPSS	SGGSSSSGPK	GNGLIPSPAH	SAHCSFYRTR	60
	TLQALSSEKK	AKKARFYRNG	DRYFKGLVFA	ISSDRFRSPD	ALLIELTRSL	SDNVNLPQGV	120
40	RTIYTTDGR	KVTSLEDELE	GESYVCASNE	PFRKVDYTKN	INPNWSVNIK	GGTSRALAAA	180
	SSVKSEVKES	KDFIKPKLVT	VIRSGVKPRK	AVRILLNKKT	AHSFEQVLTD	ITEAIKLDGS	240
	VVKRLCTLDG	KQVTCIQDF	GDDDFIACG	PEKFRYAQDD	FVLDSHSECRV	LKSSYSRSSA	300
	VKYSGSKSPG	PSRRSKSPAS	VNGTFSSQLS	TPKSTKSSSS	SPTSPGSRFG	LKISAHGRSS	360
	SNVNGGPELD	RCISPEGVNG	NRCSESSTLL	EKYKIGKVG	DGNFAVVKEC	IDRSTGKEFA	420
45	LKIIDKAKCC	GKEHLIENEV	SILRRVKHPN	IIMLVEEMET	ATELFLVME	VKGGLDFDAI	480
	TSSTKYTERD	GSAMVYNLAN	ALRYLHGLSI	VHRDIKPNEL	LVCEYPDGTK	SLKLGDFGLA	540
	TVVEGLYTV	CGTPTVVAPE	IAETGYGLK	VDIWAAGVIT	YILLCGFPFF	RENNLQEDL	600
	FDQILAGLKE	FPAPYWDNIT	DSAKELISQM	LQVNVEARCT	AGQILSHPWV	SDDAQENNM	660
50	QAEVTGKLKQ	HFNNALPKQN	STTTGVSVM	FDLTV			695
	Seq ID NO: 308 Protein Sequence						
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55	MEEMEEELKC	PVCSFYREP	IILPCSHNLC	QACARNILVQ	TPESESPQSH	RAAGSGVSDY	60
	DYLDLDKMSL	YSEADSGYGS	YGGFASAPTT	PCQKSPNGVR	VFPAMPPPPA	THLSPALAPV	120
	PRNSCITCPO	CHRSLLIDDR	GLRGFPKNRV	LEGVIDRYQQ	SKAAALKCQL	CEKAPKEATV	180
	MCEQCDVFC	DPICRLRCHP	RGPLAKHRLV	PPAQGRVSR	LSPRKVSTCT	DHELENHSMY	240
	CVQCKMPVYC	QCLEEGKHSS	HEVKALGAMW	KLHKSQSLQA	LANGLSRAKE	AKFLVLQLRN	300
60	MVQIQIENSV	EFEACLVAQC	DALIDALNRR	KAQLLARVVK	EHEHKLKVVR	DQISHCTVKL	360
	RQTGLMEYC	LEVIKENDPS	GFLQISDALI	RRVHLTDQW	GKGLTLPRMT	TDFDLSLDSN	420
	PLLQSIHQLD	FVQVKASSPV	PATPILQLEE	CCTHNSATL	SWKQPPLSTV	PADGYILELD	480
	DGNGGQFREV	YVGKETHCTV	DGLHFNSTYN	ARVKAFNKTG	VSPYSKTLVL	QTSEVAFWAF	540
	DPGSAHSDII	LSNDNLVTTC	SSYDDRVLG	KTGFSKGIHY	WELTVDRYDN	HPDPAPGVAR	600
65	MDVMKDVMLG	KDDKAWAMV	DNNRSWFMGN	NSHTNRTEGG	ITKGATIGVL	LDLNRKNLTF	660
	FINDEQGGPI	AFDNVEGLFF	PAVSLNRNVQ	VTLHTGLPVP	DFYSSRASIA		710
	Seq ID NO: 309 Protein Sequence						
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70	MEDLEEDVRF	IVDETLDFFG	LSPSDSREEE	DITVLVTPEK	PLRRGLSHRS	DPNAVAPAPQ	60
	GVRLSLGPLS	PEKLEELDE	ANRLAAQLEQ	CALQDRESAG	EGLGPRRVKP	SPRRETFVLK	120
	DSVPRDLLPT	VNSLTRSTPS	PSSLTPLRLS	NDRKGSVRAL	RATSGKRPNS	MKRESPTCNL	180
75	FPASKSPASS	PLTRSTPPVR	GRAGPSGRAA	ASPTPTIRSV	LAPQPSTNS	QRLPRPQGA	240
	AKSSSQPLIP	SAIPRPASRM	PLTSRSVPPG	RGALPPDSLS	TRKGLPRPST	AGHRVRESGH	300
	KVPVSQRLNL	PVMGATRSNL	QPPRKVAVPG	PTR			333
	Seq ID NO: 310 Protein Sequence						
	Protein Accession #: ref XP_166946.2						
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80	MGSDSRLPEM	EEKSGDGKAG	MSGALLAEVK	NQGLKCEWM	LVLKAEVVE	YTSVIVGQGG	60
	HLKMDLLKE	RHRKRYLQKP	IKRCSGLMGL	NWSLRPAISS	SPLARSQEKH	HGAKNEGKVK	120

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ALSFRKLRLK KRPPTPPSQA KSWRGRTGSA ADSPGAAAMA VQAALLSTHP FVPFGPGGSP 180
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KPGKSKRKVN HRNAPTVAAP AHGKAAPRRE ASQAAAAASL QSRSLAALFD SLRHVPGGAE 300
PAGGEVAAPA AGLGGAGTGG AGGDVAGPAG ATAIPGARKV PLRARNLPSS FFTEPSRAGG 360
GGCGPSGPDV SLGDLEKGA EVEFFELLGP DYAGTEAAV LLAAEPLDVF PAGASVLRGP 420
PELEPGLFEP PPAVVGNNLY PEPWVSPGCS PTKKSPLTAP RGGLTNEPL SPLYPAAADS 480
PGGEDGRGHL ASFAFFFFDC ALPPPPPPHQ VSYDYSAGYS RTAYSSLMRS DGVWEGAPGE 540
EGAHRD 546
  
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Seq ID NO: 311 Protein Sequence
 Protein Accession #: NP_071406.1

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1 11 21 31 41 51
| | | | |
MAPTKPSFQQ DPSRRERLQA LRKEKSRDAA RSRRGKENFE FYELAKLLPL PAATISQLDK 60
ASIIIRLTISY LKMRDFANQC DPPWNLMEG PPNTSVKGA QRRRSFALA IEVFEHLGS 120
HILQLSDGFV FALNQEGKFL YISSETVSYL GLSQVELTGS SVFDYVHPGD HVEMAEQLGM 180
KLPPGRGLLS QGTAEKGASS ASSSSQSETP EPVESTSPSL LTTDNTLERS FFIRMKSTLT 240
KRGVHIKSSG YKVIHITGRL RLRVSLSHGR TVPSQIMGLV VVAHALPPPT INEVRIDCHM 300
FVTRVMDLNL IYCNIRISD YMDLTPVDIV GKRCYFIHA EDVEGIRHSH LDLLNKQGCV 360
TKYYRWMQKN GGYIWIQSSA TIAINAKNAN EKNIWVNYL LSNPEYKDTF MDIAQLPHLP 420
EKTSESSETS DSESDDKDTG GITEDNENSK SDEKGNQSEN SEDPEPDRKK SGNACNDNMN 480
CNDGHHSSSN PDSRSDSDSF EHSDFENPKA GEDGFGALGA MQIKVERVYE SESDLRLQNC 540
ESLTSDSAKD SDSAGEAGAQ ASSKHQKRKK RKRQKGGSA SRRRLSSASS PGGLDAGLVE 600
LPRLLSSPNS ASVLKIKTEI SEPINFNDNS SIWNYPPNRE ISRNESPYSM TKPPSSEHFP 660
SPQGGGGGGG GGGGLHVAIP DSVLTPPGAD GAAARKTPG ASATAALAPV ASDPLSPPLS 720
ASPRDKHGMN GGGGGGGGGG AGGGGPSASN SLLYTGDLEA LQRLQAGNVV LPLVHRVTGT 780
LAATSTAAQR VYTTGTIRYA PAEVTLMQMS NLLPNAHAVN FVDVNSPGFG LDPKTPMEHL 840
YHKVHRLNMS GPFGAASAA SLTQMPAGNV FTTAEGLFST LPFVYSNGI HAAQTILERKE 900
D 901
  
```

Seq ID NO: 312 Protein Sequence
 Protein Accession #: NP_005797.1

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1 11 21 31 41 51
| | | | |
MDSASLVSS RPSSPEPDDL FLPARSKGSS GSAFTCGTVS SSTPSDCPPE LSAELRGAMG 60
SAGAHPGDKL GSGGFKSSSS STSSSTSSAA ASSTKKDKKQ MTEPELQQLR LKINSRERKR 120
MMDLNIAMDG LREVMPIAHG PSVRKLSKIA TLLARNYIL MLTNSLEEMK RLVSEIYGGH 180
HAGFHPSACG GLAHSAPLPA ATAHAAAAAH AAHPAVHHP ILPPAAAAAA AAAAAAVSS 240
ASLPGSLGPS VGSIRPPHGL LKSPSAAAAA PLGGGGGGSG ASGGFQHWGG MPCPCSMQCV 300
PPPHHVSAM GAGSLPRLTS DAK 323
  
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Seq ID NO: 313 Protein Sequence
 Protein Accession #: XP_045127.3

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1 11 21 31 41 51
| | | | |
MTVLEESSIS LMSSVVAADF EFEEEDPQVFN TLFPSRPPIV LSSRSMEISE TSVGISAEVD 60
MSSVTTTQVP PAHGRLSVPA SLDPATAGSL VAETQVTPSS VTTAFPSVIT SILLDSFVS 120
IANKNTPSLA VRDPSVFTPY SLVPSVSSSL FSDQERSFSF EHKPRGALDF ASSFFSTPPL 180
ELSGSISSPS EAPASLSLMP SDLSPFTSQS FSPLVETFTL FDSSDLQSSQ LSLPSSTNLE 240
FSQLQPSSEL PLNTIMLLPS RSEVSPWSSF PSDSLEFVEA STVSLTDESA HFTSAFIETT 300
SYLESSLISH ESAVTALVPP GSESPDILTA GIQATSPILT VHTTPILTES SLFSTLTTPD 360
DQISALDGHV SVLASFSKAI PTGTVLITDA YLPSGSSFVS EATPFPLPTE LTVVGVSLTP 420
TEVPLNTSTE VSTTSTGAAT GGPLDSTLMG DAASQSPSES SAAPPLPSLR PVTAFTLEAT 480
VDTPTLATAK PPYVCITVLA DAYLITTVLA RRAVQEIYIT AIKEVLRIHF NRAVELKVYE 540
LFTDFTFLVT SGPFVYTAIS VINVLINSKL VRDQTLPLS VKPSFLVPES RFQVQTVLQF 600
VPPSVDTGFC NTFQRIEKL MTALFEVRKH HQGTYNLTQV ILNITISSSR VTPRRGPVNI 660
IFAVKSTQGF LNSEVSEELL RNLSVVEFSF YLGYVPLQIA EPFQYVQLNL SQLLKSSWVR 720
TVLLGVMEKQ LQNEVFQAEK ERKLAQLLSE VSTRRRMWR ATVAAGNSV VQVNVSRLEG 780
DDNPVQLIYF VEDQDGERLS AVKSSDLINK MDLQRAAIL GYRIQGVIAQ PVDRVKRPS 840
ESQSNLWVI VGVVIVPLVV MVIVVILYWK LCRTDKLDFQ PDTVANIQR QKLQIPSVKG 900
FDFAKQLGQ HNKKDILIIH EPAPLPGLK DHTTPSENGD VSPSKSKIPS KNVRHRGRVS 960
PSDADSTVSE ESSERDAGDK TPGAVNDGRS HRAPOSGPPL PSSGNEQHSS ASIFEHVDRI 1020
SRPPEASRRV PSKIQLIAMD PIPAPPVQRP SPADRVAESN KINKEIQTAL RHKSEIEHHR 1080
NKIRLAKRR GHYEFPPVDD LSSGDTKERH RVYRRAQMOI DKILDPTASV PSVFIEPRKS 1140
SRIKRSPKPR RKHVNGCPA DAEKDLITT DSDGTYRRPP GVHNSAYIGC PSDPDLPADV 1200
QTPSSVELGR YPALPPASQ YIPPPQSIEE ARQTMHSLLD DAFALVAPSS QPASTAGVGP 1260
GVPPGLPANS TPSQBERRAT QWGSFYSPAQ TANNPCSRYE DYGMTPTGP LPRPGFGPGL 1320
LQSTELVPPD PQQPQASAEA PFAARGIYSE EMPVARPRP VGGTTGSQIQ HLTQVGIASR 1380
IGAQPVEIPP SRGSQYCGGP WPSYGEDEAG RREAVPRTSG REPSAPSGNL PHRGLQGPGL 1440
GYPTSSTEDL QPGHSSASLI KAIREELLRL SQKQSTVQNF HS 1482
  
```

Seq ID NO: 314 Protein Sequence
 Protein Accession #: BAC04820.1

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1 11 21 31 41 51
| | | | |
MAPRPLGLPV LALGAAAVL GSVLFILMKT YFGRGRERRR DRGEAWWGAE AARLPEWDEW 60
DPEDEDEEP ALEEELEQREV LVLGLDGACK STFLRVLSGK PPLEGHIPTW GFNSVRLPTK 120
DPEVDLLIIG GSONLRFYWK EHVSEVDVLV FVVDSDRLR LPWARQELHK LLDKDPDLPV 180
VVVANKQDLS EAMSMGELQR ELGLQAINQ REVFLAAASI APACPTFEED GTVHIWKLLE 240
ELLS
  
```

Seq ID NO: 315 Protein Sequence
 Protein Accession #: NP_06563.1

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1 11 21 31 41 51
| | | | |
  
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		MARRAGGARM	FGSLLLFALL	AAGVAPLSWD	LPEPRSRASK	IRVHSRGNLW	ATGHFMGKKS	60
		LEPSSPSHWG	QLPTPLRDQ	RLQLSHDLLG	ILLKKALGV	SLSRPAPQIQ	YRRLVQILQ	120
5		K						121
		Seq ID NO: 316 Protein Sequence						
		Protein Accession #: NP_002046.1						
		1	11	21	31	41	51	
10		MERRRITSAA	RRSYVSSGEM	MVGGLAPGRR	LGPGRSLSLA	RMPPPLPTRV	DFSLAGALNA	60
		GFKETRASER	AEMMELNDRF	ASYIEKVRFL	EQNKALAAE	LNQLRAKEPT	KLADVYQAEI	120
		RELRLRLDQL	TANSARLEVE	RDNLAQDLAT	VRQKLQDET	LRLEAENNLA	AYRQEADEAT	180
		LARLDLERKI	ESLEEEIRFL	RKIHEEEVRE	LQQLARQOV	HVELDVAKPD	LTAALKEIRT	240
15		QYEAMASSNM	HEAEWYRSK	FADLTDAAR	NAELLRQAGH	EANDYRRQLQ	SLTCDLESIR	300
		GTNESLERQM	REQEERHVRE	AASYQEALAR	LEEEGQSLKD	EMARHLQEYQ	DLNVLKALD	360
		IELATYRKLL	EGEENRITIP	VQTFNSNLQIR	ETSLDTKSVS	EGHLKRNIVV	KTVEMRDGEV	420
		IKESKQEHKD	VM					432
		Seq ID NO: 317 Protein Sequence						
		Protein Accession #: AAA19191.1						
		1	11	21	31	41	51	
20		MRLSSLSGGS	SVSSDAEEYQ	PPIWKSILYQ	LQQAEPKPKR	IICPREVENR	PKYYGREFHG	60
		IISREADEL	LGGVEGAYIL	RESQRQPGCY	TLALRFGNQT	LNRYLFHDGK	HFVGEKRFES	120
25		IHDLVTDGLI	TLYIETKAAE	YISKMTTNP	YEHIGYATLL	REKVSRRLSR	SKNEPRKTIV	180
		THEEHTAVEK	ISSLVRRAL	THNDNHFNYE	KTHNPKVHTF	RGPHWCEYCA	NFMWGLIAQG	240
		VRCSOGLNV	HKQCSKHVNP	DCQPLKRIK	KVYCCDLTTL	VKAHNTQRP	VVDICIREIE	300
		ARGLSSEGLY	RVSGFTEHIE	DVKMAFDRDG	EKADISANVY	PDINIITGAL	KLYFRDLPIP	360
30		VITYDTYSKF	IDAAKISNAD	ERLEAVHEVL	MLLPPAHYET	LRYLMIHLK	VTMNEKDNFM	420
		NAENLGIVFG	PTLMRPEDS	TLTTLHDMRY	QKLIVQILIE	NEDVLF		466
		Seq ID NO: 318 Protein Sequence						
		Protein Accession #: XP_113553.1						
		1	11	21	31	41	51	
35		MKRAHPEYSS	SDSELDETIE	VEKESADENG	NLSSALGMS	PTTSSQILAR	KRRRGIEIKR	60
		RDRIRNNLS	ELRRLVPSAF	EKQGSALKLE	AEILQMTVDH	LKMLHTAGGK	GYFDAHALAM	120
		DYRSLGFREC	LAEVARYLSI	IEGLDASDPL	RVRLVSHLAN	YASQREASG	AHAGLGHIPW	180
40		GTVFGHHPHI	AHPLLLPQNG	HGNAGTTASP	TEPHHQGRIG	SAHPEAPALR	APPSGSLGPV	240
		LPVVTASAKL	SPPLSSVAS	LSAFFPSFGS	FHLSPNAL	PSAFTQAANL	GKPYRPMGTE	300
		IGAF						304
		Seq ID NO: 319 Protein Sequence						
		Protein Accession #: NP_001927.2						
		1	11	21	31	41	51	
45		MTAKEPSAS	GKSVOQOEQ	LVGSNPPORN	WKGIAIALLV	ILVICSLIVT	SVILLTPAED	60
		NSLSQKKVT	VEDLFSEDFK	IHDPEAKWIS	DTEFIYREQK	GTVRLWNVET	NTSTVLIEGK	120
		KIESLRIRAY	EISPDREYAL	FSYNVEPIYQ	HSYTGYYVLS	KIPHGDPQSL	DPPEVSNAL	180
50		QYAGWGPQKQ	QLIFIFENNI	YYCAHVCKQA	IRVSTGKEG	VIYNGLSDWL	YEEIEILKTHI	240
		AHWSPDGTR	LAYAAINDSR	VPIMELPTYT	GSIIYPTVKPY	HYPKAGSENP	SISLHVIGLVN	300
		GPTHDLMMF	DDPRRMREY	ITMVKMATST	KVAVTMLNRA	QNVSLTLCD	ATTGVCTKKH	360
		EDESEAWLHR	QNEEPVFSKD	GRKFFFIIRAI	PQGGRGKPYH	ITVSSSQPNS	SNDNIQSITS	420
		GDWDVTKILA	YDEKGNKIYF	LSTEDLPRRR	QLYSANTVGN	FNRCQLSCDL	VENCTYFSAS	480
55		FSHSMDFLL	KCEGPGVPMV	TVHNTTDKKK	MFDLETNEHV	KKAINDRQMP	KVEYRDIEID	540
		DYNLPMQILK	PAITFTOTTHY	PLLLVVDGTP	GSQSVAEKFE	VSWETVMVSS	HGAVVVKCDG	600
		RSGSGFQTKL	LHEVRRRLGL	LEEKDQMEAV	RTMLKEQYID	RTRVAVFGKD	YGYLSTYIL	660
		PAKGENQGGT	FTCGSALSPI	TDFKLYASAF	SERYLGLHGL	DNRAYEMTKV	AHRVSALEEQ	720
60		QPLIHTPAD	EKIHFQHTAE	LITQLIRGKA	NYSLIQIYPDE	SHYFTSSSLK	QHLYSRIINF	780
		FVECFRIQDK	LPTVTAKED	EED				803
		Seq ID NO: 320 Protein Sequence						
		Protein Accession #: XP_087461.1						
		1	11	21	31	41	51	
65		MLPLLAALLA	AACPLPPVRG	GAADAPGLLG	VPSNASVNAS	SAASPSPRGC	WPRRPPGPPS	60
		ARARRRRRRR	RRLCNISVQR	QMLSSLLVRW	GRPRGFQCDL	LLFSTNAHGR	AFFAAAFHRV	120
		GPPLLIHHLG	LAAGGAQQDL	RLCVGCGWVR	GRRTGRLRPA	AAPSAAAATA	GAPTALPAYP	180
		AAEPPGPLNL	QGEPLHFCCL	DFSLEELQGE	PGWRLNRKPI	ESTLVACFMT	LVIVVWSVAA	240
70		LIWVPPIIAG	FLPNGMEQRR	TTASTTAATP	AAVPAGTTAA	AAAAAAAAAA	AVTSGVATK	299
		Seq ID NO: 321 Protein Sequence						
		Protein Accession #: NP_036393.1						
		1	11	21	31	41	51	
75		MDLQGRGVPS	IDRLRVLLML	FHTMAQIMAE	QEVENLSGLS	TNPEKDIFVV	RENGTTCLMA	60
		EFAAKFIVPY	DVWASNYVDL	ITEQADIALT	RGAEVKGRCG	HSQSELQVFW	VDRAVALKML	120
		FVKESHNMKS	GPEATWRLSK	VQFVYDSSEK	THPKDAVSAG	KHTANSHHLS	ALVTIPAGKSY	180
		EQQAQQTISL	ASSDPQKTIV	MILSAVHIQP	PDIIISDFVFS	EEHKCPVDER	EQLEETLPLI	240
80		LGLILGLVIM	VTLAIYVHH	KMTANQVQIP	RDRSQYKHHG			280
		Seq ID NO: 322 Protein Sequence						
		Protein Accession #: NP_653187						
		1	11	21	31	41	51	

757

PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EELARRSLA QDAPPLFVPG 120
VLLKEFTVSG NLTIRLTAA DHRQLQSLIS SCLQQLSLIM WITQCFLPVF LAQPPSGQRR 180

Seq ID NO: 330 Protein Sequence LEK6
Protein Accession #: NP_066274

1 11 21 31 41 51
MQABEQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
PRGPHGGAAS AQDGRCPGCA RRPDSRLLOF RLTAADHRQL QLSISSCLQQ LSLMLWITQC 120
FLPVFLAQAP SGQRR 135

Seq ID NO: 331 Protein Sequence
Protein Accession #: NP_008859.1

1 11 21 31 41 51
MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLQYP EWTEAQRLLDC 60
WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG QVIWVNTII NGSQVWGGQP 120
VYPQETDDAC IPFDGGPCPS GWSQKRSFV YVWKTMGQYM QVLGGFVSGL SIGTGRAMLG 180
THTMEVTVYH RRGSRYSVPL AHSSSAFTIT DQVPPSVSVS QLRALDGGNK HFLRNQPLTF 240
ALQLHDPGSGY LAEADLSYTM DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS 300
CGSSPVPVGT DGHRTAEAP NITTAQGVPTT EVVGTTPGQA PTAEPSGTTT VQVPTTEVIS 360
TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM TPAEVSIVVL SGTAAQVTT 420
TEWVETTARE LPIPEPEGPD ASSIMSTESI TGSIGPLLDG TATLRLVKRQ VPLDCVLVRY 480
GSFSVTLDIV QGIESAEILQ AVPSGEGDAF ELTVSCQGGP PKEACMEISS PGQPPAQRLL 540
CQPVLPSPAC QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV 600
GILLVLMVAV LASLIYRRRL MKQDFSVFQL PHSSSHWLRL PRIFCSCPIG ENSPLLSGQQ 660
V 661

Seq ID NO: 332 Protein Sequence
Protein Accession #: NP_001913.2

1 11 21 31 41 51
MSPLMWGFL SCLGCKILPG AQGQFPRVCM TVDSLUNKEC CPRLGAESAN VCGSQQGRGQ 60
CTEVRADTRP WSGPYILRNQ DDERELWPRKF FHRTCKCTGN FAGYNOGCK FGWTGPNCEP 120
KKPPVIRQNI HSLSPQEREQ FLGALDLAKK RVHPDYVITT QHNLGLLGN GTQPQFANCS 180
VYDFVWLHY YSVRDTLLGP GRPYRAIDFS HQGPAPVTWH RYHLLCLERD LQRLIGNESF 240
ALPYWNFATG RNECDVCTQD LFGAARPDPT TLISRNSRFS SWETVCDSD DYNHLVTLN 300
GTVEGLLRN OMGRNSMKLP TLKDIRDCLS LQKFDNPPFF QNSTFSFRNA LEGFDKADGT 360
LDSQVMSLHN LVHSFLNGTN ALPHSAANDP IFVVLHSFTD AIFDEWMKRF NPPADAWPQE 420
LAPIGNRMV NMVPPFPPT NEELFLTSQ LGYSYALDLP VSVEETPGWP TTLVVMGTL 480
VALVGLFVLL AFLQYRRLRK GYTPLMETHL SSKRYTEEA 519

Seq ID NO: 333 Protein Sequence
Protein Accession #: XP_059422.1

1 11 21 31 41 51
MNWHLPLFL ASVTLPSICS HFNPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS 60
VLGMLQLGAD GRTKKQLAMV MRYGVNGVGK ILKKINKAIV SKKNKIDIVT ANAVFVKNAS 120
EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TRDMIDNLS PDLIDGLVLR 180
LVLVNAVYFK GLWKSFRQPE NTKKRTFVAA DGKSYQVPM L AQLSVFRCS TSAPNDLWYN 240
FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRVQ VILPKFTAVA 300
QTDLKEPLKV LGITDMEDSS KANFAKITRS ENLHVSHILO KAKIEVSEDG TKASAATTAI 360
LIARSSPPWF IVDPRPLFFI RHNPTGAVLF MGQINKP 397

Seq ID NO: 334 Protein Sequence
Protein Accession #: XP_040512.2

1 11 21 31 41 51
MRQHDTRNGR IVLISGRRSF CSIFSULPYR DSTQVGDLLK DGGRQSTGAV SLKEIIGLEG 60
VELGADGKTV SYTQFLLPFN AFGARRNTID STSSFSQFRN LSHRSLSIGR ASGTQGSLLD 120
GSDLDGDMFY DPNLLDDPQW PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNETFKEKFP 180
HIKLTLSKIR SLKREMRKLA QEDCGLEET VAMAFVFEK LALKGKLNKQ NRKLCAGACV 240
LLAAKIGSD LKHEVKHLID KLEEKFRILNR RELIAFEPPV LVALEFALHL PEHEVMPHYR 300
RLVQSS 306

Seq ID NO: 335 Protein Sequence
Protein Accession #: AAH08826

1 11 21 31 41 51
MTTLGAVPR MMRPGPGQNY PRSGFPLEVS TPLQGGVRNQ LGGVFINGRP LPNHIRHKIV 60
EMAHHGIRPC VISRLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY 120
KRENPGMFSW EYRDKLLKA VCDRNTVPSV SSISRILRSK FGKGEEDAD LERKAEASE 180
KKAHSDIGI LSEASAPQS DEGSIDSEPT DLPLKRRQR SRTTFTAEQL EELERAFERT 240
HYPIYITREE LAQRAKTEA RVQVWFNSRR ARWRKQAGAN QLMAFNHLIP GGFPPPTAMPT 300
LPTVQLSETS YQTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH 360
GFSSYTDSFV PPSGSPNPMN PTIGNGLSPQ NSIRHNSLSH SKPIRVQNEG TGKSSWWMLN 420
PEGGKSGKSP RRRASMDNN SKPAKRSRA AKKASLQSG QEGAGDSPGS QFSKNPASPG 480
SHSNDPDMW STFRPRTSSN ASTISGRISP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP 540
SLSEISNPN MENLLDNLNL LSSPSTLTVS TQSSPGTMMQ QTPCYSPAPP NTSLSNPSPN 600
YQKYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 660
DPGVAQPNR VLQGNVMGMP NSVMSTYGSQ ASHNMNMPS SHTHPGHAQQ TSAVNGRPLP 720
HTVSTMPHTS GMRNLQVKT PQVPLPHPM QMSALGGYSS VSSCNGYGRM GLLHQEKLP 780
DLDMGFIERL DCDMESIIRN DLMGDTLDF NFDNVLNQS FPHSVKTTTH SWVSG 835

Seq ID NO: 336 Protein Sequence
Protein Accession #: NP_005752.1

	1	11	21	31	41	51	
5	MEVSRKAPP	RPPRPAAPLP	LLAYLLALAA	PGRGADEPVW	RSEQAIGAIA	ASQEDGVFVA	60
	SGSCLDQLDY	SLEHSLRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLLL	PYREGAAGLG	120
	GLLLTGWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPOG	STAGVYVRAG	RNNRWYLAVA	180
	ATYVLPEPET	ASRCNPAASD	HDTAIALKDT	EGRSLATQEL	GRLKLCBAG	SLHFVDAFLW	240
10	NGSIYFPPYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDCGHGHPDC	RRLLSSSLV	300
	EALDVHAGVF	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
	ERVQPIASST	LIHSDLTSVY	GTVMNRTVL	FLGTGQGQLL	KVILGENLTS	NCPEVIYEIK	420
	EETPVFYKLV	PDPVKNIIYY	LTAGKEVRR	RVANCNHKS	CSECLTATDP	HCGWCHSLQR	480
	CTFQGDGVHS	ENLENWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGSEFSP	HSKCMVKMVD	540
15	SSRELQCNKS	QPNRTCTCSI	PTRATYKDV	VNVMFSEFGS	WNLSDRNFNT	NCSSLKECPA	600
	CVETGCAMCK	SARRCIHPFT	ACDPSDYERN	QECPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
	VFYIKSIEPQ	KVSTLGKSMV	IVTGANFTRA	SNITMILKGT	STCDKDVIVQ	SHVLNDTHMK	720
	FSLPSSRKEM	KDVCIQFDGG	NCSSVGSLSY	IALPHCSLIF	PATTWISGGQ	NITMGRNFD	780
	VIDNLIISHE	LKGNINVSSEY	CVATYCGFLA	PSLKSSKVRT	NVTVKLRVQD	TYLDCGLTQY	840
20	REDPRFTGYR	VESEVDELE	VKIQKENDNF	NISKDDIET	LFHGENGQLN	CSFENITRNO	900
	DLTTILCKIK	GIKTASTIAN	SSKQVRVKLG	NLELYVEQES	VPSTWYFLIV	LPVLLLVIVF	960
	AAVGVRTRHS	KELSRKQSQ	LELLESELRK	EIRDGFAELQ	MDKLDVVDSP	GTVPFLDYKH	1020
	FALRTFPFES	GGFTHTIED	MENRDANDKN	ESLTALDALI	CNKSFLVTVI	HTLEKQKNFS	1080
	VKDRCLFASF	LTIALQTKLV	YLTSLILEVLT	RDLMQCSNM	QPKMLLRTE	SVVEKLLTNW	1140
	MSVCLSGFLR	ETVGEPPYLL	VTTLNQKINK	GPVDVITCKA	LYTLNEDWLL	WQVPEFTVA	1200
25	LNWVFEKIPE	NESADVCNRI	SVNVLDCTI	GQAKEKIPQA	FLSKNGSPYG	LQLNEIGLEL	1260
	QMGTRQKELL	DIDSSSVILE	DGITKLNTIG	HYEISNGSTI	KVFKKIANFT	SDVEYSDHHC	1320
	HLILPDESEF	QDVQGRHRG	KHKFKVKEMY	LTLLSTKVA	IHSVLEKLF	SIWSLPNSRA	1380
	PFAIKYFFDF	LDAQAENKNI	TDPDVVHIWK	TNSLPLRFVW	NILKNPQFVF	DIKKTPIHIG	1440
30	CLSVIAQAFM	DAFSLTEQQL	GKEAPTNNLL	YAKDIPTYKE	EVKSYKAIK	DLPLSSSEM	1500
	EEFLTQESKK	HENEFNEEVA	LTEIYKYIVK	YFDEILNKLE	RERGLEEAQK	QLLHVKVLFD	1560
	EKKCKNM						1568

Seq ID NO: 337 Protein Sequence
Protein Accession #: XP_063670.1

	1	11	21	31	41	51	
35	MQRILEEPAD	DCMTSTRILL	TLSEFIMSLQ	RTVYPHSEKW	RALSVPSSTY	FQELVGTQSE	60
	LALTFWHLIS	MFGFFIVSYG	FLTAFGRITL	HLDDLQPNLT	PSRFDKYTGL	FIYEIEGDGL	120
	DPCFQSMVQG	ILEVLWMSKV	ESAYHTNDGD	TAGEGVNGT	SQTRGGGGAA	RSRCREMEEP	180
40	TPEPYVDVD	KGLTLACVVF	LCLFLVVMII	RCAKIVMDPY	SAIPTSTWEE	QHLDD	235

Seq ID NO: 338 Protein Sequence
Protein Accession #: FGENSEH predicted

	1	11	21	31	41	51	
45	MEPSHSQPTM	DMGHMQERPA	ASPLKCQDGR	GSAQSPLSAA	GPQSPAPLGA	LTPAEPGLGS	60
	APRAPRARAP	VTGKRRSRRS	AVALGSAPAQ	PGPRERTGRA	SPALENNSDL	LSKASAIATG	120
	TPPCEDSTIA	RFYLPPLTTL	HPELVGTQSE	LALTFWHLIS	MFGFFIVSYG	FLTAFGRITL	180
	HLDDLQPNLT	PSRFDKYTQ	LLEPLVHYSK	VLTIHWSQGL	CIWSSHPCFA	GVNGTSTQTR	240
50	GGGGAARSRC	REMEETPEP	VYVDVKGILT	LACFVFLCLF	LVVMIIRCAK	VIMDPYSAIP	300
	TSTWEEQHL	D					311

Seq ID NO: 339 Protein Sequence
Protein Accession #: FGENSEH predicted

	1	11	21	31	41	51	
55	MGKDFMSKTP	KAMATQAKID	KWDLIKLSF	CTAKETTIRV	NRQPTWEKI	FAIYSSDEGL	60
	ISRIYNEPKQ	IYKKKTNNPI	NKWKADMRH	FSKEDIYAN	RHMCKSSSL	AIREMQIKTT	120
	TRCHLTPVRM	AIIKSGNNR	TAEQPKLRK	EAVGSIEIFR	FADGLDITLM	ILGILASLVN	180
60	GACPLMPLV	LGEMSDNLIS	GCLVQNTTN	YQNTQSQEK	LNEDMTLLT	YVVGIGVAAL	240
	IFGYIQISLW	IITAARQTKR	IRKQFFHVSU	AQDIGWFDSC	DIGELNTRMT	DDIDKISDCI	300
	GDKIALLFQ	MSTFSIGLAV	GLVKGWKLTL	VTLSPLIM	ASAAACSRMV	ISLTSKELSA	360
	YSKAGAVAE	VLSSIRTVIA	FRAQEKELQ	YTONLKDAD	FGIKRTIASK	VSLGAVYFFM	420
	NGTYGLAFWY	GTSILILNGEP	GYTIGTVLAV	FFSVIHSSYC	IGAAVPHFET	FAIARGAAFH	480
65	IFQVIDKKPS	IDNFSTAGYK	PESIEGTVEF	KNVSPNYPSR	PSIKILKGLN	LRIKSGETVA	540
	LVGLNGSGKS	TVVQLQRLY	DPDDGFIMVD	ENDIRALNVR	HYRDHIGVVS	QEPVLPFTTI	600
	SNNIKYGRDD	VDEEMERAA	REANAYDFIM	EPFNKFTLV	GEKGAQMSGG	QKQRIATARA	660
	LVRNPKLIL	DEATSALDSE	SKSAVQAAL	KDTPRYSF			698

Seq ID NO: 340 Protein Sequence
Protein Accession #: XP_166496.1

	1	11	21	31	41	51	
70	MVDENDIRAL	NVRHYRDHIG	VVSQEPVLFG	TTISNNIKYG	RDDVTDEEME	RAAREANAYD	60
75	FIMEFPNKF	TLVGEKGAQM	SGGQKQRIAI	ARALVRNPKI	LILDEATSAL	DSEKSAVQA	120
	ALEKDTPRYS	F					131

Seq ID NO: 341 Protein Sequence
Protein Accession #: XP_166305.1

	1	11	21	31	41	51	
80	MEKFRVLDL	HVGHHSALGY	GLVTLTLAGG	ERIFSAVAFQ	CPCSAAWNLP	YGLVFLLVPA	60
	LALFLGTVL	SARTWRLLTG	CCSSARASCG	SALRGSLVCT	QISAAALAP	LTWVAVALLG	120
	GAFYECAATG	SAFAQRLCL	GRNRSAAEL	PLVPCNQA	SDVQDLKLD	KAQSQVLGWI	180

LIADVIIILL IFTSVTRCLS PVSFLQLKFW KIYLEQEQQI LKSKATEHAT ELAKENIKCF 240
 FEGSHPKYFN TFSMKWQQI SSLYTFNPKG QYYSMLHKYV NRKETHSIR STEGDTVIPV 300
 LGFVDSSGIN STPEL 315

5

Seq ID NO: 342 Protein Sequence
 Protein Accession #: NP_115587.5

1 11 21 31 41 51
 | | | | |
 MARSPPATLF LFLLLGQPP PSRPQSLGTT KLRLVGPESK PEEGRLEVLH QGQWGTVCDD 60
 NFAIQEATVA CRQLGFEEAL TWAHSAKYGQ GEGPIWLDNV QCVGTESSLD QCGSNWGVVS 120
 DCSHSEVDGV ICHPRRRHGY LSETVSNALG PQGRRLEEVRL KKPILASAKQ HSPVTEGAVE 180
 VKYEGHWRQV CDQGWMTMNS RVVCGMLGFP SEVPVDSHYI RKVWDLKMRD PKSRLLSLTN 240
 KNSFWIHQVT CLGTEPHMAN CQVQVAPARG KLRPACPGGM HAVVSCVAGP HFRPPKTKPQ 300
 RKGSWAEPR VRLRSGAVG EGRVEVLAMR QMGTVCDHRW NLISASVVCRL QLGPGSAREA 360
 LFGARLGQGL GPIHLSEVRC RGYERTLSDC PALEGSQNGC QHENAAAVRC NVPNMGFQNG 420
 VRLAGGRPE EGLLVQVEV NGVPRWGSVC SENWGLTEAM VACRQLGLGF AIHAYKETWF 480
 WSGTPRAQEV VMSGVRCST ELALQCCQRH GPVCHSHGGG RFLAGVSCMD SAPDLVMNAQ 540
 LVQETAYLED RPLSQLCAH EENCLSKSAD HMDWPYGYRR LLRFSTQIYN LGRTDFRPKT 600
 GRDSWVWHQC HRHYHSIEVF THYDLLTLNG SKVAEGHKAS FCLEDTCNPT GLQRRYACAN 660
 FGEQGVTVGC WDTYRHDIDC QWVDITDVGP GNYIFQVIVN PHYEVAESDF SNNMLQCRCK 720
 YDGRHVLWLN CHTGNSYPAN AELSLEQEQRLRNLI 756

25

Seq ID NO: 343 Protein Sequence
 Protein Accession #: NP_001789.2

1 11 21 31 41 51
 | | | | |
 MENFQKVEKI GEGTYGVVYK ARNKLTGEVV ALKKIRLDTE TEGVPSTAIR EISLLKELNH 60
 PNIVKLLDVI HTENKLYLVF EFLHQDLKKF MDASALTGIP LPLIKSYLFQ LLQGLAFCHS 120
 HRVLHRDLKP QNLLINTEGA IKLADFLGAR AFGVPVRYTY HEVVTWLYRA PEILLGCKYK 180
 STAVDIWSLG CIPAEWVTR ALFPGDSEID QLFRIFTLGT TPDEVVWPGV TSMFDYKPSF 240
 PKWARQDFSK VVPLDEDEGR SLLSQMLHYD PNKRISAKAA LAHPFFQDVT KVPVHLRL 298

35

Seq ID NO: 344 Protein Sequence
 Protein Accession #: NP_439892.1

1 11 21 31 41 51
 | | | | |
 MENFQKVEKI GEGTYGVVYK ARNKLTGEVV ALKKIRLDTE TEGVPSTAIR EISLLKELNH 60
 PNIVKLLDVI HTENKLYLVF EFLHQDLKKF MDASALTGIP LPLIKSYLFQ LLQGLAFCHS 120
 HRVLHRDLKP QNLLINTEGA IKLADFLGAR AFGVPVRYTY HEVTRRALFP GDSEIDQLFR 180
 IFRTLTPTDE VVWPGVTSMP DYKPSFPKWA RQDFSKVVPV LDEDEGRSLLS QMLHYDPYKR 240
 ISAKAALAHF FQDVTKVPV HLRL 264

45

Seq ID NO: 345 Protein Sequence
 Protein Accession #: NP_116127.1

1 11 21 31 41 51
 | | | | |
 MKLGCVLMAV ALYLSLGLVW VAQMLLAASF ETLQCEGPVC TEESCHTED DLTDAEAGF 60
 QVKAYTFSEP FHLIVSYDWL ILQGPAPKVF EGDLLVLRQ AWQDWPLTQV TFYRDGSALG 120
 PPGPNREFSI TVVQKADSGH YHCSGIFQSP GPGIPETASV VAITVQELFP APILRAVPSA 180
 EPOAGSPMTL SCQTKLPLQR SAARLLFSFY KDGRIVQSRG LSSEFQIPTA SEDHSGSYWC 240
 EAATEDNQVW QKSPQLEIRV QGASSAAPP TLNPAQKSA AFGTAPEEAP GPLPPPTPS 300
 SEDPGFSSPL GMPDPHLYHQ MGLLLKHMMD VRVLLGHLML ELRELSGHQK PGTTKATAE 359

55

Seq ID NO: 346 Protein Sequence
 Protein Accession #: NP_002337.1

1 11 21 31 41 51
 | | | | |
 MKIFLPLVLA ALLGVERASS LMCFSCLNOK SNLYCLKPTI CSDQDNYCVT VSASAGIGNL 60
 VTFGHSLSKT CSPACPIPEG VNVGVASMG I SCCQSFLCNF SAADGGLRAS VTLILAGLLL 120
 SLLPALLRFP P 131

65

Seq ID NO: 347 Protein Sequence
 Protein Accession #: XP_113526.2

1 11 21 31 41 51
 | | | | |
 MEDLGENTMV LSTLRSLNMF ISQRVEGGSG LDISTSAPGS LQMYYQSMQ LEERAQIIRS 60
 KSHLIQVERE KMOMELSHKR ARVELERAAS TSARNYEREV DRNQELLTRI RQLQEREAGA 120
 EEKMQEQLER NRQCCQNLD AASKRLREKED SLAQAGETIN ALKGRISELQ HSMVDQEMRV 180
 KRLESEKQEL QEQLDLQHKK QCEANQKIQE LQASQEARAD HEQQIKDLEQ KLSLQEQDAA 240
 IVKNMKSELV RLPRLRELK QLRRESAHLR EMRETNGLLQ EELEGLQRLK GRQEKMQETL 300
 VGLELENERL LAKLQSWERL DQTMGLSIRT PEDLSRFVVE LQRELALKD KNSAVTSSAR 360
 GLEKARQQIQ EELRQVSGQL LEERKKRETH EALARRLQKR VLLLTKERDG MRAILGSYDS 420
 ELTPAIESPO LTRRMREAED MVQKVHSHA EMEAQLSQAL EELGGQKQRA DMLEMKML 480
 KSQSSAEDQS FLFSREAEOT LRLKVEELEG ERSRLSEER MLEAQLERRA LQGDYDQSR 540
 KVLHMSLNPT SVARQLRED HSQLAECER LRGLLRAMER GGTVPADLEA AAASLPSSKE 600
 VAEKKQVES AELKNQRLKE VFQTKIQEFR KACYTLTGQY IDITTENQYR LTSLYAEHPG 660
 DCLIFKATSP SGSKMQLLET EFSHTVGELI EVHLRRQDSI PAFLLSSLTLE LFSRQTVA 718

80

Seq ID NO: 348 Protein Sequence
 Protein Accession #: NP_000264.1

1 11 21 31 41 51
 | | | | |
 MTQAGRRGPG TPEPRPTQP MASPRLGTF CPTRDAATQL VLSFQPRAPH ALCLSGGLR 60
 LALGLLQLLP GRRPAGPGSP ATSPASVRI LRAAAACDLL GCLGMVIRST VWLGFNPFVD 120

5 SVSDMNHTEI WPAAFVCVGS MNIQLLYSAC FWWLFCYAVD AYLVIRRSAG LSTILLYHIM 180
AMGLATLLCV EGAAMLYYPS VSRCEGLDH AIPHYVTMYL PLLLVLVANP ILFOKTVTAV 240
ASLLKRGQGI YTENERRMGA VIKIRFFKIM LVLIICWLSN IINESLLFYL EMQTDINGGS 300
LKPVRTAAKT TWFIMGILNP AQGFLLSLAF YGWTGCSLGF QSPRKEIQWE SLTTSAAEGA 360
HPSPLMPHEN PASGKVSQVG GQTSDEALSM LSEGSDASTI EIHTASESCN KNEGDPALPT 420
HGDLL 424

10 Seq ID NO: 349 Protein Sequence
Protein Accession #: NP_647478.1
1 11 21 31 41 51
MGPKDSAKCL HRGPPQPSHWA AGDGPTQERC GPRSLGSPVL GLDTCRAWDH VDGQILGQLR 60
PLTEEEEEEAG AGATLSRGPA FPGMGSEELR LASFYDWPLT AEVPPPELLAA AGFFHTGHQD 120
KVRCCFCYGG LQSWKRGDDP WTEHAKWFPS CQFLLRSGKR DFVHSVQETH SOLLGSDPW 180
15 EEPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGGVS PAEAQRAWNV LEPPGARDVE 240
AQLRRQLEER TCKVCLDRAV SIVFVPCGHL VCAECAPGLQ LCPICRAPVR SRVRTFLS 298

20 Seq ID NO: 350 Protein Sequence
Protein Accession #: NP_071444.1
1 11 21 31 41 51
MGPKDSAKCL HRGPPQPSHWA AGDGPTQERC GPRSLGSPVL GLDTCRAWDH VDGQILGQLR 60
PLTEEEEEEAG AGATLSRGPA FPGMGSEELR LASFYDWPLT AEVPPPELLAA AGFFHTGHQD 120
KVRCCFCYGG LQSWKRGDDP WTEHAKWFPS CQFLLRSGKR DFVHSVQETH SOLLGSDPW 180
25 EEPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGARD VEAQLRRQLE ERTCKVCLDR 240
AVSIVFVPCG HLVCAECAPG LQLCPICRAP VRSRVRTFLS 280

30 Seq ID NO: 351 Protein Sequence
Protein Accession #: NP_066300.1
1 11 21 31 41 51
MGSVSSLISG HSFHSHKCR A SQYKLRKSSH LKKLNRYSDG LLRFPGFSQDS GHGKSSSKMG 60
KSEDFFYIKV SQKARGSHHP DYTALSSGDL GGQAGVDFDP STPPKLMPPFS NQLEMSEK 120
AVRPTAFKPV LPRSGAILHS SPESASHQLH PAPPDKPKEQ ELKPGLCGSA LSDSGRNSMS 180
35 SLPTHSTSSS YQLDPLVTPV GPTSRRFGGSA HNITQGIIVLQ DSNMMSLKAL SPSDGGSKLG 240
HSNKADKGPS CVRSPISDTE CSIQELEQKL LEREGALQKL QRSFEEKELA SSLAYEERPR 300
RCRDELEGPE PKGGNKLKQA SQKSQRAQOV LHLQVLQLOQ EKRLRQLELE SLMKQDLE 360
TKLRSYERK TSFGPALLET QWEVCQKSGE ISLLKQQLKE SQTEVNAKAS EILGLKAQLK 420
40 DTRGLEGLE LRTQDLEGAL RTKGLELEVC ENELQRKQNE AELLREKYNL LBQELQELRA 480
QAALARDMCP PTFPEDVPAL QRELERLRAE LREERQGHQD MSSGPOHERL VWKEEKEKVI 540
QYQKQLQSSY VAMYQRNQLR EKALQQLARG DSAGEPLEVD LEGADIPYED IIAITEI 596

45 Seq ID NO: 352 Protein Sequence
Protein Accession #: AAG41361.1
1 11 21 31 41 51
MPKNSKVVKR ELDDDVTEVS KDLLSNEDAA DDAFKTSELI VDGQEEKDIT VEEGSEVEDE 60
RPAWNSKLQY ILAQVGFVS LGNVWRFYPL CQKNGGGAYL LPYLILLMVI GIPLFFLELS 120
VQQRIRRSI GVMYIYISPKL GGIGFASCVV CYFVALYVNV IIGWSLFYFS QSFQQLPMD 180
50 QCPLVKNASH TFVEPECEQS SATTYWYRE ALNISSSISE SGLNWKMTI CLLAAMVMVC 240
LAMKGIQSSS GKIIYFSSLF PYVVLICFLI RAFLNGSID GIRHMTFPL EIMLEPKVNR 300
EAATQVFFAL GLGFGGVIAF SSYNKRDNNC HFDVAVLSFI NFFTSLVATL VVFAVLGPKA 360
NVINEKCITO NSETIMFLK MGNISQDIIP HHINLSTVTA EDYHLVYDII QKVKEEFPA 420
LHLNSCKIEE ELNKAUVQGTG LAFIAFTEAM THFPASPFWV VMFFLMLVNL GLGSMFGTIE 480
55 GIVTPIVDTF KVRKEILTIV CCLLAFICGL IFVQSGNYF VTMFDDYSAT LPLLIIVILE 540
NIAVCFVYGI DKFMEDLKM LGFAPSRYYY YMKYISPLM LLSLLIASV NMGLSPPGYN 600
ANIEDKASEE FLSYPTWGLV VCVSLVFAI LPVPVVFIVR RPNLIDSSG NIASVYTKRG 660
60 RVLKEPVNLE GDDTSLINGK IPSEMPSPNF GKNIYRKQSG SPTLDTAPNG RYIGLYLMD 720
IMPMPESDL 730

65 Seq ID NO: 353 Protein Sequence
Protein Accession #: NP_005594.1
1 11 21 31 41 51
MEGERSPLL SQETAGQKPL SVHRPPTSGC LGPVREDQA EAWGSCCPP ETKHQALSGT 60
PKKGAPSL S PGSSCVKYLI FLNFPFSL GLLALAIGLW GLAVKSLGS DLGGPLPTDP 120
MLGLALGLV VSAASLAGCL GALCENTCLL RGFSGGILAF LVLEAVAGAL VVALWGLPQD 180
70 SLEHTLRVAI AHYQDDPDLR FLDDQVQLGL RCCGAASYQD WQONLYFNCS SPGVQACSLP 240
ASCCIDPREG GASVNDQCGF GVLRLDADA QRVVYLEGCG PPLRRWLRAN LAASGYAIA 300
VLLQGAELL LAARLLGALA ARSAAAYGPG AHGEDRAGPQ SPSPGAPPAA KPARG 355

75 Seq ID NO: 354 Protein Sequence
Protein Accession #: AAL84622.1
1 11 21 31 41 51
MADPEVVVSS CSSHEENRC NFNQQTSPSE ELLLEDQMRK KLKFFFMNFC EKFWARGRKP 60
WKLAIQILKI AMVTIQLVLF GLSNQMVVAF KEENTIAFKH LFLKGYMDRM DDTYAVYTQS 120
DVIDQLIFAV NQYLQLVNV VGNHAYENKG TKQSAMAICQ HPYKRGNIYP GNDTFIDPE 180
80 IETECFFVEP DEPHIGTPA ENKLNLTLD HRLLTVELQF KLKAINLQTV RHQELPDQYD 240
FTLITFDNK AHSGRKISL DNDISIRECK DMHVSIGSIQ NTHYMIIFDA FVILTCVLSL 300
ILCIRSVIRG LQLQEFVNF FLLHYKKEVS VSDQMEFVNG WYIMIIISDI LTIIGSILKM 360
EIQAKSLTSY DVCSILGTS TMLVNLGVIR YLGFFAKYNL LILTQAAALF NVIRFCCCAA 420
MIYLYGCFQG WIVLGPYHDK FRSLNMVSEC LFSLINGDDM FATFAKMQQK SYLVWLFSLR 480
YLYSFISLFI YMILSLFIAL ITDTYETIKQ YQDGFPETE LRTFISECKD LPNSGKYRLE 540

DDPPVSLFCC CKK

553

Seq ID NO: 355 Protein Sequence
Protein Accession #: NP_000105.1

5	1	11	21	31	41	51	
	MEPGLWLLFG	LTVTSAGFV	PCSQSGDAGR	RGVSQAFTAA	RSEGDCEETV	AGPGEETVAG	60
	PGEPTVAPTA	LQGPSPGSPG	QEQAABGAPE	HHRSRRTCTF	TYKDKCEVYV	CHLDIWIINT	120
10	PEQTVPYGLS	NYRGSFRGKR	SAGPLPGNLQ	LSHRPHLRCA	CVGRYDKACL	HFCTQTLDVS	180
	SNSTRAEKTD	KEEGKVEVK	DQSKQALDL	HHPKLMPSGS	LALAPSTCPR	CLFQEGAP	238

Seq ID NO: 356 Protein Sequence
Protein Accession #: NP_005347.2

15	1	11	21	31	41	51	
	MGGCCSSHPE	DDWMENIDVC	ENCHYPIVPL	DGKGTLLIRN	GSEVRDPLVT	YEGSNPPASP	60
	LQDNLVIALH	SYEPSHDGDL	GFEKGEPLRI	LEQSGEWWKA	QSLTTGQEGF	IPFNFVAKAN	120
	SLEPEWPFWK	NLSRKDAERQ	LLAPGNTHGS	FLIRESESTA	GSFSLSVRDF	DQNGQEVVXH	180
	YKIRNLNNGG	FYISPRITFP	GLHELVRHYT	NASDGLCTRL	SRPCQTQKPK	KPWWEDEWEV	240
20	PRETLKLVER	LGAGQPGFVW	MGYYNGHTKV	AVKSLKQGSN	SPDAFLAEAN	LMKQLQHQR	300
	VRLYAVVTQE	PIYIITEYME	NGSLVDFLKT	PSGIKLTINK	LLDMAAQIAE	GMAFIEERNY	360
	IHRDLRAANI	LVSDTLSCKI	ADPGLARLIE	DNEYTAREGA	KFPIKMTAPE	AINYGTFTIK	420
	SDVMSFGLLL	TEIVTHGRIP	YFGMTNFEVI	QNLERGVRMV	RPDNCPEELY	QLMRLCWKER	480
25	PEDRPTFDYL	RSVLEDFFTA	TEGQYQPPQ				509

Seq ID NO: 357 Protein Sequence
Protein Accession #: NP_055469.1

30	1	11	21	31	41	51	
	MAIAYLGSSC	PSQPPSSAL	SLSPTPSDFE	QESGIETAMR	FSPDVALAVS	TTPAVLPTTN	60
	IQPVGTFFEE	LPSEPTLLEP	ATSPLVVTEV	PEEPSQRATT	VSTTMATTAA	TSTGDPVTAT	120
	VPATVATATP	STPAAPPFTA	TTAVIRTTGV	RRLPLPLTT	VATARATTPE	APSPPTTAIV	180
	LDTEAPTREL	VSTATSRPRA	LPRPATTEP	DIPERSTLPL	GTTAPGPTEV	AQTPTPETFL	240
	TTIRDEPEVP	VSGGSGDFE	LPEEETTQPD	TANEVVAVGG	AAAKASSPPG	TLPRGARPGP	300
35	GLLDNAIDSG	SSAAQLPQKS	ILERKEVLVA	VIVGVVVGAL	FAAFLVTLTI	YRMKKKDEGS	360
	YTLLEPKQAS	VTYQKPKQE	EFYA				384

Seq ID NO: 358 Protein Sequence
Protein Accession #: NP_008848.1

40	1	11	21	31	41	51	
	MYGNYSHFMK	PPAGYGGSPG	HTGSTMSPS	AALSTGKPMO	SHPSYTDTPV	SAPRTLSAVG	60
	TPLNALGSPY	RVITSAMGPP	SGALAAPPGI	NLVAPPSSQL	NVVNSVSSE	DIKPLPGLPG	120
	IQNMNYPSTS	PGSLVKHICA	ICGDRSSGKH	YGVYSCGCK	GFFKRTIRKO	LIYTCRDNKO	180
45	CLIDKRQNR	QCYCRQKCL	VMGMKREAVQ	EERQSRERA	ESEAECATSG	HEDMPVERIL	240
	EAELEVEPT	ESYGDMMNEN	STNDPVTNIC	HAADKQLFTL	VEWAKRIPHF	SDLTLEDQVI	300
	LLRAGWNELL	IASFHSRVS	VQDGILLATG	LHVHRSSAHS	AGVGSIFDRV	LTELVSQMKD	360
	MQMDKSELGC	LRAIVLFNPD	AKGLSNPSEV	ETLREKVYAT	LEAYTKQKYP	BQPGRFACKL	420
50	LRLPALRSIG	LKCLEHLFFF	KLIGDTPIDT	FLMEMLETPL	QIT		463

Seq ID NO: 359 Protein Sequence
Protein Accession #: NP_002176.1

55	1	11	21	31	41	51	
	MTILGTTFGM	VFSLLQVVS	ESGYAQNGDL	EDAELEDDYSF	SCYSQLEVNG	SOHSLTCAFE	60
	DPOVNTTNLE	FEICGALVEV	KCLNFRKLQE	IYFIETKKFL	LIGKSNICVK	VGEKSLTCKK	120
	IDLTTIVKPE	APFDLSVIYR	EGANDFVVT	NTSHLQKKYV	KVLMHDVAYR	QEKDENKWT	180
	VNLSSTKLTL	LQKRLQPAAM	YEIKVRSIPD	HYFKGFSEW	SPSYFFRTP	INNSSGEMDP	240
60	ILLTISILSF	FVALLVILA	CVLWKKRIKP	IVWPSLPDHK	KTLEHLCKKP	RKNLNVSPNP	300
	ESFLDQCIHR	VDDIQARDEV	EGFLQDTFPQ	QLESEKORL	GGDVQSPNCP	SEDVVVTPES	360
	FGRDSSLTCL	AGNVASADAP	ILSSSRSLDC	RESGKNGPHV	YQDLLLSLGT	TNSTLPPPPS	420
	LQSGITLTLN	VAQQQPIILTS	LGSNQEEAYV	TMSSFFYQNG			459

Seq ID NO: 360 Protein Sequence
Protein Accession #: NP_006263.1

65	1	11	21	31	41	51	
	MSELEKAMVA	LIDVFHQYSG	REGDKHKLKK	SELKELINNE	LSHFLEEIKE	QEVVDKVMET	60
70	LDNDGDEGCD	QEFMAFVAM	VTTACHEFFE	HE			92

Seq ID NO: 361 Protein Sequence
Protein Accession #: NP_006148.1

75	1	11	21	31	41	51	
	MPMDLILVVM	FCVCTARTVV	GFGMDPDLQM	DIVTELDLVN	TTLGVAQVSG	MHNASKAFLF	60
	QDIEREIHAA	PHVSEKLIQL	FQNKSEFTIL	ATVQOKPSTS	GVILSIRELE	HSYFELESSG	120
	LRDEIRYHYI	HNGKPRTEAL	PYRMADGQWH	KVALSVSASH	LLLHVDCNRI	YERVIDPPDT	180
80	NLPFGNLNLW	QQRNQKHGLF	KGIIQDGKII	FMPNGYITQC	PNLNHTCPTC	SDFLSLVQGI	240
	MDLQELLAKM	TAKLYNAETR	LSQLENCHCE	KTCQVSGLLY	RDQDSWVDGD	HCRNCTCKSG	300
	AVECRRMSCP	PLNCSPPDSL	VHIAQGCCKV	CRPKCIYGGK	VLAEGQRILT	KSCRECRGGV	360
	LVKITMCPFP	LNCSEKDHIL	PENQCCRVCR	GHNFCABGPK	CGENSECKNW	NTKATCECKS	420
	GYISVQGDSA	YCEDIDECAA	KMHYCHANTV	CYNLPGLYRC	DCVPGYIRVD	DFSCTEHDEC	480

		GSGQHNCNEN	AICTNTVQGH	SCTCKPGYVG	NGTICRAFCE	EGCRYGGTCV	APNKCVCPSG	540	
		FTGSHCEKDI	DECSGIEIEC	HNHSRCVNL	P	GWYHCECRSG	FHDDGTYSLS	GESCIDIDEC	600
		ALRTHTCWND	SACINLAGGF	DCLCPSPGSC		SGDCPHEGGL	KHNGQVWTLK	EDRCSVCSCK	660
5		DGKIFCRRTA	CDQCNPSADL	FCCPECDTRV	TSQCLDQNGH	KLYRSGDNWT	HSCQCCRCLE	720	
		GEVDCWPLTC	PNLSCEYTAI	LEGECCPRCV	SDPCLADNIT	YDIRKTC LDS	YGVSRLSGSV	780	
		WTMAGSPCTT	CKCKNGRVCC	SVDFECLQNN				810	
Seq ID NO: 362 Protein Sequence									
Protein Accession #: NP_057264.1									
10		1	11	21	31	41	51		
		MGSNSQAGR	HIYKSLADGG	PFDSEVPPKR	PTSRLIMHSM	AMFGREFCYA	VEAAYVTPVL	60	
		LSVGLPSSLY	SIWFLSPIL	GFLIQPVVGS	ASDHCRSRWG	RRRPYILTIG	VMMLVGMALY	120	
15		LNGATVVAAL	IANPRRKLVM	AISVTMIGVV	LFDFAADFID	GPIKAYLFDV	CSHQDKEKGL	180	
		HYHALFTGFG	GALGYLLGAI	DWAHLELGR	LGTEFQVMFF	FSALVLTLCF	TVHLCSISEA	240	
		PLTEVAKGIP	PQQTPODPPL	SSDGMVEYGS	IEKVNGYVN	PELAMQGAKN	KNHAEQTRRA	300	
		MTLKSLLRAL	VNMPPHYRYL	CISHLIGWTA	FLSNMLPFTD	FMGQIVYRGD	PYSAHNSTEF	360	
		LIYERGVEVG	CWGFICINSVF	SSLYSYFQKV	LVSYIGLKGL	YFTGYLLFGL	GTGFIGLFPN	420	
20		VYSTLVLCSL	FGVMSSTLYT	VPFNLITEYH	REEEKERQQA	PGGDPDNVSR	GKGMDCATLT	480	
		CMVQLAQILV	GGGLGFLVNT	AGTVVVVVIT	ASAVALIGCC	FVALFVRYVD		530	
Seq ID NO: 363 Protein Sequence									
Protein Accession #: NP_036532.1									
25		1	11	21	31	41	51		
		MELALLQGLV	VMAGVPIIQG	GILNLMKMKV	QVTGKMPILS	YWPYGCCHGL	GGRGQPKDAT	60	
		DWCQTHDCC	YDLKLTQCCS	IYKDYRYNPF	SQGNIHCSDK	GSWCEQQLCA	CDKEVAFCLK	120	
		RNLDTYQKRL	RFYWRPHCRG	QTPGC				145	
30	Seq ID NO: 364 Protein Sequence								
Protein Accession #: NP_061313.1									
		1	11	21	31	41	51		
35		MRLPDLRPWT	SLLLVDAALL	WLLQGPLGTL	LPQGLPGLWL	EGTLRLGLGW	GLLKLRLGLG	60	
		FVGTLLPLC	LATPLTVSLR	ALVAGASRAP	PARVASAPWS	WLLVGYGAAG	LSWSLWAVLS	120	
		PPGAQEKEQD	QVNNKVLMMR	LKLSRPDL	LLVAAFFFLV	LAVLGETLIP	HYSGRVIDIL	180	
		GGDFDPHAF	SAIFFMCLFS	FGSSLSAGCR	GGCFTYTMSR	INLRIREQLF	SSLLRQDLGF	240	
		FQETKTGELN	SRLSSDTTLM	SNWLPLNANV	LLRSLVKVVG	LYGFMLSISP	RLTLSSLHLM	300	
40		PFTIAAEKVY	NTRHQEVLRE	IQDAVARAQ	VVREAVGGLQ	TVRSFGAEH	EVCRYKEALE	360	
		QCRQLYWRD	LERALYLLIR	RVLHLGVQML	MLSCGLQOMQ	DGELTQGSLL	SFMIYQESVG	420	
		SYVQTLVYIY	GDMLSNVGA	EKVFSYMDRQ	PNLSPSGTLA	PTTLQGVVVF	QDVSPAYPNR	480	
		PDRPVLKGLT	FTLRPGEVTA	LVGPNNGSGKS	TVAALLQNLV	QPTGGQVLLD	EKPISQYEHC	540	
		YLHSQVSVG	QEPVLFSGSV	RNNIAYGLQS	CEDDKVMAAA	QAAHADDIFIQ	EMEHEGIYTDV	600	
45		GEKGSQLAAG	QKQLALARA	LVRDPRVLIL				630	
Seq ID NO: 365 Protein Sequence									
Protein Accession #: NP_002407									
50		1	11	21	31	41	51		
		MKKSGVLFL	GIILLVLIGV	QGTFFVRKGR	CSCISTNQGT	IHLQSLKDLK	QFAPSPPSCEK	60	
		IEIATLKNG	VQTCNLPDSA	DVKELIKKWE	KQVSQKKKQK	NGKGHQKKKV	LKVRKSQSR	120	
		QKKTT							
55	Seq ID NO: 366 Protein Sequence								
Protein Accession #: NP_006524.1									
		1	11	21	31	41	51		
		MARSLVCLGV	IILLSAFSGP	GVRGGPMPLK	ADRLCADQE	CSHPISMAVA	LQDYMADPCR	60	
		FLTIHRGQVV	YVFSKLKGRG	RLFWGGSVQG	DYYGDLAARL	GYFPSSIVRE	DQTLKPGKVD	120	
60		VKTDKWDIFYC	Q					131	

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-68 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.
- 1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.
- 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.
- 1 4. The method of Claim 2, wherein said nucleic acids are mRNA
- 1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.
- 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-68.
- 1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-68; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.
- 1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-68.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-68.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targetting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- a) contacting said compound with a pathology-associated polypeptide, said polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and
- b) determining the functional effect of said compound upon said polypeptide.

19. A drug screening assay comprising the steps of:

- a) administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and
- b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of said polynucleotide in a control cell or mammal, wherein a test compound that modulates said level of expression of the polynucleotide is a candidate for the treatment of said pathology.

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 March 2003 (27.03.2003)

PCT

(10) International Publication Number
WO 03/025138 A3

(51) International Patent Classification⁷: **C12Q 1/68**

(21) International Application Number: **PCT/US02/29560**

(22) International Filing Date:
17 September 2002 (17.09.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/323,469 17 September 2001 (17.09.2001) US
60/323,887 20 September 2001 (20.09.2001) US
60/350,666 13 November 2001 (13.11.2001) US
60/355,145 8 February 2002 (08.02.2002) US
60/355,257 8 February 2002 (08.02.2002) US
60/372,246 12 April 2002 (12.04.2002) US

(71) Applicant (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway, Boulevard, South San Francisco, CA 94080 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

Published:

— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:
8 May 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 03/025138 A3

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68

US CL : 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 7.1, 287.2; 436/63, 64

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P — Y,P	US 6,426,186 B1 (JONES et al.) 30 July 2002 (30.07.2002), see especially Detailed Description of the Invention and Sequence 62.	1-6 — 7
X — Y	US 6,194,158 B1 (KROES et al.) 27 February 2001 (27.02.2001), see especially Background of the Invention and Detailed Description of the Invention.	2-5 — 1, 6, 7
X,P — Y,P	US 6,440,676 B1 (KROES et al.) 27 August 2002 (27.08.2002), see especially Background of the Invention and Detailed Description of the Invention.	2-5 — 1, 6, 7
Y,P	US 6,500,938 B1 (AU-YOUNG et al.) 31 December 2002 (31.12.2002), see especially Summary of the Invention and Description of the Invention.	1-7
Y	SMYTH TEMPLETON et al. Cloning and Characterization of Human Tumor Cell Interstitial Collagenase. September 1990, Volume 50, Number 17, pages 5431-5437, especially Figure 2.	1-7

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:		*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	*X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier application or patent published on or after the international filing date	*Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*&	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

03 March 2003 (03.03.2003)

Date of mailing of the international search report

24 MAR 2003

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

Box PCT

Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Carolyn Smith

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet x

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; It is covered by claims Nos.: 1-7 for Specie A(hemangiomas) and B (SEQ ID NO: 1)

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

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This application contains the following inventions or groups of inventions, which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Groups 1-104,648, claim(s) 1-7, drawn to a method for determining the presence or absence of a pathological (Specie A) cell in a patient via detection of polynucleotides that are at least 80% identical to listed sequences (Specie B). If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

Groups 104,649-105,060, claim(s) 8-12, drawn to an isolated nucleic acid molecules from Tables 2A-68, expression vectors, host cells, and polypeptides encoded by nucleic acid molecules with listed sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,061-105,472, claim(s) 13-14, drawn to an antibody that binds to a polypeptide encoded by a polynucleotide with sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,473-105,884, claim(s) 15, drawn to a method for targeting a compound to a pathological cell in a patient via administering an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,885-106,296, claim(s) 16-17, drawn to a method for determining the presence or absence of a pathological cell in a patient via contacting the sample with an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,297-106,708, claim(s) 18, drawn to a method for identifying a compound that modulates a pathology-associated polypeptide encoded by a polynucleotide that hybridizes to a sequence in Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,709-211,356, claim(s) 19, drawn to drug screening assay by administering a compound to a mammal or cell having a pathology (of Table 1) and comparing the level of gene expression of a polynucleotide that hybridizes to a sequence that is 80% identical to sequences as described in Tables 2A-68 (Species B) to gene expression in control cells or mammals. If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

This International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons indicated below:

The inventions listed as all Group Sets (Groups 1-211,356) do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

Groups 1-104,648 and Groups 105,472-211,356 are directed to methods or assays which vary in one or more of the following: reactants, steps, and/or goals which are not coextensive and which do not share the same technical feature. Groups 104,649-105,472 have two separate special technical features, a nucleic acid and an antibody, respectively. These are directed to different chemical entity types regarding the critical limitations featuring different structures and functions. The antibodies undergo recognition and binding reactions

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

wherein what is bound is different from what is bound by the compositions including the nucleic acids. Thus, in summary, each Group is directed to a different special technical feature and thus supports this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

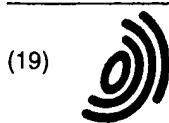
The claims in the Groups 1-104,648 and 106,709-211,356 include a series of species A directed to different pathologies which are listed in Table 1. Each of these types of pathologies are separate entities which affect patients differently, meaning each has its own special technical feature.

The claims in all Groups (1-211,356) include a series of species B directed to nucleic acid sequence listed (412 possibilities) which are considered separate as each defines its own special technical feature.

The first listed pathology (Specie A) and SEQ ID NO: 1 (Species B) will be automatically searched. For each additional Group with a specie combination elected, the fee is an additional \$210.00.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, PUBMED, BIOSIS, CAPLUS, MEDLINE, SCISEARCH, EMBASE searching terms: diagnosis, cancer, screen, modulator, pathological cell, patient, nucleic acid, tissue, mRNA, detect, probe, biochip, array, therapeutic



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 1 469 072 A2**

(12) **EUROPEAN PATENT APPLICATION**

(43) Date of publication:
20.10.2004 Bulletin 2004/43

(21) Application number: **04009160.5**

(22) Date of filing: **16.04.2004**

(51) Int Cl.⁷: **C12N 15/12, C12N 1/21,
C12N 5/10, C07K 16/28,
C12N 15/11, C12Q 1/68,
A61K 38/17, A61K 39/395,
A61K 31/7088, A61K 31/40,
G01N 33/68**

(84) Designated Contracting States:
**AT BE BG CH CY CZ DE DK EE ES FI FR GB GR
HU IE IT LI LU MC NL PL PT RO SE SI SK TR**
Designated Extension States:
AL HR LT LV MK

(30) Priority: **17.04.2003 EP 03008753
04.09.2003 EP 03019626**

(60) Divisional application:
04018640.5

(71) Applicant: **NeuroNova Aktiengesellschaft
80804 München (DE)**

(72) Inventors:
• **Barden, Nicholas
Sainte-Foy, Québec G1W 3H1 (CA)**
• **Sillaber, Inge
80802 Munich (DE)**
• **Paez-Pereda, Marcelo
80809 Munich (DE)**

(74) Representative: **VOSSIUS & PARTNER
Siebertstrasse 4
81675 München (DE)**

(54) **Means and methods for diagnosing and treating affective disorders**

(57) The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the

present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R.

The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases.

Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

EP 1 469 072 A2

Description

[0001] The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R. The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases. Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

[0002] Up to 10% of persons visiting a physician are afflicted with an affective disorder (also known as behavioural disorder, mood disorder). Nonetheless, most cases remain undiagnosed or inadequately treated. Affective disorders include among others, depression, anxiety, and bipolar disorder. These diseases are well described in the literature; see, for example, Diagnostic and Statistical Manual of Mental Disorders-4th Edition Text Revision (DMS-IV-TR), American Psychiatric Press, 2000.

Depression, also known as unipolar affective disorder, is characterized by a combination of symptoms such as lowered mood, loss of energy, loss of interest, feeling of physical illness, poor concentration, altered appetite, altered sleep and a slowing down of physical and mental functions resulting in a relentless feeling of hopelessness, helplessness, guilt, and anxiety. The primary subtypes of this disease are major depression, dysthymia (milder depression), and atypical depression. Other important forms of depression are premenstrual dysphoric disorder and seasonal affective disorder. Present treatment of depression consists of psychotherapy, antidepressant drugs, or a combination of both. Most antidepressive drugs target the transport of the neurotransmitters serotonin and/or norepinephrine, or the activity of the enzyme monoamine oxidase. They include: Selective serotonin-reuptake inhibitors (e.g., fluoxetine, paroxetine, sertraline, fluvoxamine), tricyclic antidepressants (e.g., amitriptyline, imipramine, desipramine, nortriptyline), monoamine oxidase inhibitors (e.g., phenelzine, isocarboxazid, tranylcypromine), and designer antidepressants such as mirtazapine, reboxetine, nefazodone. However, all existing antidepressive drugs possess shortcomings such as long latency until response, high degree of non-responders and undesirable side effects (Holsboer, Biol. Psychol. 57 (2001), 47-65). Therefore, a need exists in the medical community for new antidepressive drugs with improved pharmacological profile (Baldwin, Hum. Psychopharmacol. Clin. Exp. 16 (2001), S93-S99).

Anxiety disorders are defined by an excessive or inappropriate aroused state characterized by feelings of apprehension, uncertainty, or fear. They are classified according to the severity and duration of their symptoms and specific affective characteristics. Categories include: (1) Generalized anxiety disorder, (2) panic disorder, (3) phobias, (4) obsessive-compulsive disorder, (5) post-traumatic stress disorder, and (6) separation anxiety disorder. The standard treatment for most anxiety disorders is a combination of cognitive-behavioural therapy with antidepressant medication. Additional medications include benzodiazepines and buspirone.

[0003] Bipolar disorder, also known as manic-depression, is characterized by mood swings between periods of mania (i.e. mood elevation including exaggerated euphoria, irritability) and periods of depression. Bipolar disorder is classified according to the severity of the symptoms. Patients diagnosed with bipolar disorder type I suffer from manic or mixed episodes with or without major depression. In Bipolar Disorder type II, patients have episodes of hypomania and episodes of major depression. With hypomania the symptoms of mania (euphoria or irritability) appear in milder forms and are of shorter duration. The current drugs used to treat bipolar disorders are lithium, valproate and lamotrigine, which stimulates the release of the neurotransmitter glutamate. As with antidepressive drugs, they take weeks to become effective and can result in undesirable side effects, for example, high levels of lithium in the blood can be fatal. Compelling evidence suggest that affective disorders are biological diseases. However, there are no laboratory tests or other procedures that a common physician can use to make a definitive diagnosis. Instead, a specially trained physician or psychiatrist must diagnose the illness based on a group of symptoms that occur together. This process is often time consuming and laborious requiring several visits for the physician to perform a careful history of the symptoms that the patient is currently experiencing as well as any symptoms he or she has had in the past. Therefore,

an easy and effective method for the accurate diagnosis of affective disorders is of high interest to the medical community (Wittchen et al., J. Clin. Psychiatry 62, suppl. 26 (2001), 23-28).

Most patients afflicted with affective disorders have family antecedents and identical twins studies suggest a strong genetic component. For example, genetic mapping on an isolated population of the central valley of Costa Rica suggests a locus for severe bipolar disorder at chromosome 18q22-q23 (Freimer et al., Nature Genetics 12 (1996), 436-441). Moreover, genetic studies performed on the Old Order Amish population suggest that genes on chromosomes 6, 13, and 15 may contribute to the susceptibility of bipolar affective disorder (Ginns et al., Nature Genetics 12 (1996), 431-435). Recently, a genome-wide search in a homogenous population found in the Saguenay/Lac-St-Jean region of Quebec suggests the presence of a major locus for bipolar disorder on chromosome 12q23-q24 (Morissette et al., Am. J. Med. Genet. (Neuropsychiatr. Genet.) 88 (1999), 567-587). Susceptibility loci on chromosomes 5 and 21 were also found in this study. Other groups report minimal evidence for linkage in the region of 12q23 (Kelsoe et al., Proc. Natl. Acad. Sci. USA 98 (2001), 585-590; Sklar, Annu. Rev. Genomics Hum. Genet. 3 (2002), 371-413). Given the various loci mentioned in the above studies (e.g., links to chromosomes 5, 6, 12, 13, 15, 18, 21), a definite genetic link for affective diseases remains to be found.

[0004] Thus, although several genes have been assumed to be linked with affective disorders as mentioned hereinabove, however, no clear correlation has so far been shown. Since no well-suited medication nor diagnosis on a molecular level for affective disorders is available, there is a need for identifying a gene whose mutations cause the whole spectrum of affective disorders as well as for providing medicaments and methods for diagnosis and treatment of affective disorders.

[0005] Thus, the technical problem underlying the present invention is to provide means and methods for diagnosis and treating affective disorders.

[0006] The solution to said technical problem is achieved by providing the embodiments characterized in the claims.

[0007] Accordingly, the present invention relates to a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

(a) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 5'UTR region corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(b) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of the ATP-gated ion channel P2X7R, wherein in the exon as indicated in column "Exon" of the following Table A the amino acid residue as indicated in column "Amino acid residue" of Table A corresponding to the position as indicated in column "Position in wild-type" of Table A of the wild-type ATP-gated ion channel P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue

Table A

Exon	Amino acid residue	Position in wild-type
exon 3	R (Arg)	117
exon 5	G (Gly)	150
exon 6	E (Glu)	186
exon 6	L (Leu)	191
exon 8	R (Arg)	270
exon 13	I (Ile)	568
exon 13	R (Arg)	578

(c) a nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in exon 5 or 8 corresponding to position 32548 or position 37633 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide

(d) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted;

(e) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R, wherein in the intron as indicated in column "Intron" of the following Table B the nucleotide as indicated in column "Replaced nucleotide" of Table B

corresponding to the position as indicated in column "Position in wild-type" of Table B of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1 is replaced by another nucleotide

Table B

Intron	REPLACED NUCLEOTIDE	Position in wild-type
intron 1	G	3166
intron 1	C	24778
intron 1	C	24830
intron 3	A	26308
intron 3	G	26422
intron 4	G	32394
intron 4	T	32434
intron 5	A	32783
intron 6	G	35641
intron 6	A	35725
intron 6	T	36001
intron 7	G	36378
intron 7	T	36387
intron 7	G	36398
intron 9	C	47214
intron 11	T	47563
intron 12	C	54307
intron 12	G	54308

(f) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 3'UTR region corresponding to position 55169, 55170, 55171, 55917 or 54925 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(g) a nucleotide sequence comprising at least 20 or 21 nucleotides and comprising the mutations or deletions as defined in any one of (a) to (f);

(h) a nucleic acid sequence comprising a nucleotide sequence as shown in any one of SEQ ID NOs: 13 to 51;

(i) a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NOs: 5 to 12;

(j) a nucleotide sequence which hybridizes to a nucleotide sequence defined in any one of (a) to (g) or to the nucleotide sequence of (h) and having a mutation as defined in any one of (a) to (f); and

(k) a nucleic acid sequence being degenerate as a result of the genetic code to the nucleic acid sequence as defined in (j).

[0008] It has surprisingly been found that mutations in the P2X7R gene which encodes the ATP-gated ion channel P2X7R can cause the whole spectrum of affective disorders. Six different mutations in the 5'UTR of the P2X7R gene, seven different mutations in exons 3, 5, 6, 8 and 13 of the P2X7R gene leading to an amino acid replacement of the corresponding amino acid in the wild-type sequence of P2X7R depicted in SEQ ID NO: 3 or 4 and two mutations in exons 5 and 8 of said gene, respectively, leading to a replacement of a nucleotide by another nucleotide, a deletion of nucleotides in exon 13 of said gene, 18 mutations in introns 1, 3, 4, 5, 6, 7, 9, 11 and 12 and 5 mutations in the 3'UTR of the P2X7R gene have been identified to co-segregate with the affection status in 41 unrelated families affected with affective disorders. The term "affective disorder" when used in the context of the present invention means to include, but is not limited to, depression, anxiety, unipolar disorder, bipolar disorder type I, bipolar disorder type II, mania, attention deficit hyperactive disorder, substance abuse, and any other disorders affecting the normal behaviour, or mood of an individual.

Each mutation causes alterations that can explain affective disorders as shown in the Examples hereinbelow.

[0009] P2X7R is an ATP-gated ion channel belonging to the P2X ionotropic channel family. The gene was first isolated from rat brain (Surprenant et al., (1996), 272, 735-738; Genbank accession number NM_019256) and subsequently from a human monocyte library (Rassendren et al., J. Biol. Chem. 272 (1997), 5482-5486; Genbank accession numbers NM_002562, Y09561) by virtue of its sequence homology with the other members of the P2X family. It was later found that P2X7R corresponded to the unidentified P2Z receptor which mediates the permeabilising action of ATP on mast cells and macrophages (Dahlgvist and Diamant, Acta Physiol. Scand. 34 (1974), 368-384; Steinberg and Silverstein, J. Biol. Chem. 262 (1987), 3118-3122; Gordon, Biochem. J. 233 (1986), 309-319). The P2X7R has two hydrophobic membrane-spanning domains, an extracellular loop, and forms transmembrane ion channels. P2X7 receptors seem to function only in homooligomeric form and bear a pharmacological profile markedly different from other P2X homo- or heteromers (North and Surprenant, Annual Rev. Pharmacology Toxicology 40 (2000), 563-580). P2X7R requires levels of ATP in excess of 1 mM to achieve activation, whereas other P2X receptors activate at ATP concentrations of $\leq 100 \mu\text{M}$ (Steinberg et al., J. Biol. Chem. 262 (1987), 8884-8888; Greenberg et al., J. Biol. Chem. 263 (1988), 10337-10343) 32). While all P2X receptors demonstrate non-selective channel-like properties following ligation, the channels formed by the P2X7R can rapidly transform into pores that can allow the passage of molecules of up to 900 Dalton (Virginio et al., J. Physiol. 519 (1999), 335-346).

P2X7R is expressed in hematopoietic cells, mast cells and macrophages (Surprenant et al., Science 272 (1996), 3118-3122), where it is organized in tetrameric or hexameric form (Kim et al., J. Biol. Chem. 276 (2001), 23262-23267). P2X7R is *inter alia* involved in the regulation of the immune function and inflammatory response.

[0010] Activation of P2X7R by ATP in macrophages is associated with mitogenic stimulation of T cells (Baricordi et al., Blood 87 (1996), 682-690), the release of cytokines such as interleukin-1 β (Griffiths et al., J. Immunol. 154 (1995), 2821-2828), and formation of macrophage polykaryons (Falzoni et al., J. Clin. Invest. 95 (1995), 1207-1216). Stimulation of the P2X7R with ATP can also result in cell death by triggering massive transmembrane ion fluxes (particularly influx of Ca^{2+} and Na^{+} , and efflux of K^{+}) and the formation of non-selective plasma membrane pores (Di Virgilio et al., Cell Death Differ. 5 (1998), 191-199).

In the brain, P2X7R was originally thought to be restricted to microglia (resident macrophage of the brain) and ependymal cells rather than neurons (Collo et al., Neuropharmacology 36 (1997), 1277-1283) suggesting a role of P2X7R in neurodegeneration. However, P2X7R has since been found in neurons of the rat retina (Brandle et al., Brain Research Molecular Brain Res. 62 (1998), 106-109), cochlear ganglion cells (Brandle et al., Neuroscience Letters 273 (1999), 105-108), and presynaptic terminals of neurons throughout the brainstem and spinal cord (Deuchards et al., J. Neurosci. 21 (2001), 7143-7152). Subsequent studies also suggest that P2X7R regulates the release of neurotransmitters such as glutamate and GABA in neurons of the hippocampus (Armstrong et al., J. Neuroscience 22 (2002), 5938-5945, Sperlagh et al., J. Neurochem. 81 (2002), 1196-1211). Organisation of P2X7R in glial cells and astrocytes of the brain appears monomeric (Kim et al., J. Biol. Chem. 276 (2001), 23262-23267).

Several agonists and antagonists of P2X7R have been identified. Brilliant Blue (Jiang et al., Mol. Pharmacol. 58 (2000), 82-88), the isoquinolines 1-[N,O-Bis(5-isoquinolinesulfonyl)-N-methyl-L-tyrosyl]-4-phenylpiperazine and N-[1-[N-methyl-p-(5-isoquinolinesulfonyl)benzyl]-2-(4-phenylpiperazine)ethyl]-5-isoquinolinesulfonamide (Humphreys et al., Mol. Pharmacol., 54 (1998), 22-32), adamantane derivatives (WO 99/29660, WO 99/29661, WO 00/61569, WO 01/42194, WO 01/44170, WO 01/44213), substituted phenyl compounds (WO 00/71529), piperidine and piperazine derivatives (WO 01/46200) are antagonists of P2X7R while Oxidized ATP (oATP) acts as an irreversible inhibitor of the receptor (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203). Some of these antagonists are presently being evaluated for the treatment of inflammatory, immune, and cardiovascular diseases. BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate ($\text{C}_{24}\text{H}_{24}\text{N}_5\text{O}_{15}\text{P}_3$)) acts as agonist of P2X7R (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). WO 99/55901 describes a method for identifying compounds that modulate the activity of a mammalian purinoreceptor selected from the group consisting of P2X2, P2X3, P2X4, P2X5, P2X6 and P2X7 and suggests a role of said purinoreceptors in therapy of behavioural disorders such as epilepsy, depression and aging-associated degenerative diseases.

[0011] Mutant mice lacking P2X7R are healthy, fertile and demonstrate no overt phenotype. However, in contrast to their wild-type counterparts, LPS-activated peritoneal macrophages from *P2X7R*^{-/-} animals fail to generate mature interleukin-1 β (IL-1 β) when challenged with ATP suggesting an inability of peritoneal macrophages to release IL-1 in response to ATP (Solle et al., J. Biol. Chem. 276 (2001), 125-132). A detailed behavioural study of the *P2X7R*^{-/-} mice was not performed. In humans, a Glu-496 to Ala polymorphism leads to the loss of P2X7 function (Gu et al., J. Biol. Chem. 276 (2001), 11135-11142) and is associated with B-cell chronic lymphocytic leukaemia (Thunberg, et al., The Lancet 360 (2002), 1935-1939). Additional polymorphisms in the putative P2X7R promoter region, and coding region have been reported (Li et al., FEBS Lett. 531 (2002), 127-131; EP 1199372).

Despite the abundant literature concerning P2X7R, a role in affective disorders has never been suggested or alluded to in the prior art.

[0012] Before the present invention is described in detail, it is to be understood that this invention is not limited to

the particular methodology, protocols, cell lines, vectors, and reagents described herein as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art.

Preferably, the terms used herein are defined as described in "A multilingual glossary of biotechnological terms: (IUPAC Recommendations)", Leuenberger, H.G.W, Nagel, B. and Kölbl, H. eds. (1995), Helvetica Chimica Acta, CH-4010 Basel, Switzerland).

[0013] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. Several documents are cited throughout the text of this specification. Each of the documents cited herein (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the", include plural referents unless the context clearly indicates otherwise. Thus, for example, reference to "a reagent" includes one or more of such different reagents, and reference to "the method" includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[0014] In accordance with the present invention, the term "nucleic acid sequence" means the sequence of bases comprising purine- and pyrimidine bases which are comprised by nucleic acid molecules, whereby said bases represent the primary structure of a nucleic acid molecule. Nucleic acid sequences include DNA, cDNA, genomic DNA, RNA, synthetic forms and mixed polymers, both sense and antisense strands, or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those skilled in the art.

[0015] When used herein, the term "polypeptide" means a peptide, a protein, or a polypeptide which encompasses amino acid chains of a given length, wherein the amino acid residues are linked by covalent peptide bonds. However, peptidomimetics of such proteins/polypeptides wherein amino acid(s) and/or peptide bond(s) have been replaced by functional analogs are also encompassed by the invention as well as other than the 20 gene-encoded amino acids, such as selenocysteine. Peptides, oligopeptides and proteins may be termed polypeptides. The terms polypeptide and protein are often used interchangeably herein. The term polypeptide also refers to, and does not exclude, modifications of the polypeptide, e.g., glycosylation, acetylation, phosphorylation and the like. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature.

[0016] The term "position" used in accordance with the present invention means the position of either an amino acid within an amino acid sequence depicted herein or the position of a nucleotide within a nucleic acid sequence depicted herein.

[0017] The term "ATP-gated ion channel P2X7R", in accordance with this invention, denotes a polypeptide which can be classified as a member of the P2X ionotropic receptor family. They are also known as purinergic receptors. P2X receptors are ligand-gated ion channels. The ligand for these receptors may be ATP and/or another natural nucleotide such as ADP, UTP and UDP, or a synthetic nucleotide such as 2-methylthioATP. The criteria for the classification are: (1) a sequence homology that is higher than 39% across the family or different species; (2) signal transduction mechanism involving ion conductance (Khakh et al., Pharmacol Rev. 253 (2001), 107-18). Accordingly, the term "ATP-gated ion channel P2X7R" is interchangeable with the terms "ionotropic receptor" or "purinergic receptor". Preferably, the term "ATP-gated ion channel P2X7R" denotes a polypeptide which can be classified as an ATP-gated ion channel P2X7R on the basis of one or more structural and/or functional characteristics, preferably those described above. Structural characteristics refer to certain structural features which allow to classify a polypeptide as being a P2X7R protein. One such feature is the amino acid sequence. In the context of the present invention a polypeptide is classified as an ATP-gated ion channel P2X7R if it shows a certain degree of sequence identity over its own length to the amino acid sequence of the human P2X7R protein depicted in SEQ ID NO: 3 or 4. This degree of sequence identity is at least 40%, more preferably at least 50%, even more preferably at least 60%, at least 70%, at least 80%, at least 90% or at least 95%. It is particularly preferred that the degree of sequence identity is at least 65%.

[0018] Moreover, structural characteristics of P2X7R proteins are two hydrophobic membrane-spanning domains, an extra cellular loop which could be analyzed by using the program TMPRED (Hofmann Biol. Chem. 347 (1993), 166) or TMHMM (Krogh J. Mol. Bio. 305 (2001), 567-580). Additionally, P2X7R may exist as a single polypeptide, as dimer, tetramer or the like.

[0019] Thus, in the context of the present invention a protein is preferably classified as a P2X7R protein if it displays at least one of the above-mentioned structural characteristics. Functional characteristics refer to properties related to the biological activity of the P2X7R protein. In particular, P2X7R is an ATP-gated ion channel which allows calcium and sodium ions to pass from extracellular solution to intracellular solution, and allows potassium ions to pass from

intracellular to extracellular solution. Moreover, the ATP-gated ion channel P2X7R forms naturally a homooligomeric form. The characteristics of P2X7R receptor proteins can be determined as mentioned hereinbelow. The term "ATP-gated ion channels P2X7R" comprises functional and non-functional forms of the ATP-gated ion channels P2X7R. A functional ATP-gated ion channel P2X7R is understood to be a P2X7R protein which has at least one of the above-mentioned functional characteristics which can be measured by methods known in the art. A non-functional ATP-gated ion channel P2X7R is a protein which can be classified as a P2X7R protein due to structural characteristics as described above but which has lost at least one, preferably all, functional characteristics of a P2X7R protein as described above. Non-functionality of the P2X7R protein can, e.g., be determined by measuring whether calcium and sodium ions can flow into cells or whether potassium ions can exit from cells. Thus, it is possible to determine the occurrence of a mutation in the ATP-gated ion channel P2X7R by measuring either calcium and/or sodium influx or efflux of cells. Cells harbouring a mutation in the P2X7R gene show an altered ion influx and/or efflux in comparison to cells harbouring a wild-type P2X7R protein.

Additionally, there are different methods that could be used to determine whether the P2X7R is functional or non-functional, for example, altered. One method consists of measuring the rate of ATP-induced incorporation of ethidium into cells, e.g. cells isolated from an individual. Ethidium is incorporated into the cells through P2X7R pores, when the pore formation is activated by ATP. Cells are then incubated with or without ATP in the presence of ethidium, then they are analyzed by flow cytometry. Ethidium fluorescence is measured and compared in the presence or absence of ATP. If the P2X7R has lower activity, the ethidium fluorescence induced by ATP will be lower than in control cells. Such a method was used to verify P2X7R activity in isolated B-lymphocytes and T-lymphocytes from leukaemia patients (Wiley et al., *Lancet* 359 (2002), 1114-1119). Briefly, isolated cells are incubated in 1 ml of Hepes buffered potassium chloride at 37°C with continuous stirring. Ethidium is then added at a concentration of 25 mol/l, followed 40 seconds later by the addition of 10 µl of 100 mmol/l ATP stock. Cells are analyzed at 1,000 events/s by flow cytometry using a Coulter Elite flow cytometer (Coulter, Hialeah, FL) with argon laser excitation at 488 nm. Fluorescent emission was collected using a 590-nm long-pass filter. The linear mean channel fluorescence intensity for each gated subpopulation over successive 5-s intervals was analyzed with the use of Win-MDI software (Joseph Trotter, version 2.7) and plotted against time.

Another method of determining P2X7R activity is to measure calcium entry into isolated cells incubated with fluorescent dyes that emit only upon binding to calcium. The cells have to be loaded with the dye and then the calcium entry has to be stimulated. Examples of such dyes include Fura-2, Calcium green, calcium orange, calcium crimson (all available from Molecular Probes). Methods of measuring calcium transport are well known in the art; see for example, Takahashi et al., *Physiol Rev.* 79 (1999), 1089-1125. Furthermore, calcium entry into the cells produces changes in the membrane electric potential. This changes can be measured by electrophysiology (patch clamp) or by using dyes which are sensitive to voltage change. Such methods are also well known in the art, see for example, Gonzalez et al., *DDT* 4 (1999), 431-439; González and Tsien, *Chemistry & Biology* 4 (1997), 269-277; González and Tsien, *Biophysical Journal* 69 (1995), 1272-1280.

Yet another method is to measure uptake of ¹³³Ba²¹. Ba²¹ is a good surrogate for Ca²¹ and once inside the cell is neither pumped nor sequestered by transport ATPases. Ba²¹ uptake can be measured over 60 s using ¹³³BaCl₂ (final concentration, 0.2 mM). At time 0, a prewarmed stock solution of ¹³³Ba²¹ (0.4 mM and 1 µCi/ml) is added in equal volumes to prewarmed isolated cells in 150 mM KCl with HEPES (pH 7.4) at 37°C. ATP (1 mM) is added either 10 minutes before or simultaneously with the ¹³³Ba²¹ isotope. Aliquots of 0.8 ml are taken at time points between 0 and 60 s and are immediately mixed with 0.2 ml of ice-cold 50 mM MgCl₂ (in KCl-HEPES medium) that had been previously layered over 250 µl of oil mixture (di-n-butyl phthalate and di-iso-octyl phthalate, 7:3 vol/vol) and then centrifuged at 8,000 g for 30 s. The supernatants and the oil are aspirated, and the cell pellets are counted in a Wallac Wizard 3 automatic gamma-counter or in any other suitable gamma measuring unit.

[0020] The present invention is based on the finding that mutations of different kinds in the P2X7R gene are linked to the occurrence of affective disorders. The first type of mutations are mutations in the 5'UTR. Examples of such mutations are single nucleotide replacements at positions corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as described in SEQ ID NO: 1.

[0021] The position with respect to nucleotide sequences mentioned herein refer to the sequence shown in SEQ ID NO: 1. This sequence represents the nucleic acid sequence of the P2X7R gene encoding the ATP-gated ion channel P2X7R. It is possible for the skilled person to identify the position in the genomic sequence corresponding to a position in SEQ ID NO: 1 by aligning the sequences. Moreover, the exact locations of the exons and introns are indicated in SEQ ID NO: 1 hereinbelow. Additionally, the person skilled in the art is able to identify exons and introns of the P2X7R gene by comparing SEQ ID NO: 1 with SEQ ID NO: 2 which shows the cDNA sequence of the P2X7R gene.

[0022] Preferably, at position 362 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a thymine (T) is replaced by another nucleotide, preferably a purine base. More preferably, at said position said thymine is replaced by a pyrimidine base. Particularly preferred, said thymine is replaced by a cytosine (C).

[0023] At position 532 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a thymine

(T) is preferably replaced by another nucleotide, preferably a pyrimidine base. More preferably, at said position said thymine is replaced by a purine base. Particularly preferred, said thymine is replaced by a guanine (G).

[0024] The adenine (A) residues at positions 1100 and 1122, respectively, in the 5'UTR of the genomic sequence of the P2X7R gene is preferably replaced by a pyrimidine base. More preferably, said adenine is replaced by a purine base and particularly preferred said adenine is replaced by a guanine (G).

[0025] At position 1171 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a cytidine (C) is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, said cytidine is replaced by a purine base and even more preferred, said cytidine is replaced by a guanine (G).

[0026] The guanine at position 1702 in the 5'UTR of the genomic sequence of the gene P2X7R depicted in SEQ ID NO: 1 is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, said guanine is replaced by a purine base and particularly preferred it is replaced by an adenine (A).

[0027] A second type of mutation found in the P2X7R gene are mutations in exons which lead to amino acid substitutions in the corresponding amino acid sequence. These are the mutations listed under item (b), supra. In this context, the term "an amino acid residue as indicated in column 'Amino acid residue' of Table A corresponding to position X of the wild-type ATP-gated ion channel P2X7R as depicted in column 'Position in wild-type' "has the following meaning: The amino acid residue in question would be located at position X in the sequence of SEQ ID NO: 3 or 4 if the sequence in which said amino acid residue occurs is compared and aligned with the amino acid sequence of SEQ ID NO: 3 or 4. The amino acid sequence shown in SEQ ID NO: 3 or 4 is the amino acid sequence of the human P2X7R gene and is used as a reference sequence in the present invention.

In order to determine whether an amino acid residue or nucleotide residue in a given P2X7R sequence corresponds to a certain position in the amino acid sequence or nucleotide sequence of SEQ ID NO: 1, 3 or 4, the skilled person can use means and methods well-known in the art, e.g., alignments, either manually or by using computer programs such as those mentioned further down below in connection with the definition of the term "hybridization" and degrees of homology.

[0028] For example, BLAST2.0, which stands for Basic Local Alignment Search Tool (Altschul, Nucl. Acids Res. 25 (1997), 3389-3402; Altschul, J. Mol. Evol. 36 (1993), 290-300; Altschul, J. Mol. Biol. 215 (1990), 403-410), can be used to search for local sequence alignments. BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying similar sequences. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP). An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user. The BLAST approach is to look for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output.

Analogous computer techniques using BLAST (Altschul (1997), loc. cit.; Altschul (1993), loc. cit.; Altschul (1990), loc. cit.) are used to search for identical or related molecules in nucleotide databases such as GenBank or EMBL. This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score which is defined as:

$$\frac{\% \text{sequence identity} \times \% \text{maximum BLAST score}}{100}$$

and it takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1-2% error; and at 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

[0029] As mentioned above, the second group of mutations identified in the P2X7R gene are mutations in the exons of the P2X7R gene which lead to amino acid substitutions. In this respect SEQ ID NO 2 shows the cDNA sequence of the P2X7R gene. In exon 3 at position 117 of the corresponding wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 an arginine (R) residue is replaced by another amino acid residue, preferably by an aliphatic, acidic or basic amino acid residue. More preferably, by an aromatic amino acid residue which is particularly preferred to be a tryptophane (W). The resulting polypeptide is shown in SEQ ID NO: 5.

[0030] In exon 5 at position 150 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 a glycine (G) residue is replaced by another amino acid residue, preferably by an aliphatic, aromatic or acidic amino acid

residue. More preferably, by a basic amino acid residue and particularly preferred by an arginine (R). The resulting polypeptide is shown in SEQ ID NO: 6.

[0031] At position 186 in exon 6 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 a glutamate residue (E) is replaced by another amino acid residue, preferably by an aliphatic, aromatic or acidic amino acid residue. More preferably, said glutamate is replaced by a basic amino acid residue which is particularly preferred a lysine (K). The resulting polypeptide is shown in SEQ ID NO: 7.

[0032] In exon 6 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 at position 191 a leucine residue (L) is replaced by another amino acid residue. Said amino acid residue is preferably an aliphatic, acidic or basic amino acid residue. More preferably, said amino acid residue is an aromatic amino acid residue which is particularly preferred to be a proline (P). The resulting polypeptide is shown in SEQ ID NO: 8.

[0033] In exon 8 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 at position 270 an arginine residue (R) is replaced by another amino acid residue. Said amino acid residue is preferably an aromatic, acidic or basic amino acid residue. More preferably, said amino acid residue is an aliphatic amino acid residue which is particularly preferred to be a cysteine (C). The resulting polypeptide is shown in SEQ ID NO: 9.

[0034] At position 568 in exon 13 of the wild-type amino acid residue of P2X7R depicted in SEQ ID NO: 3 or 4 an isoleucine (I) residue is replaced by another amino acid residue. More preferably, said isoleucine is replaced by an aromatic, basic or acidic amino acid residue. Even more preferred, said isoleucine is replaced by an aliphatic amino acid residue which is particularly preferred to be an asparagine (N). The resulting polypeptide is shown in SEQ ID NO: 10.

[0035] In exon 13 at position 578 in the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 an argine residue (R) is replaced by another amino acid residue. Said amino acid residue is preferably an aromatic, acidic or basic amino acid residue. More preferably, it is an aliphatic amino acid residue and particularly preferred it is a glutamine (Q) residue. The resulting polypeptide is shown in SEQ ID NO: 12.

[0036] It is envisaged that the above-mentioned mutations in the exons of the P2X7R gene occur due to point mutations caused by, e.g. chemical and/or physical means or inaccuracy of the replication complex followed by a failure of the reparation machinery of a cell, can result in a change of a single codon. Possible types of point mutations are transitions, i.e. change of a purine or pyrimidine base for another purine or pyrimidine base, e.g. adenine to guanine or thymidine to cytosine or transversions, i.e. change of a purine or pyrimidine base for another pyrimidine or purine base, e.g., adenine to thymidine or guanine to cytosine. Additionally a point mutation can also be caused by insertion or deletion of one or more nucleotides.

[0037] The mutations leading to the replacement of the amino acids as mentioned hereinabove and hereinbelow are indicated in Table 1 hereinbelow.

[0038] The third group of mutations in the P2X7R gene has been identified to be in exons 5 and 8 of the P2X7R gene depicted in SEQ ID NO: 1 and to be silent, i.e. they do not lead to amino acid changes. In particular, at position 32548 in exon 5 of the wild-type genomic sequence P2X7R gene depicted in SEQ ID NO: 1 a cytidine residue is replaced by another nucleotide. Said nucleotide is preferably a pyrimidine base and particularly preferred a thymine. The exchange of the cytidine residue at position 32548 in exon 5 of the P2X7R gene by another nucleotide preferably does not lead to the replacement of the amino acid cysteine by another amino acid residue.

[0039] In exon 8 of the wild-type P2X7R gene depicted in SEQ ID NO: 1 at position 37633 a cytidine residue is replaced by another nucleotide residue. Said nucleotide residue is preferably a pyrimidine base and particularly preferred thymine. Due to this replacement the amino acid aspartate (D) encoded by the respective codon in which at position 37633 a replacement has taken place is preferably not replaced by another amino acid residue.

The above-mentioned mutations in exons 5 and 8 at positions 32548 and 37633, respectively; of the wild-type P2X7R gene depicted in SEQ ID NO: 1 are mutations at the third position of a triplet codon, i.e. at the wobble base, which lead to so-called silent mutations. Silent mutations do normally not lead to a change of the amino acid due to the degeneracy of the genetic code, i.e. 64 triplets encode at all 20 naturally occurring amino acids. However, said silent mutations lead to a change in the codon encoding its respective amino acids insofar that the newly generated codon may not fit so well into the codon usage of an organism. Namely, the newly generated codon is not translated by the ribosome with the same efficiency as the "old" codon. This may lead to insufficient amounts of the corresponding polypeptide causing an distinct phenotype.

[0040] The fourth group of mutations in the P2X7R gene described hereinabove in item (d) is a deletion of 7 amino acids corresponding to positions 488 to 494 of the wild-type P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4. Thus, the present invention also relates to nucleic acid sequences encoding a P2X7R protein in which amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted. This means, according to the present invention, that a fragment encompassing amino acid positions 488 to 494 of the corresponding wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4 is deleted which results in a shortened polypeptide. An example for such a shortened polypeptide is depicted in SEQ ID NO: 11. This type of mutation as described herein preferably encodes a non-functional ATP-gated ion channel P2X7R. In the present in-

vention the deletion of a fragment encompassing amino acids 488 to 494 of the wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4 is the result of a deletion in exon 13. The resulting protein depicted in SEQ ID NO: 11 lacks amino acids 488 to 494 of the corresponding wild type amino acid sequence depicted in SEQ ID NO: 3 or 4 such that amino acid position 494 of the deleted polypeptide depicted in SEQ ID NO: 11 corresponds to amino acid position 502 of the wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4. Preferably, the nucleic acid sequence of the invention encodes a P2X7R polypeptide in which exactly amino acids corresponding to positions 488 to 494 of SEQ ID NO: 3 or 4 are deleted. However, also mutants are comprised in which either more or less amino acids within the P2X7R amino acid sequence set forth in SEQ ID NO: 3 or 4 may be deleted due to, for example, atypical splicing or deletion of nucleotides of the nucleic acid molecule encoding P2X7R or wrong posttranslational processes, as long as the P2X7R ATP-gated ion channel is non-functional. For example, it is also possible that further amino acids preceding amino acid position 488 or amino acids succeeding amino acid position 494 may be deleted or that less amino acids are deleted.

Preferably at least one, more preferably at least two, even more preferably at least three and most preferably at least 5 amino acid residues are further deleted upstream from the position corresponding to amino acid residue 488 and/or downstream of the position corresponding to amino acid residue 494 of SEQ ID NO: 3 or 4.

However, it is preferred that not more than 20, preferably not more than 15, even more preferably not more than 10 and most preferably not more than 7 amino acid residues are further deleted upstream of the position corresponding to amino acid residue 488 of SEQ ID NO: 3 or 4 or downstream of the position corresponding to amino acid residue 494 of SEQ ID NO: 3 or 4.

[0041] Another group of mutation (mentioned in item (e), supra) resides in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 of the wild-type genomic sequence of P2X7R depicted in SEQ ID NO: 1. Said mutations in said introns are point mutations as shown in Table B hereinabove and in Table 1, hereinbelow.

[0042] At the respective position indicated in the column "Position in wild-type" in Table B or indicated in the column "Polymorphism" in Table 1 the position of the nucleotide residue in the respective intron which is replaced by another nucleotide residue is shown. Accordingly, the term "a nucleotide as indicated in column "Intron" of the Table B corresponding to the position as indicated in column "Replaced nucleotide" of Table B corresponding to the position as indicated in column "Position in wild-type" of Table B is replaced by another nucleotide means that a nucleotide residue in a P2X7R encoding sequence would be located at position Y in SEQ ID NO: 1 when the P2X7R sequence is compared and aligned with the sequence of SEQ ID NO: 1.

If the nucleotide at the respective position is a purine base such as adenine or guanine it is preferred that due to a transition it is replaced by another purine base.

For example, an adenine is replaced by a guanine or a guanine is replaced by an adenine. If the nucleotide at the respective position is a pyrimidine base it is preferred that due to a transition it is replaced by another pyrimidine base. For example, thymine is replaced by a cytidine and a cytidine is replaced by a thymine.

[0043] It is also preferred that due to a transversion a purine base is replaced by a pyrimidine base or vice versa. For example, an adenine is replaced by a thymine and a guanine is replaced by a cytidine. Particularly preferred, said nucleotide in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 of the P2X7R gene depicted in SEQ ID NO: 1 is replaced by the nucleotide depicted in column "Polymorphism" of Table 1, hereinbelow.

[0044] A last group of mutations that has been identified relates to mutations which reside in the 3'UTR of the wild-type P2X7R gene depicted in SEQ ID NO: 1. The mutations were found at positions 54925, 55169, 55170, 55171 or 55917 respectively, of the wild-type P2X7R gene depicted in SEQ ID NO: 1.

[0045] At position 54925 a guanine residue was found to be replaced by another nucleotide. Preferably, said guanine residue is replaced by a pyrimidine base, more preferably by a purine base and particularly preferred by an adenine.

[0046] At position 55169 a cytidine residue is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, it is replaced by a purine base and particularly preferred, it is replaced by an adenine.

At positions 55170 and 55171 an adenine residue is replaced by another nucleotide residue, preferably by a purine base. More preferably, said adenine residue is replaced by a pyrimidine base and particularly preferred said adenine residue is replaced by a cytidine residue. It was also found that at position 55917 a cytidine residue is replaced by another nucleotide. Preferably, said nucleotide residue is a purine base, more preferably a pyrimidine base and particularly preferable a thymine.

[0047] As is evident from the above, not all identified mutations are located in exons or lead to a change in the amino acid sequence. Some of the mutations are located in the 5'UTR, the 3'UTR or in introns.

[0048] It is known that polymorphisms in promoter and enhancer regions can affect gene function by modulating transcription, particularly if they are situated at recognition sites for DNA binding proteins (Fishman et al., J. Clin. Invest. 102 (1998), 1369-1376). The term "polymorphism" which is used in the present invention means single nucleotide substitution, nucleotide insertion and nucleotide deletion which in the case of insertion and deletion includes insertion or deletion of one or more nucleotides at a position of a gene and corresponding alterations in expressed proteins. Polymorphisms in the 5' untranslated region (5'UTR) of genes can affect the efficiency with which proteins are trans-

lated. A representative example of this is in the c-myc gene where a C-G SNP that creates an internal ribosome entry site is associated with increased efficiency of c-myc translation and myeloma (Chappell et al., *Oncogene* 19 (2000), 4437-4440). Polymorphisms in the 3'UTR can affect gene function by altering the secondary structure of RNA and efficiency of translation or by affecting motifs in the RNA that bind proteins which regulate RNA degradation. Polymorphisms within introns can affect gene function by affecting RNA splicing resulting in aberrant polypeptides. Another way in which intronic polymorphisms can affect gene function is when they affect regulatory motifs within introns. Examples are the Sp1 binding site polymorphism within intron 1 of the COLIA1 gene (Mann et al., *J. Clin. Invest* 107 (2001), 899-907) and a repeat polymorphisms within the IL-1Ra gene (Keen et al., *Bone* 23 (1998), 367-371). Further examples between intronic SNPs and gene function are described in Caceres and Komblitt, *Trends Genet.* 4 (2002), 186-93. Example 4 on page 52, line 30 to page 53, line 51 of the text describes potential alternative splicing events and aberrant protein production associated with three SNPs disclosed in the application.

[0049] The nucleic acid sequences described hereinabove may comprise at least 56580 nucleotides, preferably at least 10000 nucleotides, at least 5000 nucleotides, at least 1000 nucleotides, at least 500 nucleotides, at least 100 nucleotides. More preferably, said nucleic acid sequences comprise at least 50 nucleotides and particularly preferred they comprise at least 20 or 21 nucleotides comprising the mutations or deletions as described hereinabove. Most preferably such a nucleic acid sequence has a sequence as depicted in any one of SEQ ID NOs: 13 to 51.

[0050] The nucleic acid sequences described hereinabove which comprise mutations in exons leading to a replacement of the corresponding amino acid sequence of the P2X7R wild-type polypeptide depicted in SEQ ID NO: 3 or 4 encode polypeptides shown in SEQ ID NOs: 5 to 10 and 12

Additionally, the nucleic acid sequences described hereinabove which comprise a deletion leading to a truncated polypeptide in comparison to the full-length polypeptide of the wild-type P2X7R polypeptide shown in SEQ ID NO: 3 or 4 is shown in SEQ ID NO: 11.

[0051] The present invention also relates to nucleic acid molecules which hybridize to one of the above described nucleic acid molecules and which shows a mutation as described hereinabove.

The term "hybridizes" as used in accordance with the present invention may relate to hybridizations under stringent or non-stringent conditions. If not further specified, the conditions are preferably non-stringent. Said hybridization conditions may be established according to conventional protocols described, for example, in Sambrook, Russell "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, N.Y. (2001); Ausubel, "Current Protocols in Molecular Biology", Green Publishing Associates and Wiley Interscience, N.Y. (1989), or Higgins and Hames (Eds.) "Nucleic acid hybridization, a practical approach" IRL Press Oxford, Washington DC, (1985). The setting of conditions is well within the skill of the artisan and can be determined according to protocols described in the art. Thus, the detection of only specifically hybridizing sequences will usually require stringent hybridization and washing conditions such as 0.1xSSC, 0.1% SDS at 65°C. Non-stringent hybridization conditions for the detection of homologous or not exactly complementary sequences may be set at 6xSSC, 1% SDS at 65°C. As is well known, the length of the probe and the composition of the nucleic acid to be determined constitute further parameters of the hybridization conditions. Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility. Hybridizing nucleic acid molecules also comprise fragments of the above described molecules. Such fragments may represent nucleic acid sequences which code for a non-functional ATP-gated ion channel P2X7R or a non-functional fragment thereof, and which have a length of at least 12 nucleotides, preferably at least 15, more preferably at least 18, more preferably of at least 21 nucleotides, more preferably at least 30 nucleotides, even more preferably at least 40 nucleotides and most preferably at least 60 nucleotides. Furthermore, nucleic acid molecules which hybridize with any of the aforementioned nucleic acid molecules also include complementary fragments, derivatives and allelic variants of these molecules. Additionally, a hybridization complex refers to a complex between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g., Cot or Rot analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., membranes, filters, chips, pins or glass slides to which, e.g., cells have been fixed). The terms complementary or complementarity refer to the natural binding of polynucleotides under permissive salt and temperature conditions by base-pairing. For example, the sequence "A-G-T" binds to the complementary sequence "T-C-A". Complementarity between two single-stranded molecules may be "partial", in which only some of the nucleic acids bind, or it may be complete when total complementarity exists between single-stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands.

The term "hybridizing sequences" preferably refers to sequences which display a sequence identity of at least 40%, preferably at least 50%, more preferably at least 60%, even more preferably at least 70%, particularly preferred at least 80%, more particularly preferred at least 90%, even more particularly preferred at least 95% and most preferably at least 97% identity with a nucleic acid sequence as described above encoding a P2X7R protein having a described mutation. Moreover, the term "hybridizing sequences" preferably refers to sequences encoding a P2X7R protein having a sequence identity of at least 40%, preferably at least 50%, more preferably at least 60%, even more preferably at least 70%, particularly preferred at least 80%, more particularly preferred at least 90%, even more particularly preferred at least 95% and most preferably at least 97% identity with an amino acid sequence of a P2X7R mutant as described herein above.

In accordance with the present invention, the term "identical" or "percent identity" in the context of two or more nucleic acid or amino acid sequences, refers to two or more sequences or subsequences that are the same, or that have a specified percentage of amino acid residues or nucleotides that are the same (e.g., 60% or 65% identity, preferably, 70-95% identity, more preferably at least 95% identity), when compared and aligned for maximum correspondence over a window of comparison, or over a designated region as measured using a sequence comparison algorithm as known in the art, or by manual alignment and visual inspection. Sequences having, for example, 60% to 95% or greater sequence identity are considered to be substantially identical. Such a definition also applies to the complement of a test sequence. Preferably the described identity exists over a region that is at least about 15 to 25 amino acids or nucleotides in length, more preferably, over a region that is about 50 to 100 amino acids or nucleotides in length. Those having skill in the art will know how to determine percent identity between/among sequences using, for example, algorithms such as those based on CLUSTALW computer program (Thompson Nucl. Acids Res. 2 (1994), 4673-4680) or FASTDB (Brutlag Comp. App. Biosci. 6 (1990), 237-245), as known in the art.

Although the FASTDB algorithm typically does not consider internal non-matching deletions or additions in sequences, i.e., gaps, in its calculation, this can be corrected manually to avoid an overestimation of the % identity. CLUSTALW, however, does take sequence gaps into account in its identity calculations. Also available to those having skill in this art are the BLAST and BLAST 2.0 algorithms (Altschul Nucl. Acids Res. 25 (1977), 3389-3402). The BLASTN program for nucleic acid sequences uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, and an expectation (E) of 10. The BLOSUM62 scoring matrix (Henikoff Proc. Natl. Acad. Sci., USA, 89, (1989), 10915) uses alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

[0052] Moreover, the present invention also relates to nucleic acid molecules the sequence of which is degenerate in comparison with the sequence of an above-described hybridizing molecule. When used in accordance with the present invention the term "being degenerate as a result of the genetic code" means that due to the redundancy of the genetic code different nucleotide sequences code for the same amino acid.

[0053] The present invention also related to nucleic acid molecules which comprise one or more of the above-described mutations or deletions.

[0054] The nucleic acid molecules according to the invention may be derived from any organism encoding corresponding P2X7R ATP-gated ion channels. For example, P2X7R ATP-gated ion channels have been reported in various organisms, for example, rat (see, Suprenant (1996), loc. cit.), mouse (Genbank Accession No. AJ 489297), xenopus (Genbank Accession No. AJ 345114), chicken (Genbank Accession No. BM 491404) or Bos Taurus (Genbank Accession No. AF 083073). In a preferred embodiment the nucleic acid molecule of the invention is derived from a vertebrate, preferably from a mammal, even more preferably the nucleic acid molecule is derived from rabbit or guinea pig, and most preferably the nucleic acid is derived from mouse, rat or human.

[0055] The nucleic acid molecule according to the invention may be any type of nucleic acid, e.g. DNA, RNA or PNA (peptide nucleic acid).

For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by Nielsen et al., Science 254:1497 (1991); and Egholm et al., Nature 365:666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point (T.sub.m) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

[0056] The DNA may, for example, be cDNA. In a preferred embodiment it is a genomic DNA. The RNA may be, e.g., mRNA. The nucleic acid molecule may be natural, synthetic or semisynthetic or it may be a derivative, such as

peptide nucleic acid (Nielsen, Science 254 (1991), 1497-1500) or phosphorothioates. Furthermore, the nucleic acid molecule may be a recombinantly produced chimeric nucleic acid molecule comprising any of the aforementioned nucleic acid molecules either alone or in combination.

[0057] Preferably, the nucleic acid molecule of the present invention is part of a vector. Therefore, the present invention relates in another embodiment to a vector comprising the nucleic acid molecule of this invention. Such a vector may be, e.g., a plasmid, cosmid, virus, bacteriophage or another vector used e.g. conventionally in genetic engineering, and may comprise further genes such as marker genes which allow for the selection of said vector in a suitable host cell and under suitable conditions.

[0058] The nucleic acid molecules of the present invention may be inserted into several commercially available vectors. Nonlimiting examples include plasmid vectors compatible with mammalian cells, such as pUC, pBluescript (Stratagene), pET (Novagen), pREP (Invitrogen), pCRTopo (Invitrogen), pcDNA3 (Invitrogen), pCEP4 (Invitrogen), pMC1 neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2neo, pBPV-1, pDBPVMNTneo, pRSVgpt, pRS-Vneo, pSV2-dhfr, pUCTag, pIZD35, pLXIN and pSIR (Clontech) and pIRES-EGFP (Clontech). Baculovirus vectors such as pBlueBac, BacPacz Baculovirus Expression System (CLONTECH), and MaxBacTM Baculovirus Expression System, insect cells and protocols (Invitrogen) are available commercially and may also be used to produce high yields of biologically active protein. (see also, Miller (1993), Curr. Op. Genet. Dev., 3, 9; O'Reilly, Baculovirus Expression Vectors: A Laboratory Manual, p. 127). In addition, prokaryotic vectors such as pcDNA2; and yeast vectors such as pYes2 are nonlimiting examples of other vectors suitable for use with the present invention. For vector modification techniques, see Sambrook and Russel (2001), loc. cit. Vectors can contain one or more replication and inheritance systems for cloning or expression, one or more markers for selection in the host, e. g., antibiotic resistance, and one or more expression cassettes.

The coding sequences inserted in the vector can be synthesized by standard methods, isolated from natural sources, or prepared as hybrids. Ligation of the coding sequences to transcriptional regulatory elements (e. g., promoters, enhancers, and/or insulators) and/or to other amino acid encoding sequences can be carried out using established methods.

[0059] Furthermore, the vectors may, in addition to the nucleic acid sequences of the invention, comprise expression control elements, allowing proper expression of the coding regions in suitable hosts. Such control elements are known to the artisan and may include a promoter, translation initiation codon, translation and insertion site or internal ribosomal entry sites (IRES) (Owens, Proc. Natl. Acad. Sci. USA 98 (2001), 1471-1476) for introducing an insert into the vector. Preferably, the nucleic acid molecule of the invention is operatively linked to said expression control sequences allowing expression in eukaryotic or prokaryotic cells. Particularly preferred are in this context control sequences which allow for correct expression in neuronal cells and/or cells derived from nervous tissue.

Control elements ensuring expression in eukaryotic and prokaryotic cells are well known to those skilled in the art. As mentioned above, they usually comprise regulatory sequences ensuring initiation of transcription and optionally poly-A signals ensuring termination of transcription and stabilization of the transcript. Additional regulatory elements may include transcriptional as well as translational enhancers, and/or naturally-associated or heterologous promoter regions. Possible regulatory elements permitting expression in for example mammalian host cells comprise the CMV-HSV thymidine kinase promoter, SV40, RSV-promoter (Rous sarcome virus), human elongation factor 1 α -promoter, CMV enhancer, CaM-kinase promoter or SV40-enhancer.

For the expression for example in nervous tissue and/or cells derived therefrom, several regulatory sequences are well known in the art, like the minimal promoter sequence of human neurofilament L (Charron, J. Biol. Chem. 270 (1995), 25739-25745). For the expression in prokaryotic cells, a multitude of promoters including, for example, the tac-lac-promoter, the lacUV5 or the trp promoter, has been described. Beside elements which are responsible for the initiation of transcription such regulatory elements may also comprise transcription termination signals, such as SV40-poly-A site or the tk-poly-A site, downstream of the polynucleotide. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pRc/CMV, pcDNA1, pcDNA3 (Invitrogen, as used, inter alia in the appended examples), pSPORT1 (GIBCO BRL) or pGEMHE (Promega), or prokaryotic expression vectors, such as lambda gt11.

[0060] An expression vector according to this invention is at least capable of directing the replication, and preferably the expression, of the nucleic acids and protein of this invention. Suitable origins of replication include, for example, the Col E1, the SV40 viral and the M 13 origins of replication. Suitable promoters include, for example, the cytomegalovirus (CMV) promoter, the iacZ promoter, the gai10 promoter and the Autographa californica multiple nuclear polyhedrosis virus (AcMNPV) polyhedral promoter. Suitable termination sequences include, for example, the bovine growth hormone, SV40, iacZ and AcMNPV polyhedral polyadenylation signals. Examples of selectable markers include neomycin, ampicillin, and hygromycin resistance and the like. Specifically-designed vectors allow the shuttling of DNA between different host cells, such as bacteria-yeast, or bacteria-animal cells, or bacteria-fungal cells, or bacteria invertebrate cells.

Beside the nucleic acid molecules of the present invention, the vector may further comprise nucleic acid sequences

encoding for secretion signals. Such sequences are well known to the person skilled in the art. Furthermore, depending on the expression system used leader sequences capable of directing the expressed polypeptide to a cellular compartment may be added to the coding sequence of the nucleic acid molecules of the invention and are well known in the art. The leader sequence(s) is (are) assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein, or a part thereof, into, inter alia, the extracellular membrane. Optionally, the heterologous sequence can encode a fusion protein including an C- or N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and, as desired, the collection and purification of the proteins, antigenic fragments or fusion proteins of the invention may follow. Of course, the vector can also comprise regulatory regions from pathogenic organisms.

Furthermore, said vector may also be, besides an expression vector, a gene transfer and/or gene targeting vector. Gene therapy, which is based on introducing therapeutic genes (for example for vaccination) into cells by ex-vivo or in-vivo techniques is one of the most important applications of gene transfer. Suitable vectors, vector systems and methods for in-vitro or in-vivo gene therapy are described in the literature and are known to the person skilled in the art; see, e.g., Giordano, Nature Medicine 2 (1996), 534-539; Schaper, Circ. Res. 79 (1996), 911-919; Anderson, Science 256 (1992), 808-813, Isner, Lancet 348 (1996), 370-374; Muhlhauser, Circ. Res. 77 (1995), 1077-1086; Wang, Nature Medicine 2 (1996), 714-716; WO 94/29469; WO 97/00957; Schaper, Current Opinion in Biotechnology 7 (1996), 635-640 or Verma, Nature 389 (1997), 239-242 and references cited therein.

The nucleic acid molecules of the invention and vectors as described herein above may be designed for direct introduction or for introduction via liposomes, or viral vectors (e.g. adenoviral, retroviral) into the cell. Additionally, baculoviral systems or systems based on vaccinia virus or Semliki Forest Virus can be used as eukaryotic expression system for the nucleic acid molecules of the invention. In addition to recombinant production, fragments of the protein, the fusion protein or antigenic fragments of the invention may be produced by direct peptide synthesis using solid-phase techniques (cf Stewart et al. (1969) Solid Phase Peptide Synthesis; Freeman Co., San Francisco; Merrifield, J. Am. Chem. Soc. 85 (1963), 2149-2154). In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer, Foster City CA) in accordance with the instructions provided by the manufacturer. Various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

[0061] The present invention in addition relates to a host transformed with a vector of the present invention or to a host comprising the nucleic acid molecule of the invention. Said host may be produced by introducing said vector or nucleotide sequence into a host cell which upon its presence in the cell mediates the expression of a protein encoded by the nucleotide sequence of the invention or comprising a nucleotide sequence or a vector according to the invention wherein the nucleotide sequence and/or the encoded polypeptide is foreign to the host cell.

By "foreign" it is meant that the nucleotide sequence and/or the encoded polypeptide is either heterologous with respect to the host, this means derived from a cell or organism with a different genomic background, or is homologous with respect to the host but located in a different genomic environment than the naturally occurring counterpart of said nucleotide sequence. This means that, if the nucleotide sequence is homologous with respect to the host, it is not located in its natural location in the genome of said host, in particular it is surrounded by different genes. In this case the nucleotide sequence may be either under the control of its own promoter or under the control of a heterologous promoter. The location of the introduced nucleic acid molecule or the vector can be determined by the skilled person by using methods well-known to the person skilled in the art, e.g., Southern Blotting. The vector or nucleotide sequence according to the invention which is present in the host may either be integrated into the genome of the host or it may be maintained in some form extrachromosomally. In this respect, it is also to be understood that the nucleotide sequence of the invention can be used to restore or create a mutant gene via homologous recombination.

[0062] Said host may be any prokaryotic or eukaryotic cell. Suitable prokaryotic/bacterial cells are those generally used for cloning like *E. coli*, *Salmonella typhimurium*, *Serratia marcescens* or *Bacillus subtilis*. Said eukaryotic host may be a mammalian cell, an amphibian cell, a fish cell, an insect cell, a fungal cell, a plant cell or a bacterial cell (e.g., *E. coli* strains HB101, DH5a, XL1 Blue, Y1090 and JM101). Eukaryotic recombinant host cells are preferred. Examples of eukaryotic host cells include, but are not limited to, yeast, e.g., *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis* or *Pichia pastoris* cells, cell lines of human, bovine, porcine, monkey, and rodent origin, as well as insect cells, including but not limited to, *Spodoptera frugiperda* insect cells and *Drosophila*-derived insect cells as well as zebra fish cells. Mammalian species-derived cell lines suitable for use and commercially available include, but are not limited to, L cells, CV-1 cells, COS-1 cells (ATCC CRL 1650), COS-7 cells (ATCC CRL 1651), HeLa cells (ATCC CCL 2), C1271 (ATCC CRL 1616), BS-C-1 (ATCC CCL 26) and MRC-5 (ATCC CCL 171).

[0063] In a particularly preferred embodiment said mammalian cell is a neuronal cell and/or a cultured cell like, inter alia, a HEK 293 (human embryonic kidney) cell, a CHO, HeLa, NIH3T3, BHK, PC12 cell or a neuronal stem cell preferably derived from a mammal and more preferably from a human.

In another more preferred embodiment said amphibian cell is an oocyte. In an even more preferred embodiment said oocyte is a frog oocyte, particularly preferred a *Xenopus laevis* oocyte.

[0064] In a more preferred embodiment, the host according to the invention is a non-human transgenic organism. Said non-human organism may be a mammal, amphibian, a fish, an insect, a fungus or a plant. Particularly preferred non-human transgenic animals are *Drosophila* species, *Caenorhabditis elegans*, *Xenopus* species, zebra fish, *Spodoptera frugiperda*, *Autographa californica*, mice and rats. Transgenic plants comprise, but are not limited to, wheat, tobacco, parsley and *Arabidopsis*. Transgenic fungi are also well known in the art and comprise, inter alia, yeasts, like *S. pombe* or *S. cerevisiae*, or *Aspergillus*, *Neurospora* or *Ustilago* species or *Pichia* species.

[0065] In another embodiment, the present invention relates to a method for producing the polypeptide encoded by a nucleic acid molecule of the invention comprising culturing/raising the host of the invention and isolating the produced polypeptide.

A large number of suitable methods exist in the art to produce polypeptides in appropriate hosts. If the host is a unicellular organism or a mammalian or insect cell, the person skilled in the art can revert to a variety of culture conditions that can be further optimized without an undue burden of work. Conveniently, the produced protein is harvested from the culture medium or from isolated (biological) membranes by established techniques. Furthermore, the produced polypeptide may be directly isolated from the host cell. Said host cell may be part of or derived from a part of a host organism, for example said host cell may be part of the CNS of an animal or the harvestable part of a plant. Additionally, the produced polypeptide may be isolated from fluids derived from said host, like blood, milk or cerebrospinal fluid.

[0066] Additionally the present invention relates to polypeptides depicted in SEQ ID NOs: 5 to 12 which are encoded by the nucleic acid molecules of the invention or produced by the method of the invention. The polypeptide of the invention may accordingly be produced by microbiological methods or by transgenic mammals. It is also envisaged that the polypeptide of the invention is recovered from transgenic plants. Alternatively, the polypeptide of the invention may be produced synthetically or semi-synthetically.

For example, chemical synthesis, such as the solid phase procedure described by Houghton Proc. Natl. Acad. Sci. USA (82) (1985), 5131-5135, can be used. Another method is in vitro translation of mRNA. A preferred method involves the recombinant production of protein in host cells as described above. For example, nucleotide acid sequences comprising all or a portion of any one of the nucleotide sequences according to the invention can be synthesized by PCR, inserted into an expression vector, and a host cell transformed with the expression vector. Thereafter, the host cell is cultured to produce the desired polypeptide, which is isolated and purified. Protein isolation and purification can be achieved by any one of several known techniques; for example and without limitation, ion exchange chromatography, gel filtration chromatography and affinity chromatography, high pressure liquid chromatography (HPLC), reversed phase HPLC, preparative disc gel electrophoresis. In addition, cell-free translation systems can be used to produce the polypeptides of the present invention. Suitable cell-free expression systems for use in accordance with the present invention include rabbit reticulocyte lysate, wheat germ extract, canine pancreatic microsomal membranes, *E. coli* S30 extract, and coupled transcription/translation systems such as the TNT-system (Promega). These systems allow the expression of recombinant polypeptides or peptides upon the addition of cloning vectors, DNA fragments, or RNA sequences containing coding regions and appropriate promoter elements. As mentioned supra, protein isolation/purification techniques may require modification of the proteins of the present invention using conventional methods. For example, a histidine tag can be added to the protein to allow purification on a nickel column. Other modifications may cause higher or lower activity, permit higher levels of protein production, or simplify purification of the protein.

[0067] In a further embodiment, the present invention relates to an antibody specifically directed to a polypeptide of the invention, wherein said antibody specifically reacts with an epitope generated and/or formed by the mutation in the ATP-gated ion channel P2X7R selected from the group consisting of:

(i) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein the R (Arg), G (Gly), E (Glu), L (Leu), R (Arg), I (Ile) or R (Arg) residue corresponding to position 117, 150, 186, 191, 270, 568 or 578 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue; and

(ii) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted.

[0068] With respect to preferred embodiments of (i) and (ii) the same applies as described above in connection with the nucleic acid molecules. The term "specifically" in this context means that the antibody reacts with the mutant P2X7R protein but not with a wild-type P2X7R protein. Preferably this term also means that such an antibody does not bind to other mutant forms of the P2X7R protein, in particular those described herein. Whether the antibody specifically reacts as defined herein above can easily be tested, inter alia, by comparing the reaction of said antibody with a wild-type ATP-gated ion channel P2X7R (or a subunit or a fragment thereof) with the reaction of said antibody with a mutant

P2X7R polypeptide of the invention.

The antibody of the present invention can be, for example, polyclonal or monoclonal. The term "antibody" also comprises derivatives or fragments thereof which still retain the binding specificity. Techniques for the production of antibodies are well known in the art and described, e.g. in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. These antibodies can be used, for example, for the immunoprecipitation and immunolocalization of the polypeptides of the invention as well as for the monitoring of the presence of such polypeptides, for example, in recombinant organisms or in diagnosis. They can also be used for the identification of compounds interacting with the proteins according to the invention (as mentioned herein below). For example, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of the polypeptide of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13).

The present invention furthermore includes chimeric, single chain and humanized antibodies, as well as antibody fragments, like, inter alia, Fab fragments. Antibody fragments or derivatives further comprise F(ab')₂, Fv or scFv fragments; see, for example, Harlow and Lane, loc. cit.. Various procedures are known in the art and may be used for the production of such antibodies and/or fragments. Thus, the (antibody) derivatives can be produced by peptidomimetics. Further, techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778) can be adapted to produce single chain antibodies to polypeptide(s) of this invention. Also, transgenic animals may be used to express humanized antibodies to polypeptides of this invention. Most preferably, the antibody of this invention is a monoclonal antibody. For the preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples for such techniques include the hybridoma technique (Köhler and Milstein Nature 256 (1975), 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96). Techniques describing the production of single chain antibodies (e.g., US Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptides as described above. Furthermore, transgenic mice may be used to express humanized antibodies directed against said immunogenic polypeptides. It is in particular preferred that the antibodies/antibody constructs as well as antibody fragments or derivatives to be employed in accordance with this invention or capable to be expressed in a cell. This may, inter alia, be achieved by direct injection of the corresponding proteinaceous molecules or by injection of nucleic acid molecules encoding the same. Furthermore, gene therapy approaches are envisaged. Accordingly, in context of the present invention, the term "antibody molecule" relates to full immunoglobulin molecules as well as to parts of such immunoglobulin molecules. Furthermore, the term relates, as discussed above, to modified and/or altered antibody molecules, like chimeric and humanized antibodies. The term also relates to monoclonal or polyclonal antibodies as well as to recombinantly or synthetically generated/synthesized antibodies. The term also relates to intact antibodies as well as to antibody fragments thereof, like, separated light and heavy chains, Fab, Fab/c, Fv, Fab', F(ab')₂. The term "antibody molecule" also comprises bifunctional antibodies and antibody constructs, like single chain Fvs (scFv) or antibody-fusion proteins. It is also envisaged in context of this invention that the term "antibody" comprises antibody constructs which may be expressed in cells, e.g. antibody constructs which may be transfected and/or transduced via, inter alia, viruses or vectors. It is in particular envisaged that such antibody constructs specifically recognize the polypeptides of the present invention. It is, furthermore, envisaged that said antibody construct is employed in gene therapy approaches.

[0069] The present invention relates also to an aptamer specifically binding to a polypeptide according to the invention wherein said aptamer reacts with an epitope of a polypeptide of the present invention. The present invention furthermore relates to an aptamer specifically directed to a corresponding nucleic acid molecule according to the invention.

In accordance with the present invention, the term "aptamer" means nucleic acid molecules that can bind to target molecules. Aptamers commonly comprise RNA, single stranded DNA, modified RNA or modified DNA molecules. The preparation of aptamers is well known in the art and may involve, inter alia, the use of combinatorial RNA libraries to identify binding sides (Gold, Ann. Rev. Biochem. 64 (1995), 763-797).

[0070] Furthermore, the present invention relates to a primer or pair of primers capable of specifically amplifying the nucleic acid molecules of the present invention. The term "primer" when used in the present invention means a single-stranded nucleic acid molecule capable of annealing the nucleic acid molecule of the present application and thereby being capable of serving as a starting point for amplification. Said term also comprises oligoribo- or deoxyribonucleotides which are complementary to a region of one of the strands of a nucleic acid molecule of the present invention. According to the present invention the term "pair of primers" means a pair of primers that are with respect to a complementary region of a nucleic acid molecule directed in the opposite direction towards each other to enable, for example, amplification by polymerase chain reaction (PCR).

The term "amplifying" refers to repeated copying of a specified sequence of nucleotides resulting in an increase in the amount of said specified sequence of nucleotides. and allows the generation of a multitude of identical or essentially identical (i.e. at least 95% more preferred at least 98%, even more preferred at least 99% and most preferred at least

99.5% such as 99.9% identical) nucleic acid molecules or parts thereof. Such methods are well established in the art; see Sambrook et al. "Molecular Cloning, A Laboratory Manual", 2nd edition 1989, CSH Press, Cold Spring Harbor. They include polymerase chain reaction (PCR) and modifications thereof, ligase chain reaction (LCR) to name some preferred amplification methods.

When used in the context of primers the term "specifically" means that only the nucleic acid molecules as described herein above are amplified and nucleic acid molecules encoding the wild-type P2X7R ATP-gated receptor as depicted in SEQ ID NO: 1 are not amplified. Thus, a primer according to the invention is preferably a primer which binds to a region of a nucleic acid molecule of the invention which is unique for this molecule and which is not present in the wild-type P2X7R encoding sequence, i.e. the primer binds in a region in which one of the above described mutations occur. In connection with a pair of primers according to the invention it is possible that one of the primers of the pair is specific in the above described meaning or both of the primers of the pair are specific. In both cases, the use of such a pair of primers would allow to specifically amplify a mutant of the invention as described herein-above but not the wild-type P2X7R encoding sequence.

The 3'-OH end of a primer is used by a polymerase to be extended by successive incorporation of nucleotides. The primer or pair of primers of the present invention can be used, for example, in primer extension experiments on template RNA according to methods known by the person skilled in the art. Preferably, the primer or pair of primers of the present invention are used for amplification reactions on template RNA or template DNA, preferably cDNA or genomic DNA. The terms "template DNA" or "template RNA" refers to DNA or RNA molecules or fragments thereof of any source or nucleotide composition, that comprise a target nucleotide sequence as defined above. The primer or pair of primers can also be used for hybridization experiments as known in the art. Preferably, the primer or pair of primers are used in polymerase chain reactions to amplify sequences corresponding to a sequence of the nucleic acid molecule of the present invention. It is known that the length of a primer results from different parameters (Gillam, Gene 8 (1979), 81-97; Innis, PCR Protocols: A guide to methods and applications, Academic Press, San Diego, USA (1990)). Preferably, the primer should only hybridize or bind to a specific region of a target nucleotide sequence. The length of a primer that statistically hybridizes only to one region of a target nucleotide sequence can be calculated by the following formula: $(\frac{1}{4})^x$ (whereby x is the length of the primer). For example a hepta- or octanucleotide would be sufficient to bind statistically only once on a sequence of 37 kb. However, it is known that a primer exactly matching to a complementary template strand must be at least 9 base pairs in length, otherwise no stable-double strand can be generated (Goulian, Biochemistry 12 (1973), 2893-2901). It is also envisaged that computer-based algorithms can be used to design primers capable of amplifying the nucleic acid molecules of the invention. Preferably, the primers of the invention are at least 10 nucleotides in length, more preferred at least 12 nucleotides in length, even more preferred at least 15 nucleotides in length, particularly preferred at least 18 nucleotides in length, even more particularly preferred at least 20 nucleotides in length and most preferably at least 25 nucleotides in length. The invention, however, can also be carried out with primers which are shorter or longer.

It is also envisaged that the primer or pair of primers is labeled. The label may, for example, be a radioactive label, such as ³²P, ³³P or ³⁵S. In a preferred embodiment of the invention, the label is a non-radioactive label, for example, digoxigenin, biotin and fluorescence dye or a dye.

In another preferred embodiment said primers are selected from the group consisting of SEQ ID NOs: 52 to 111.

[0071] In yet another embodiment, the present invention relates to a composition comprising a nucleic acid molecule, a vector, a polypeptide, an antibody, an aptamer and/or a primer or pair of primers of the invention.

The term "composition", as used in accordance with the present invention, relates to compositions which comprise at least one nucleic acid molecule, vector, polypeptide, an antibody and/or primer or pair of primers of this invention. It may, optionally, comprise further molecules capable of altering the characteristics of the component of the invention thereby, for example, suppressing, blocking, modulating and/or activating their function which have neuroprotective, nootropic, antidepressive and/or cell-protective properties as will also be described herein below. The composition may be in solid, liquid or gaseous form and may be, inter alia, in the form of (a) powder(s), (a) tablet(s), (a) solution(s) or (an) aerosol(s).

[0072] In a preferred embodiment the composition according to the invention is a diagnostic composition, optionally further comprising suitable means for detection. As described above, the present invention is based on the surprising finding that mutations in the P2X7R protein are connected with affective disorders. Thus, this knowledge now allows to diagnose affective disorders in an easy way. The diagnostic composition comprises at least one of the aforementioned compounds of the invention. The diagnostic composition may be used, inter alia, for methods for determining the presence and/or expression of the nucleic acids and/or polypeptides of the invention. This may be effected by detecting, e.g., the presence of a corresponding gene in the genetic material of an individual or the presence of the corresponding mRNA which comprises isolation of DNA or RNA from a cell derived from said individual, contacting the DNA or RNA so obtained with a nucleic acid probe as described above under hybridizing conditions, and detecting the presence of mRNAs hybridized to the probe. Alternatively, the diagnostic composition may also be used for detecting the presence of a nucleic acid molecule of the invention by PCR. Furthermore, polypeptides of the invention can be

detected with methods known in the art, which comprise, inter alia, immunological methods, like, RIA, FIA, ELISA, FACS or Western blotting.

Furthermore, the diagnostic composition of the invention may be useful, inter alia, in detecting the prevalence, the onset or the progress of a disease related to the expression of a polypeptide of the invention. Accordingly, the diagnostic composition of the invention may be used, inter alia, for assessing the prevalence, the onset and/or the disease status of affective disorders, as defined herein above. It is also contemplated that the diagnostic composition of the invention may be useful in discriminating (the) stage(s) of a disease.

[0073] The diagnostic composition optionally comprises suitable means for detection. The nucleic acid molecule(s), vector(s), host(s), antibody(ies), aptamer(s), polypeptide(s) described above are, for example, suitable for use in immunoassays in which they can be utilized in liquid phase or bound to a solid phase carrier. Examples of well-known carriers include glass, polystyrene, polyvinyl ion, polypropylene, polyethylene, polycarbonate, dextran, nylon, amyloses, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble or insoluble for the purposes of the invention.

Solid phase carriers are known to those in the art and may comprise polystyrene beads, latex beads, magnetic beads, colloid metal particles, glass and/or silicon chips and surfaces, nitrocellulose strips, membranes, sheets, duracytes and the walls of wells of a reaction tray, plastic tubes or other test tubes. Suitable methods of immobilizing nucleic acid molecule(s), vector(s), host(s), antibody(ies), aptamer(s), polypeptide(s), etc. on solid phases include but are not limited to ionic, hydrophobic, covalent interactions or (chemical) crosslinking and the like. Examples of immunoassays which can utilize said compounds of the invention are competitive and non-competitive immunoassays in either a direct or indirect format. Commonly used detection assays can comprise radioisotopic or non-radioisotopic methods. Examples of such immunoassays are the radioimmunoassay (RIA), the sandwich (immunometric assay) and the Northern or Southern blot assay. Furthermore, these detection methods comprise, inter alia, IRMA (Immune Radioimmunometric Assay), EIA (Enzyme Immuno Assay), ELISA (Enzyme Linked Immuno Assay), FIA (Fluorescent Immuno Assay), and CLIA (Chemiluminescent Immune Assay). Furthermore, the diagnostic compounds of the present invention may be

are employed in techniques like FRET (Fluorescence Resonance Energy Transfer) assays. Appropriate labels and methods for labeling are known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include inter alia, fluorochromes (like fluorescein, rhodamine, Texas Red, etc.), enzymes (like horse radish peroxidase, β -galactosidase, alkaline phosphatase), radioactive isotopes (like ^{32}P , ^{33}P , ^{35}S or ^{125}I), biotin, digoxigenin, colloidal metals, chemi- or bioluminescent compounds (like dioxetanes, luminol or acridiniums).

[0074] A variety of techniques are available for labeling biomolecules, are well known to the person skilled in the art and are considered to be within the scope of the present invention and comprise, inter alia, covalent coupling of enzymes or biotinyl groups, phosphorylations, biotinylations, random priming, nick-translations, tailing (using terminal transferases). Such techniques are, e.g., described in Tijssen, "Practice and theory of enzyme immunoassays", Burden and von Knippenburg (Eds), Volume 15 (1985); "Basic methods in molecular biology", Davis LG, Diber MD, Battey Elsevier (1990); Mayer, (Eds) "Immunochemical methods in cell and molecular biology" Academic Press, London (1987); or in the series "Methods in Enzymology", Academic Press, Inc. Detection methods comprise, but are not limited to, autoradiography, fluorescence microscopy, direct and indirect enzymatic reactions, etc.

Said diagnostic composition may be used for methods for detecting the presence and/or abundance of a nucleic acid molecule of the invention in a biological and/or medical sample and/or for detecting expression of such a nucleic acid molecule (e.g. by determining the mRNA or the expressed polypeptide). Furthermore, said diagnostic composition may also be used in methods of the present invention, inter alia, for the detection of specific antagonists or agonists for P2X7R ATP-gated ion channels (see herein below).

[0075] In a further embodiment the present invention provides a method of diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R protein expressed in the cells of said individual is non-functional, shows an altered ATP-gating in comparison to the wild-type P2X7R protein or is over- or under-expressed in comparison to the P2X7R protein level of an unaffected individual.

The term "over- or under-expressed in comparison to the P2X7R protein level" in the context of the present invention means that the P2X7R protein level is higher or lower than the P2X7R level of a healthy individual, i.e. an individual not affected with an affective disorder. The over-expression may result, e.g. from an increased amount of P2X7R mRNA caused by enhanced transcription rates due to increased activity of the RNA-polymerase II. The amount of mRNA may accordingly lead to an increased translation and, thus, to a higher protein level of P2X7R. It may also be possible that a higher amount of P2X7R protein is caused by increased stability of the protein. An under-expression of P2X7R protein may be caused by low transcription rates of the P2X7R gene and, thus, insufficient amounts of P2X7R mRNA give only rise to a low P2X7R protein amount. Another reason may be that the P2X7R protein is unstable and, thus, is not present in amounts comparable to the wild-type protein level.

The under- or over-expression of P2X7R protein may be determined by methods well-known to the person skilled in the art. These include, but are not limited, to methods for determining the amount of mRNA or the amount and/or activity of the protein. Examples are Northern Blot analysis or immuno based techniques, such as Western Blotting.

"Non-functional" means that the P2X7R protein has lost at least one functional property displayed by the wild-type P2X7R protein as described herein above. Preferably, "non-functional" means that the P2X7R protein does no longer function as a channel. Non-functionality may, e.g., be caused by the fact that one allele occurring in an individual codes for a P2X7R protein which leads to non-functional dimers (dominant negative mutation). Whether a P2X7R protein in an individual is functional or non-functional can be determined by the methods described herein above and in the examples.

The term "altered ATP-gating" means that the respective P2X7R protein reacts in a different way to ATP than the wild-type P2X7R protein. This can be determined as described in the appended examples or as described hereinabove.

In the context of diagnosis, not only the activity of the P2X7R could be of diagnostic value but also the amount of expression. For example, if a polymorphism affects RNA stability or translation efficiency, this could lead to lower expression of the P2X7 protein not only in the hippocampus but also in the blood. Therefore, one could speculate that a lower amount of P2X7 detected by western blot in blood cells could be related to depression.

[0076] Another aspect of the present invention is a method for diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R gene sequence or encoded protein thereof comprises a mutation in comparison to the wild-type P2X7R sequence.

[0077] A preferred embodiment of the present invention is a method, wherein a mutation is a mutation in a P2X7R sequence as defined hereinabove and/or a nucleotide replacement or deletion selected from the following Table C indicating in column "Region of P2X7R" the region of the P2X7R genomic nucleotide sequence in which the replacement or deletion occurs, in column "Nucleotide" of Table C the nucleotide which is replaced by another nucleotide or the nucleotides which are deleted and in column "Position in wild-type" of Table C the corresponding position in the nucleotide sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1

Table C

Region of P2X7R	Nucleotide	Position in wild-type
5'UTR	T	362
5'UTR	T	532
5'UTR	A	1100
5'UTR	A	1122
5'UTR	C	1171
5'UTR	T	1351
5'UTR	G	1702
5'UTR	T	1731
5'UTR	C	1860
5'UTR	C	2162
5'UTR	C	2238
5'UTR	A	2373
5'UTR	G	2569
5'UTR	G	2702
intron 1	G	3166
intron 1	C	24778
intron 1	C	24830
exon 2	T	24942
exon 3	C	26188
exon 3	A	26308

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Table C (continued)

	Region of P2X7R	Nucleotide	Position in wild-type
5	exon 3	G	26422
	intron 4	G	32394
	intron 4	T	32434
	exon 5	G	32493
10	exon 5	G	32506
	exon 5	C	32507
	exon 5	C	32548
15	intron 5	A	32783
	intron 5	T	35309
	intron 5	C	35374
	intron 5	A	35378
20	exon 6	G	35438
	exon 6	T	35454
	intron 6	T	35549
25	intron 6	G	35641
	intron 6	A	35725
	intron 6	T	36001
	intron 6	A	36064
30	intron 6	deletion of GTTT	36091 to 36094
	intron 6	C	36108
	intron 7	C	36374
35	intron 7	G	36378
	intron 7	T	36387
	intron 7	G	36398
	intron 7	C	37439
40	intron 7	T	37513
	exon 8	C	37604
	exon 8	G	37605
45	exon 8	G	37623
	exon 8	C	37633
	intron 9	C	47214
	exon 11	G	47383
50	exon 11	C	47411
	intron 11	T	47563
	intron 12	C	54307
55	intron 12	G	54308
	exon 13	C	54399

Table C (continued)

Region of P2X7R	Nucleotide	Position in wild-type
exon 13	A	54480
exon 13	C	54523
exon 13	deletion of CCCTGAGAGCCACAGGTGCCT	54562 to 54582
exon 13	A	54588
exon 13	C	54664
exon 13	G	54703
exon 13	A	54804
exon 13	G	54834
exon 13	G	54847
3'UTR	G	54925
3'UTR	C	55169
3'UTR	A	55170
3'UTR	A	55171
3'UTR	C	55917

[0078] As indicated hereinabove, if the respective nucleotide which is replaced by another nucleotide is a purine base, it is preferred to be replaced by another purine base. If it is a pyrimidine base, it is preferred to be replaced by another pyrimidine base. It is also preferred that a purine base is replaced by a pyrimidine base and that a pyrimidine base is replaced by a purine base. Most preferably, the nucleotides indicated in Table C are replaced by the nucleotides indicated at the respective position in Table 12 hereinbelow (see Example 3).

[0079] In a preferred embodiment the present invention relates to diagnostic composition designed for use in a method in which the occurrence of the mutation in the ATP-gated ion channel P2X7R gene is determined by PCR, immunological methods and/or electrophysiological methods as described herein below and in the appended Examples. Additionally, it is possible to determine the occurrence of a mutation in the ATP-gated ion channel P2X7R as described hereinabove.

[0080] In yet another aspect the present invention relates to the use of a nucleic acid molecule, a vector, a polypeptide, an antibody, aptamer and/or a primer or pair of primers of the present invention for the preparation of a diagnostic composition for the detection of an affective disorder.

[0081] It is also envisaged that the present invention relates to methods of diagnosing an affective disorder of an individual comprising:

- (a) isolating DNA from cells obtained from an individual;
- (b) determining all or part of the nucleotide composition of the P2X7R gene; and
- (c) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism, mutation or allelic variation.

[0082] The term "gene" means a nucleotide sequence associated with the production of a protein, including promoter sequences, enhancer sequences, intron sequences, exon sequences, coding regions, 5' untranslated region (5'UTR), 3' untranslated region (3'UTR), and splice variants.

[0083] In a preferred embodiment of the described method the individual is a mammal and more preferably human. Moreover, the cells are preferably derived from skin, blood, urine or cerebral spinal fluid.

[0084] The method of the present invention allows for the diagnosis of an affective disorder according to the composition of a genetic marker corresponding to the P2X7R gene. As is demonstrated by the appended examples, polymorphisms in the P2X7R are genetically linked to patients suffering from an affective disorder.

[0085] In accordance with this embodiment of the present invention, the diagnosis of an affective disorder can, e.g., be effected by isolating cells from an individual, and isolating the genomic DNA of said cells. Such cells can be collected from body fluids, skin, hair, biopsies and other sources. Collection and analysis of cells from bodily fluids such as blood,

urine and cerebrospinal fluid is well known to the art; see for example, Rodak, "Haematology: Clinical Principles & Applications" second ed., WB Saunders Co, 2002; Brunzel, "Fundamentals of Urine and Body Fluids Analysis", WB Saunders Co, 1994; Herndon and Brumback (Ed.), "Cerebrospinal Fluid", Kluwer Academic Pub., 1989. In addition, methods for DNA isolation are well described in the art; see, for example, Sambrook et al., "Molecular Cloning: A Laboratory Manual", 3rd edition, Cold Spring Harbor Laboratory, 2001.

[0086] Once DNA has been isolated, various oligonucleotide primers spanning the P2X7R locus may be designed in order to amplify the genetic material by Polymerase Chain Reaction (PCR). Conventional methods for designing, synthesizing, producing said oligonucleotide primers and performing PCR amplification may be found in standard textbooks, see, for example Agrawal (Ed.), "Protocols for Oligonucleotides and Analogs: Synthesis and Properties (Methods in Molecular Biology, 20)", Humana Press, 1993; Innis et al. (Ed.), "PCR Applications: Protocols for Functional Genomics", Academic Press, 1999; Chen and Janes (Ed.), "PCR Cloning Protocols: From Molecular Cloning to Genetic", 2nd edition, Humana Press, 2002. Primers for the detection of P2X7R polymorphisms are also given in, but not limited to, SEQ ID NO: 52 to SEQ ID NO: 111. Once DNA has been amplified, nucleotide structure can be analysed by sequencing methods and compared to normal P2X7R DNA.

[0087] Sequencing may be performed manually by any molecular biologist of ordinary skills or by an automated sequencing apparatus. These procedures are common in the art, see, for example, Adams et al. (Ed.), "Automated DNA Sequencing and Analysis", Academic Press, 1994; Alphey, "DNA Sequencing: From Experimental Methods to Bioinformatics", Springer Verlag Publishing, 1997.

[0088] Detection and analysis of polymorphisms in P2X7R can also be performed using amplification refractory mutation system (ARMSTM), amplification refractory mutation system linear extension (ALEXTM), single-strand conformation polymorphism (SSCP), heteroduplex analysis, PCR-SSCP, fluorescent SSCP in an automated DNA sequencer, denaturing gradient gel electrophoresis, RNase protection assays, detection of mutations by sequence specific oligonucleotide hybridization, chemical cleavage methods, enzyme mismatch cleavage methods, cleavage fragment length methods, allele-specific oligonucleotide hybridization on DNA chips, and other such methods known in the art, see, for example Nollau et al, Clin. Chem. 43 (1997), 1114-1128; Burczak and Mardis (Ed.), "Polymorphism Detection & Analysis Techniques", Eaton Pub Co, 2000; Cotton et al. (Ed.), "Mutation Detection: A Practical Approach", Irl Press, 1998; Taylor (Ed.), "Laboratory Methods for the Detection of Mutations and Polymorphisms in DNA", CRC Press, 1997.

[0089] The present invention also relates to a method of diagnosing an affective disorder in an individual comprising:

- (a) isolating RNA from cells obtained from an individual;
- (b) converting the RNA into cDNA;
- (c) determining all or part of the nucleotide composition of the cDNA so obtained; and
- (c) analyzing said nucleotide composition for the presence of one or more polymorphism(s) or allelic variation.

[0090] With respect to the preferred embodiments the same applies as already described above.

[0091] Detection and analysis of polymorphisms in the P2X7R RNA can be performed according to the methods described above.

[0092] The present invention also relates to a method for diagnosing an affective disorder in an individual comprising:

- (a) isolating RNA or proteins from cells obtained from an individual;
- (b) determining the levels of P2X7R RNA or protein; and
- (c) comparing the levels of P2X7R RNA or protein with the corresponding levels from a normal individual not afflicted with an affective disorder.

[0093] With respect to the preferred embodiments the same applies as already described above.

[0094] As is demonstrated by the appended examples, a relationship exists between the expression, or protein level of P2X7R and an affective disorder. This and other embodiments of the present invention will readily occur to those of ordinary skill in the art in view of the disclosure herein.

[0095] According to another aspect on the invention, there is provided a polynucleotide comprising at least 20 bases of the human P2X7R gene and comprising a mutation or polymorphism selected from any of the following:

Table 1:

Novel polymorphisms in the human P2X7R		
Region in P2X7	Polymorphism	Protein Modification
5'UTR	362 T-C	
5'UTR	532 T-G	
5'UTR	1100 A-G	
5'UTR	1122 A-G	
5'UTR	1171 C-G	
5'UTR	1702 G-A	
Intron01	3166 G-C	
Intron01	24778 C-T	
Intron01	24830 6C-T	
Exon03	26188 C-T	Arg117Trp
Intron03	26308 A-G	
Intron03	26422 G-A	
Intron04	32394 G-A	
Intron04	32434 T-C	
Exon05	32493 G-A	Gly150Arg
Exon05	32548 C-T	Silent Cys168
Intron05	32783 A-C	
Exon06	35438 G-A	Glu186Lys
Exon06	35454 T-C	Leu191Pro
Intron06	35641 G-C	
Intron06	35725 A-C	
Intron06	36001 T-G	
Intron07	36378 G-A	
Intron07	36387 T-A	
Intron07	36398 G-C	
Exon08	37604 C-T	Arg270Cys
Exon08	37633 C-T	Silent Asp279
Intron09	47214 C-T	
Intron11	47563 T-C	
Intron12	54307 C-T	
Intron12	54308 G-A	
Exon 13	54562-54582 deletion of CCCTGAGA GCCACAGGTGCCT	deletion of 7aa 488 to 494 (PESHRCL)
Exon 13	54804 A-T	Ile568Asn
Exon 13	54834 G-A	Arg578Gln
3'UTR	55169 C-A	

Table 1: (continued)

Novel polymorphisms in the human P2X7R		
Region in P2X7	Polymorphism	Protein Modification
3'UTR	55170 A-C	
3'UTR	55171 A-C	
3'UTR	55917 C-T	
3'UTR	54925 G-A	

[0096] The polymorphism describes the position and the variation observed. The position and numbering of the polymorphism corresponds to the human P2X7R gene as defined in SEQ ID No 1. Primers used for SNP amplification and sequencing are shown in Table 1 a and listed in SEQ ID NO: 52 to SEQ ID NO: 111.

Table 1a. Primer sequences for SNP amplification and sequencing

Primer Name	Orientation	Sequence	Begin	End
P2RX7_01.for	Sense	cgtaggacttggcgcttct	2785	2803
P2RX7_01.rev	Anti sense	gagcacgtctcagattcgaaa	3224	3244
P2RX7_02.for	Sense	ccatgaggcaggatgactattc	24665	24687
P2RX7_02.rev	Antisense	ctcctggatctcaccagtt	25168	25187
P2RX7_03.for	Sense	ctcgtccagctttgatattaagc	25966	25988
P2RX7_03.rev	Antisense	ggcccttagtgctagaaccaga	26426	26447
P2RX7_04.for	Sense	attcatccgtcagtgcc	30794	30811
P2RX7_04.rev	Antisense	gccatgtgaattttctaccgat	31277	31298
P2RX7_05.for	Sense	ttcgtttgtggttaggatggg	32314	32333
P2RX7_05.rev	Antisense	caaggatgctcagggtagtagc	32805	32826
P2RX7_06.for	Sense	cactaggttgctgtatccatttct	35277	35301
P2RX7_06.rev	Antisense	gcaactgtgtgagagcttgg	35731	35750
P2RX7_07.for	Sense	tcaacctgggtccagtggtg	35950	35968
P2RX7_07.rev	Antisense	caccaagtagctctcactcataagg	36424	36448
P2RX7_08.for	Sense	caataacactttgtgcgagttaggt	37380	37403
P2RX7_08.rev	Antisense	catctgtttgccttggaacc	37750	37770
P2RX7_09.for	Sense	gtgagtggtaatcctgtactgc	45321	45343
P2RX7_09.rev	Antisense	aggccactcctgtactcg	45743	45761
P2RX7_10_11.for	Sense	ccaagtccacagcatgaggc	47119	47137
P2RX7_10_11.rev	Antisense	accagcgacgtatccac	47632	47649
P2RX7_12.for	Sense	aagcatgggggtccatttc	50252	50268
P2RX7_12.rev	Antisense	gcataaaagggaactcctgctagta	50691	50714
P2RX7_13a.for	Sense	gcttacagaacacatgcatgg	54232	54252
P2RX7_13a.rev	Antisense	gcacctgtaggcacagtgc	54739	54757
P2RX7_13b.for	Sense	atcaccacctcagagctgttc	54620	54640
P2RX7_13b.rev	Antisense	gttaacatggctactgcagcc	55203	55223
P2RX7_13d.for	Sense	gcttagaaaggaggcgactcc	54484	54504
P2XR7_Pro13.for	Sense	ttgtgacatttgcaaggctgcc	2617	2638
P2XR7_Pro7.rev	Antisense	tctgaagctctgctcctgag	1955	1974
P2XR7_Pro8.rev	Antisense	ctcaccttctggcttccagt	1611	1630
P2XR7_Pro9.for	Sense	cttaccactcccaggactaa	1496	1515
P2XR7_Pro10.for	Sense	gtctgcctgttctactgcat	1149	1168
P2XR7_Pro1.for	Sense	cagagaccttcagaaacttcg	1841	1861
P2XR7_Pro2.rev	Antisense	agatcaccagggaacacagtg	2261	2280
P2XR7_Pro3.for	Sense	ctcaactccactttcctcgg	2133	2152
P2XR7_Pro4.rev	Antisense	cctttcacttttttggtctcatg	2655	2677
P2XR7_Pro5.for	Sense	gggagaattctgaaaatgcc	2691	2711
P2XR7_Pro6.rev	Antisense	ggaccagagctctactcttc	2951	2970
P2XR7_Pro11.for	Sense	aggtcatagatcgacctgcc	2296	2315
P2XR7_Pro12.rev	Antisense	aagaagcgccaagtccctacg	2785	2804
P2XR7_Pro14.for	Sense	gcaatccagactgaagttgac	2051	2071
P2XR7_Pro15.rev	Antisense	actctgggtctgcagttggtg	2428	2447
P2XR7_Pro21.for	Sense	cctttaaaatcagagaccttcaga	1831	1854
P2XR7_Pro22.for	Sense	gcccacctctgaacacat	2708	2727
P2XR7_3UTR10.for	Sense	cccttggaactcttgctatcg	55804	55824
P2XR7_3UTR1.for	Sense	ggcagtacagtggttcaaga	54858	54878
P2XR7_3UTR2.rev	Antisense	gtgggacagtttgctgtgcct	55150	55170

P2XR7_3UTR3.for	Sense	gagtccttaccaatagcagg	55183	55202
P2XR7_3UTR4.rev	Antisense	gtcaaagaatttgtggccacc	55643	55663
P2XR7_3UTR5.for	Sense	catgaactgtcttttaatgtgtaaag	55515	55540
P2XR7_3UTR6.rev	Antisense	gagatacgggtttcaccatgttg	55955	55976
P2XR7_3UTR7.for	Sense	aattagctgggcatggtgcg	55992	56011
P2XR7_3UTR8.rev	Antisense	ttgagatggagctctcgtctg	56122	56140
P2XR7_3UTR9.rev	Antisense	cactgtccacgtgactgctt	56208	56227
P2XR7_11.For	Sense	tcctacttcggtctggttaagagatt	47281	47305
P2XR7_11.Rev	Antisense	gggcctaattttcgtgcat	47591	47609
P2XR7_13G.For	Sense	aagaacctagaacctgagggctt	54333	54355
P2XR7_13G.Rev	Antisense	ttgagatgggaggcagctt	54541	54559
P2XR7_13H.For	Sense	ttcggctcccaggacat	54773	54789
P2XR7_13H.Rev	Antisense	cacagagctttgcaggtgaa	55248	55267

[0097] Another aspect of the present invention is in the form of a diagnostic kit for affective disorders comprising a specific oligonucleotide probe, or primer corresponding to P2XR7 polymorphisms. The diagnostic kit may comprise appropriate packaging and instructions for the use in the method of the invention. Said kit may further comprise appropriate buffer, and enzymes such as reverse transcriptase, and thermostable polymerases.

[0098] In a preferred embodiment of the invention, diagnosis can be performed on a mouse, rat or human. The invention is generally applied in vitro, e.g. using cells or other material obtained from an individual. However, it can also be applied on a living individual, or post mortem.

[0099] In accordance with the embodiments of the present invention, diagnosis of an affective disorder may be followed by prescription, or administration of an antidepressant drug. Administration and dosage of antidepressive drugs can vary between patients and are well known in the medical art, see, for example Benkert and Hippus, "Kompendium der Psychiatrischen Pharmakotherapie", Springer Verlag Publishing, 2000; Albers, "Handbook of Psychiatric Drugs: 2001-2002 Edition", Current Clinical Strategies Publishing, 2000. Preferred examples include between 5 mg and 80 mg per day, preferably 20 mg, fluoxetine; between 5 mg and 50 mg per day, preferably 20 mg, paroxetine; between 5 mg and 200 mg per day, preferably 50 mg, sertraline; between 5 mg and 300 mg per day, preferably 100 mg, fluvoxamine; between 5 mg and 100 mg per day, preferably 30 mg, mirtazapine; between 4 mg and 50 mg, preferably 8 mg, reboxetine; between 5 mg and 600 mg per day, preferably 200 mg, nefazodone; between 450 mg and 1800 mg per day, preferably 900 mg, lithium carbonate.

[0100] The P2XR7 protein is also useful for monitoring the efficacy and/or dosing of a drug or the likelihood of a patient to respond to a drug. Thus, in yet another embodiment the invention relates to a method for, monitoring the efficacy and/or dosing of a drug, e.g. an antidepressive drug, and/or the likelihood of a patient to respond to said drug which comprises determining the level of expression and/or activity of the P2XR7 protein in a patient before and after administration of the respective drug. As presented in the examples below, treatment with an antidepressive drug results in an upregulation in P2XR7 activity. In humans, P2XR7 activity can be monitored by Positron Emission Tomography (PET) or Single Photon Emission Computerised Tomography (SPECT) using a radiolabelled ligand tracer for P2XR7. Examples of P2XR7 ligands can be, but are not limited to, ATP, an antagonist binding P2XR7, an agonist binding P2XR7, or a small polynucleotide comprising at least 20 bases of the human P2XR7 gene. A modulation of P2XR7 activity, membrane distribution or expression levels would reflect the activity and potency of the antidepressive drug. Methods and techniques required for PET analysis are well known in the art, see, for example Paans and Vaalburg, Curr. Pharmac. Design 6 (2000), 1583-1591; van Waarde, Curr. Pharmac. Design. 6 (2000), 1593-1610; Paans et al, Methods 27 (2002), 195-207; Passchier et al., Methods 27 (2002), 278-286; Laruelle et al., Methods 27 (2002), 287-299.

[0101] In accordance with the present invention by the term "sample" is intended any biological sample obtained from an individual, cell line, tissue culture, or other source containing polynucleotides or polypeptides or portions thereof. As indicated, biological samples include body fluids (such as blood, sera, plasma, urine, synovial fluid and spinal fluid) and tissue sources found to express the polynucleotides of the present invention. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. A biological sample which includes genomic DNA, mRNA or proteins is preferred as a source.

[0102] As described herein above, mutations of the P2XR7 encoding gene can occur on DNA level or on mRNA level and may result in an altered expression of P2XR7 or in the expression of P2XR7 ATP-gated ion channels which show either an altered function or no function when compared to the wild-type P2XR7 ATP-gated ion channel as described herein. Thus, various methods on DNA level, RNA level or protein level exist for determining whether the

ATP-gated ion channel P2X7R gene shows a mutation as described herein above. Consequently, mRNA, cDNA, DNA and genomic DNA are the preferred nucleic acid molecules to be used in the below mentioned methods. Also polypeptides or fragments thereof are preferred if a mutation in the P2X7R ATP-gated ion channel protein as described herein is to be determined.

[0103] Preferably, a point mutation leading to the replacement of an amino acid residue at the positions as indicated in Table 1 of the corresponding wild-type P2X7R amino acid sequence depicted in SEQ ID NO: 3 or 4 by another amino acid can be determined by PCR. Said PCR is followed by a restriction fragment length polymorphism (RFLP) analysis if due to the point mutation a recognition site for a restriction endonuclease is generated which is not present in the wild-type nucleotide sequence or a recognition site for a restriction enzyme is created which does not occur in the wild-type P2X7R. More preferably said mutation can be determined by PCR using primers and conditions that allow only an amplification of the wild-type nucleotide sequence encoding the corresponding wild-type amino acid at the respective position, but not of the nucleotide sequence of a nucleic acid molecule encoding a different amino acid residue at the corresponding position. It is even more preferred that PCR is performed to determine a mutation using primers and conditions that allow no amplification if the wild-type nucleotide sequence is present, but only if another amino acid residue is encoded at the respective position. Particularly preferred is a method using PCR and primers under conditions that allow amplification of a fragment comprising at least the nucleotide residues encoding the amino acid residue corresponding to positions of SEQ ID NO: 1.

Said PCR is followed by e.g., sequencing and/or single strand conformation analysis (SSCA). Said fragment is preferably of at least 25 nucleotides in length, more preferred of at least 50 nucleotides in length, even more preferred of at least 75 nucleotides in length, particularly preferred of at least 100 nucleotides in length, more particularly preferred of at least 200 nucleotides in length, also more particularly preferred at least 250 nucleotides in length, even more particularly preferred at least 300 nucleotides in length and most particularly preferred at least 600 nucleotides in length. Said primers are preferably of at least 12 nucleotides in length, more preferred of at least 15 nucleotides in length, even more preferred of at least 18 nucleotides in length and most preferred of at least 21 nucleotides in length as depicted in SEQ ID NOs: 52 to 111. The temperature for annealing said primers is preferably at least 50°C, more preferred at least 55°C and most preferred at least 58°C. The temperature for denaturation is preferably at least 95°C for preferably at least 10 sec, more preferably at least 20 sec, even more preferred at least 30 sec and most preferred at least 60 sec. However, depending on the length and the G-C content of the nucleic acid sequence to be amplified the temperature for denaturation may be shorter or longer. The temperature for extension of the annealed primers is preferably at least 10 sec, more preferably at least 20 sec, even more preferred at least 30 sec and most preferred at least 60 sec. A PCR reaction comprising the aforementioned conditions is exemplified in the Examples herein below. The subsequent sequencing and/or SSCA is carried out as known in the art. Preferably, the PCR fragments are separated on a 10% polyacrylamide gel at 4°C or also preferred at room temperature. PCR fragments showing a SSCA band shift are amplified with the primers under conditions as mentioned above and are subsequently sequenced. Alternatively, it is also possible to directly sequence genomic DNA in order to determine whether a mutation in the CLCN2 gene has occurred. A direct genomic sequencing approach is, for example, demonstrated for baker's yeast in Horecka, Yeast 16 (2000), 967-970.

Preferably, a deletion is determined by using hybridization techniques as known in the art. In particular, a primer is designed as mentioned herein above that is capable to only hybridize to wild-type genomic DNA as depicted in SEQ ID NO: 1 but not to a nucleotide sequence comprising a deletion of a fragment between nucleotides 54562 and 54582 of SEQ ID NO: 1. Also preferred is the method of fluorescent in situ hybridization (FISH) for determining on whole chromosomes, in particular on chromosome 12q23-q24 that said chromosome has the above mentioned deletion. Even more preferred is that a deletion of nucleotide residues as described herein may be determined by using PCR, wherein one primer of a pair of primers is located within the region of genomic DNA comprising said deletion. Preferably, said deletion is between nucleotide positions 54562 and 54582 as depicted in SEQ ID NO: 1. Thus, under the appropriate conditions no PCR fragment will result if the genomic DNA comprises said deletion. It is particularly preferred that PCR using primers which are located upstream or downstream of the deletion is performed to determine said deletion. Under appropriate conditions as mentioned herein above, both a fragment of genomic DNA of the wild-type nucleotide sequence as set forth in SEQ ID NO: 1 and a fragment of the nucleotide sequence comprising a deletion of preferably the nucleotides between positions 54562 and 54582 as depicted in SEQ ID NO: 1 will be amplified.

[0104] It is also possible to determine the above-described P2X7R mutations on the protein level. Some of the mutations described above lead to shortened versions of the P2X7R protein. Thus, it is conceivable to determine the occurrence of these mutations by determining the length or molecular weight of the P2X7R protein expressed in an individual, e.g. by SDS PAGE.

It is also possible to determine the mutations of the P2X7R ATP-gated channel as described herein by using the antibodies of the present invention. Said antibodies specific for said mutations of P2X7R proteins will be determined by assay techniques such as radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assay. Also preferred are classical immunohistological methods.

[0105] The finding, described in the present invention, that certain mutations in the P2X7R encoding gene and/or the corresponding protein are connected with affective disorder is indicative that the non- or dysfunction of the P2X7R protein is responsible for various forms of affective disorders. Thus, the finding of these mutations not only allows the diagnosis of affective disorders by determining whether the above-described mutations occur in an individual. It also allows to develop a treatment of affective disorders which has been diagnosed to be the result of a mutation in the P2X7R encoding gene. Such a treatment can, e.g., comprise the introduction of a nucleic acid molecule encoding a non-functional or functional wild-type P2X7R protein thereby restoring in said individual the P2X7R activity or the activation or repression of (a) P2X7R gene(s) in vivo. The term "activation or repression" in this context means that the expression of the gene is either enhanced (activation) or reduced (repression). An enhancement of expression can, e.g., be achieved by increasing the efficiency of transcription initiation, for example, by using suitable compounds which have an activating effect on transcription. Alternatively, an enhancement can be achieved by replacing the naturally occurring promoter by a more efficient promoter.

A repression may be achieved by suppressing expression of the gene, e.g., by specifically suppressing transcription from the respective promoter by suitable compounds or by rendering the promoter less efficient or non-functional.

[0106] In another embodiment the present invention also relates to a pharmaceutical composition. In accordance with the present invention the term "pharmaceutical composition" relates to a composition comprising a nucleic acid molecule comprising a nucleotide sequence which encodes an ATP-gated ion channel P2X7R and which is selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence as depicted in SEQ ID NO: 3 or 4;
- (b) a nucleotide sequence comprising the nucleotide sequence as depicted in SEQ ID NO: 1 or SEQ ID NO: 2;
- (c) a nucleotide sequence which hybridizes to the nucleotide sequence of (a) or (b); and
- (d) a nucleotide sequence which is degenerated as a result of the genetic code to the nucleotide sequence of (c).

[0107] Such pharmaceutical compositions comprise a therapeutically effective amount of a nucleic acid molecule encoding a functional P2X7R protein and, optionally, a pharmaceutically acceptable carrier. The pharmaceutical composition may be administered with a physiologically acceptable carrier to a patient, as described herein. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency or other generally recognized pharmacopoeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered.

[0108] Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium ion, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the aforementioned compounds, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In another preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The pharmaceutical composition of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric

acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

In vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems. Preferably, the pharmaceutical composition is administered directly or in combination with an adjuvant.

The pharmaceutical composition is preferably designed for the application in gene therapy. The technique of gene therapy has already been described above in connection with the nucleic acid molecules of the invention and all what has been said there also applies in connection with the pharmaceutical composition. For example, the nucleic acid molecule in the pharmaceutical composition is preferably in a form which allows its introduction, expression and/or stable integration into cells of an individual to be treated.

[0109] For gene therapy, various viral vectors which can be utilized, for example, adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (Ha-MuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV). A number of additional retroviral vectors can also incorporate multiple genes. All of these vectors can transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting a P2X7R sequence of interest encoding a functional P2X7R protein into the viral vector, along with another gene which encodes, for example, the ligand for a receptor on a specific target cell, for example, the vector is now target specific.

Retroviral vectors can be made target specific by inserting, for example, a polynucleotide encoding a sugar, a glycolipid, or a protein. Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral genome to allow target specific delivery of the retroviral vector containing the inserted polynucleotide sequence.

Since recombinant retroviruses are preferably defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packaging mechanism to recognize an RNA transcript for encapsidation. Helper cell lines which have deletions of the packaging signal include, but are not limited to w2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced. Alternatively, NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes gag, pol and env, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium. Another targeted delivery system for P2X7R polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles in vitro and in vivo. It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-4.0 μm can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, et al., Trends Biochem. Sci., 6:77, 1981). In addition to mammalian cells, liposomes have been used for delivery of polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high efficiency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Mannino, et al., Biotechniques, 6:682, 1988). The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations. Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerbrosides, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine. The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to

cells of the reticulo-endothelial system (RES) in organs which contain sinusoidal capillaries.

[0110] In another aspect the present invention relates to a method of treating an affective disorder comprising administering a therapeutically effective amount of the pharmaceutical composition comprising a nucleotide sequence encoding a functional ATP-gated ion channel as described herein above to a subject suffering from said disorder.

[0111] In the context of the present invention the term "subject" means an individual in need of a treatment of an affective disorder. Preferably, the subject is a vertebrate, even more preferred a mammal, particularly preferred a human.

The term "administered" means administration of a therapeutically effective dose of the aforementioned nucleic acid molecule encoding a functional P2X7R protein to an individual. By "therapeutically effective amount" is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art and described above, adjustments for systemic versus localized delivery, age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

The methods are applicable to both human therapy and veterinary applications. The compounds described herein having the desired therapeutic activity may be administered in a physiologically acceptable carrier to a patient, as described herein. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways as discussed below. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt %. The agents maybe administered alone or in combination with other treatments.

The administration of the pharmaceutical composition can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-arterial, intranodal, intramedullary, intrathecal, intratracheal, intranasally, intrabronchial, transdermally, intranodally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the candidate agents may be directly applied as a solution dry spray.

The attending physician and clinical factors will determine the dosage regimen. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. A typical dose can be, for example, in the range of 0.001 to 1000 µg; however, doses below or above this exemplary range are envisioned, especially considering the aforementioned factors.

[0112] The dosages are preferably given once a week, however, during progression of the treatment the dosages can be given in much longer time intervals and in need can be given in much shorter time intervals, e.g., daily. In a preferred case the immune response is monitored using herein described methods and further methods known to those skilled in the art and dosages are optimized, e.g., in time, amount and/or composition. Dosages will vary but a preferred dosage for intravenous administration of DNA is from approximately 10^6 to 10^{12} copies of the DNA molecule. If the regimen is a continuous infusion, it should also be in the range of 1 µg to 10 mg units per kilogram of body weight per minute, respectively. Progress can be monitored by periodic assessment. The pharmaceutical composition of the invention may be administered locally or systemically. Administration will preferably be parenterally, e.g., intravenously. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium ion solution, Ringer's dextrose, dextrose and sodium ion, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

It is also envisaged that the pharmaceutical compositions are employed in co-therapy approaches, i.e. in co-administration with other medicaments or drugs, for example other drugs for preventing, treating or ameliorating affective disorders.

[0113] Another aspect of the present invention is a pharmaceutical composition comprising a compound, the administration of which to cells leads to a reduction or increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells or comprising a nucleic acid molecule the expression of which in cells or the administration of which to cells leads to a reduction or increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells. Said pharmaceutical composition may be useful for treating individuals having an increased or reduced amount of the P2X7R protein or expression level as described hereinabove. Preferably, said pharmaceutical composition leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells.

[0114] It is envisaged that the above-mentioned pharmaceutical composition, the administration of which to cells leads to a reduction of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R is an antisense

nucleic acid, a ribozyme, a co-suppressive nucleic acid, iRNA or siRNA.

An siRNA approach is, for example, disclosed in Elbashir ((2001), Nature 411, 494-498)). It is also envisaged in accordance with this invention that for example short hairpin RNAs (shRNAs) are employed in accordance with this invention as pharmaceutical composition. The shRNA approach for gene silencing is well known in the art and may comprise the use of st (small temporal) RNAs; see, inter alia, Paddison (2002) Genes Dev. 16, 948-958.

As mentioned above, approaches for gene silencing are known in the art and comprise "RNA"-approaches like RNAi or siRNA. Successful use of such approaches has been shown in Paddison (2002) loc. cit., Elbashir (2002) Methods 26, 199-213; Novina (2002) Mat. Med. June 3, 2002; Donze (2002) Nucl. Acids Res. 30, e46; Paul (2002) Nat. Biotech 20, 505-508; Lee (2002) Nat. Biotech. 20, 500-505; Miyagishi (2002) Nat. Biotech. 20, 497-500; Yu (2002) PNAS 99, 6047-6052 or Brummelkamp (2002), Science 296, 550-553. These approaches may be vector-based, e.g. the pSUPER vector, or RNA polIII vectors may be employed as illustrated, inter alia, in Yu (2002) loc. cit.; Miyagishi (2002) loc. cit. or Brummelkamp (2002) loc. cit.

A compound which leads to a reduction of the expression of the P2X7R gene may, e.g., be a compound which acts on the regulatory region of the gene and thereby reduces the level of transcription. Such compounds can be identified by methods as described herein below.

[0115] The invention also relates to the use of a nucleic acid molecule encoding a functional P2X7R protein as described herein above in connection with the pharmaceutical composition for the preparation of a pharmaceutical composition for treating an affective disorder.

[0116] Furthermore, the present invention relates to a method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule according to the invention or a therapeutically effective amount of the corresponding encoded polypeptide to a subject suffering from said disorder.

[0117] In another preferred embodiment the present invention relates to a pharmaceutical composition comprising, inter alia, the polynucleotides according to the present invention, i.e. polynucleotides having mutations and/or deletions as described hereinabove. Such pharmaceutical compositions may, e.g., be useful for treating individuals having an increased or decreased amount of the P2X7R protein or having a P2X7R protein showing an increased or decreased activity which can be determined as described hereinabove. Preferably, such a pharmaceutical composition may be useful for treating individuals having a decreased amount of the P2X7R protein or having a P2X7R protein showing a decreased activity which can be determined as described hereinabove. It is envisaged that, e.g. a non-functional or preferably a hyperfunctional P2X7R protein comprised by said pharmaceutical composition is incorporated in a P2X7R complex which naturally exists in cells as described hereinabove. It is also envisaged that the above-described techniques for gene therapy can be used for treating an individual with the nucleic acid molecules of the present invention, mutatis mutandis.

[0118] With respect to the possible modes of administration and preferred embodiments the same applies as has been set forth above.

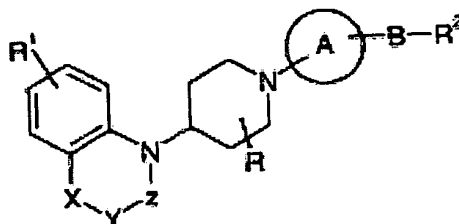
[0119] Additionally, the present invention also envisages the use of the nucleic acid molecules, the vectors, the polypeptides, the antibody and/or the aptamer according to the invention for the preparation of a pharmaceutical composition for the treatment of an affective disorder.

[0120] A further aspect of the present invention is the use of a modulator of P2X7R activity or expression for the preparation of a pharmaceutical composition for treating an affective disorder. In the context of the present invention the term "modulator" means (a) compound(s), a complex of compounds, (a) substance(s) or complex of substances which can modify, i.e. modulate the activity of P2X7R or the expression of P2X7R either directly or indirectly. The modulation can, for example, occur at the protein level. Particularly, the P2X7R protein may interfere with the modulator such that it is either more active or less active. The modulation can also occur on nucleic acid level. Namely, the gene is transcribed more frequently or less frequently giving rise to more or less protein. Modulation can also influence RNA or protein stability. Since it was surprisingly found that agonists of P2X7R improve the symptoms of mice selected for anxiety and depressive behaviour, the modulator of P2X7R activity used for the preparation of a pharmaceutical composition for treating an affective disorder is preferably an agonist. The term "agonist" means an agent or a compound that can interact with a receptor and initiate a physiological or a pharmacological response characteristic of that receptor. Examples of P2X7R agonist include but are not restricted to ATP, ATP-4, BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)) and tenidap (5-chloro-2,3-dihydro-2-oxo-3-(2-thienylcarbonyl)-indole-1-carboxamide, i.e. C₁₅H₁₁ClN₂O₂S) or a derivative thereof. Particularly preferred, said agonist used to treat depression or anxiety is BzATP as demonstrated in Example 9 hereinbelow.

Although it was reported that activation of P2X7R could induce apoptosis and cell death in vitro (Di Virgilio et al., Cell Death Differ. 5 (1988), 191-199; Virginio et al., J. Physiol. 519 (1999), 335-346), the present application demonstrates in Example 9 hereinbelow that treatment of the brain of mice selected for anxiety and depressive behaviour with BzATP revealed no significant difference in the numbers of apoptotic cells between control mice and mice treated with BzATP. This result indicates that activation of P2X7R did not result in cerebral cell death in vivo which, thus, renders BzATP to be a candidate drug for treatment of affective disorders.

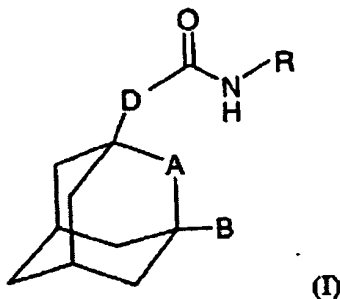
[0121] It is furthermore envisaged that said modulator is selected from the group consisting of piperidine and piperazine derivatives, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate and 3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate as, for example, described in WO 99/29660, WO 99/29661; WO 99/296896; WO 00/61569; WO 01/42194; WO 01/44170; WO 01/44213; WO 00/71529; WO 01/46200. The following compounds illustrate compounds which are also preferred to be used as modulators of P2X7R activity.

A compound of general formula:



where A is phenyl or a 5- or 6-membered heterocyclic ring containing one or two heteroatoms selected from O, N or S; and optionally substituted by C₁₋₆alkyl, halogen, nitro, amino, alkylamino, CF₃, SO₂Me, NHSO₂Me or cyano; B is S; and optionally substituted by C₁₋₆alkyl, halogen, nitro, amino, alkylamino, CF₃, SO₂Me, NHSO₂Me or cyano; C is C=O, NH or SO₂; X is C=O, CH(Me), O or (CH₂)_p where p is 0 or 1; Y is O, CH₂, NH or S; Z is C=O or SO₂, provided that when Z is C=O, then Y is O, CH₂ or S; R is hydrogen or C₁₋₆alkyl; R¹ is hydrogen, halogen; R² is phenyl optionally substituted by CO₂H, CO₂alkyl, CONH₂ or R² is OH, NHR³, NHCH(R⁴)(CHR⁵)_nR⁶, NH-R⁷-R⁸, SO₂NHalkyl, NHCOalkyl, NHSO₂alkyl, morpholine, NR⁹R¹⁰, piperazine substituted by phenyl, alkoxyphenyl, pyridyl or fluorophenyl; n is 0, 1 or 2; R³ is hydrogen, a bi- or tricyclic saturated ring system optionally containing a nitrogen atom, piperidinyl, alkylpyrrolidine, ethynylcyclohexyl, a 5-membered aromatic ring containing 2 or 3 heteroatoms, C₄₋₆ cycloalkyl optionally substituted by alkyl, cyano or hydroxy, or C₁₋₈ alkyl optionally containing an oxygen atom in the alkyl chain and being optionally substituted by one or more substituents selected from ethynyl, cyano, fluoro, dialkylamino, hydroxy, thioalkyl, CO₂R¹¹ or CONH₂; R⁴ is hydrogen or alkyl optionally substituted by hydroxy or alkoxy; R⁵ is hydrogen or hydroxy; R⁶ is CO₂R¹¹, NHCO₂R¹², CONH₂ or a 5 or 6-membered saturated ring containing an oxygen atom, a 5-membered heterocyclic ring containing one or two heteroatoms selected from O, N or S, or phenyl optionally substituted by one or more groups selected from alkyl, hydroxy, amino, alkoxy, or nitro; R⁷ is a cyclopentane ring; R⁸ is phenyl; R⁹ and R¹⁰ are independently hydrogen, benzyl, alkenyl, cycloalkyl, alkyl optionally substituted by hydroxy, alkoxy, cyano, dialkylamino, phenyl, pyridyl or CO₂R¹¹ or R⁹ and R¹⁰ together form a 5- to 7-membered saturated or partially saturated ring optionally containing a further heteroatom and optionally substituted by one or more groups selected from alkyl (optionally containing an oxygen atom in the chain and optionally substituted by hydroxy), COalkyl, CO₂R¹¹, COR¹³R¹⁴, CHO or piperidine, R¹¹ is hydrogen or alkyl; R¹² is alkyl; and R¹³ and R¹⁴ are independently hydrogen or alkyl, is or a pharmaceutically acceptable salt or solvate thereof.

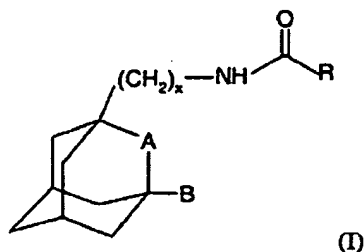
[0122] A compound of general formula:



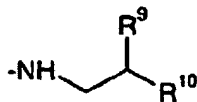
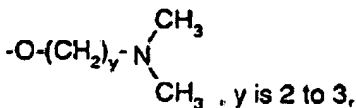
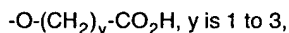
wherein A represents a group CH₂ or an oxygen atom; B represents a hydrogen or halogen atom; D represents a group CH₂, OCH₂, NHCH₂ or CH₂CH₂; R represents a phenyl, benzothiazolyl, indolyl, indazolyl, purinyl, pyridyl, pyrimidinyl or thiophenyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or a cyano, carboxyl, hydroxyl, nitro, halo-C_{1-C₆}-alkyl, -N(R¹)-C(=O)-R², -C(O)-NR³R⁴, -NR⁵R⁶, C_{3-C₈}-cycloalkyl, 3- to 8-membered heterocyclyl, C_{3-C₈}-cycloalkyloxy, C_{1-C₆}-alkylcarbonyl, phenoxy, benzyl, C_{1-C₆}-

alkylthio, phenylthio, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphinyl or C₁-C₆-alkylsulphonyl group, or a C₁-C₆-alkyl or C₁-C₆-alkoxy group optionally substituted by one or more substituents independently selected from a halogen atom or an amino, carboxyl, hydroxyl, C₁-C₆-alkoxy, (di)C₁-C₆-alkylamino, C₁-C₆-alkoxycarbonyl, imidazolyl, morpholinyl, piperidinyl or pyrrolidinyl group; R¹ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R² represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; and R³, R⁴, R⁵ and R⁶ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; with the provisos that when A is CH₂, B is H and D is CH₂, then R does not represent a phenyl, ortho-carboxyphenyl, methylphenyl or para-phenoxyphenyl group, and that when A is CH₂, D is CH₂ or CH₂CH₂ and R represents a substituted phenyl group, the substituent or substituents present do not comprise, in an ortho position, a C₁-C₆-alkoxy group substituted by an amino, (di)C₁-C₆-alkylamino, imidazolyl, morpholinyl, piperidinyl or pyrrolidinyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0123] A compound of general formula:

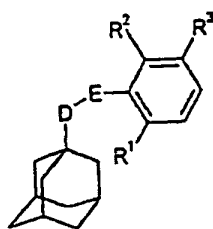


wherein x represents 1 or 2; A represents a group CH₂ or an oxygen atom; B represents a hydrogen or halogen atom; R represents a phenyl, pyridyl, indolyl, indazolyl, pyrimidinyl or thiophenyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or an amino, cyano, carboxyl, hydroxyl, nitro, C₁-C₆-alkyl, halo-C₁-C₆-alkyl, -N(R¹)-C(=O)-R², -C(O)NR³R⁴, -NR⁵R⁶, C₃-C₈-cycloalkyl, 3- to 8-membered heterocyclyl, C₃-C₈-cycloalkyloxy, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphinyl or C₁-C₆-alkylsulphonyl group, or a C₁-C₆-alkoxy, C₁-C₆-alkylamino, phenoxy, benzyl, C₁-C₆-alkylthio or phenylthio group optionally substituted by one or more substituents independently selected from a 15 halogen atom or an amino, cyano, carboxyl, hydroxyl, nitro, 1-pyrrolidinyl, 1-piperidinyl, C₁-C₆-alkyl, C₁-C₆-alkoxy, (di)C₁-C₆-alkylamino, halo-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl or one of the following groups:



R¹ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R² represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R³ and R⁴ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁶ represents a C₃-C₈-cycloalkyl group and, additionally, a C₁-C₆-alkyl group when R⁵ is not a hydrogen atom; R⁷ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁸ represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁹ represents a hydrogen atom or a hydroxyl group; and R¹⁰ represents a hydrogen atom or a phenyl or imidazolyl group; with the provisos that R does not represent an unsubstituted pyridyl group when A represents a group CH₂ and B represents a hydrogen atom, and that when R represents a substituted phenyl, indolyl or indazolyl group, the substituent or substituents present do not comprise an amido, carboxyl, (di)C₁-C₆-alkylamido or C₁-C₆-alkoxycarbonyl group in an ortho position; or a pharmaceutically acceptable salt or solvate thereof.

[0124] A compound of general formula:

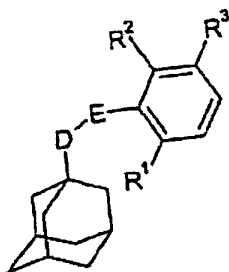


wherein D represents CH_2 or CH_2CH_2 ; E represents $\text{C}(\text{O})\text{NH}$ or $\text{NHC}(\text{O})$; R^1 and R^2 each independently represent a hydrogen or halogen atom, or an amino, nitro, $\text{C}_1\text{-C}_6$ -alkyl or trifluoromethyl group; R^3 represents a group of formula:

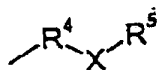


X represents an oxygen or sulphur atom or a group NH , SO or SO_2 ; Y represents an oxygen or sulphur atom or a group NR^{11} , SO or SO_2 ; Z represents a group $-\text{OH}$, $-\text{SH}$, $-\text{CO}_2\text{H}$, $\text{C}_1\text{-C}_6$ -alkoxy, $\text{C}_1\text{-C}_6$ -alkylthio, $\text{C}_1\text{-C}_6$ -alkylsulphinyl, $\text{C}_1\text{-C}_6$ -alkylsulphonyl, $-\text{NR}^6\text{R}^7$, $-\text{C}(\text{O})\text{NR}^8\text{R}^9$, imidazolyl, 1-methylimidazolyl, $-\text{N}(\text{R}^{10})\text{C}(\text{O})\text{-C}_1\text{-C}_6$ -alkyl, $\text{C}_1\text{-C}_6$ -alkylcarbonyloxy, $\text{C}_1\text{-C}_6$ -alkoxycarbonyloxy, $-\text{OC}(\text{O})\text{NR}^{12}\text{R}^{13}$, $-\text{OCH}_2\text{OC}(\text{O})\text{R}^{14}$, $\text{OCHOC}(\text{O})\text{OR}^{15}$ or $-\text{OC}(\text{O})\text{OCH}_2\text{OR}^{16}$, R^4 represents a $\text{C}_2\text{-C}_6$ -alkyl group; R^5 represents a $\text{C}_1\text{-C}_6$ -alkyl group; R^6 , R^7 , R^8 , R^9 , R^{10} , R^{12} , and R^{13} each independently represent a hydrogen atom, or a $\text{C}_1\text{-C}_6$ -alkyl group optionally substituted by at least one hydroxyl group; R^{11} represents a hydrogen atom, or a $\text{C}_1\text{-C}_6$ -alkyl group optionally substituted by at least one substituent independently selected from hydroxyl and $\text{C}_1\text{-C}_6$ -alkoxy; and R^{14} , R^{15} and R^{16} each independently represent a $\text{C}_1\text{-C}_6$ -alkyl group; with the provisos that (i) when E represents $\text{NEC}(\text{O})$, X represents O, S or NH and Y represents O, then Z represents $-\text{NR}^6\text{R}^7$ where R^6 represents a hydrogen atom and R^7 represents either a hydrogen atom or a $\text{C}_1\text{-C}_6$ -alkyl group substituted by at least one hydroxyl group, and (ii) when E represents $\text{NHC}(\text{O})$, X represents O, S or NH, Y represents NH, and R^5 represents CH_2CH_2 , then Z is not $-\text{OH}$ or imidazolyl; or a pharmaceutically acceptable salt or solvate thereof.

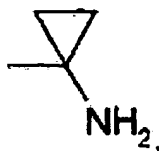
[0125] A compound of general formula:



wherein D represents CH_2 or CH_2CH_2 ; E represents $\text{C}(\text{O})\text{NH}$ or $\text{NHC}(\text{O})$; R^1 and R^2 each independently represent hydrogen, halogen, amino, nitro, $\text{C}_1\text{-C}_6$ -alkyl or trifluoromethyl, but R^1 and R^2 may not both simultaneously represent hydrogen; R^3 represents a group of formula

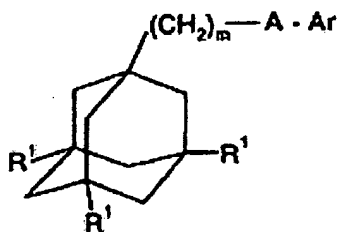


R^4 represents a $\text{C}_1\text{-C}_6$ -alkyl group; X represents an oxygen or sulphur atom or a group NR^{13} , SO or SO_2 ; R^5 represents hydrogen, or R^5 represents $\text{C}_1\text{-C}_6$ -alkyl or $\text{C}_2\text{-C}_6$ -alkenyl, each of which may be optionally substituted by at least one substituent selected from halogen, hydroxyl, (di) $\text{C}_1\text{-C}_6$ -alkylamino, $-\text{Y-R}^6$,

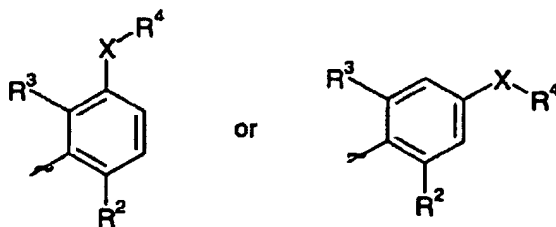


and a 5- or 6-membered heteroaromatic ring comprising from 1 to 4 heteroatoms independently selected from nitrogen, oxygen and sulphur which heteroaromatic ring may itself be optionally substituted by at least one substituent selected from halogen, hydroxyl and C₁-C₆-alkyl; Y represents an oxygen or sulphur atom or a group NH, SO or SO₂; R⁶ represents a group -R⁷Z where R⁷ represents a C₂-C₆-alkyl group and Z represents an -OH, -CO₂H, -NR⁸R⁹, -C(O)NR¹⁰R¹¹ or -N(R¹²)C(O)-C₁-C₆-alkyl group, and, in the case where Y represents an oxygen or sulphur atom or a group NH, R⁶ additionally represents hydrogen, C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, -C(O)NR¹⁴R¹⁵, -CH₂OC(O)R¹⁶, -CH₂OC(O)OR¹⁷ or -C(O)OCH₂OR¹⁸; R⁸, R⁹, R¹⁰, R¹¹ and R¹² each independently represent a hydrogen atom or a C₁-C₆-alkyl group; R¹³ represents hydrogen, C₃-C₈-cycloalkyl, C₃-C₈-cycloalkylmethyl, or R¹³ represents a C₁-C₆-alkyl group optionally substituted by at least one substituent selected from hydroxyl to and C₁-C₆-alkoxy; and R¹⁴, R¹⁵, R¹⁶, R¹⁷, and R¹⁸ each independently represent a C₁-C₆-alkyl group; with the proviso that when E is C(O)NH, X is O, NH or N(C₁-C₆-alkyl), then R⁵ is other than a hydrogen atom or an unsubstituted C₁-C₆-alkyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0126] A compound of general formula:



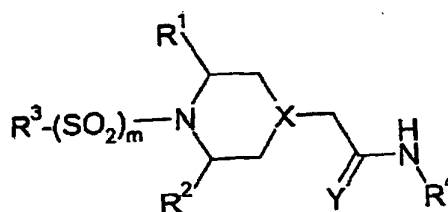
wherein m represents 1, 2 or 3; each R¹ independently represents a hydrogen or halogen atom; A represents C(O)NH or NHC(O); Ar represents a group



X represents a bond, an oxygen atom or a group CO, (CH₂)₁₋₆, CH=, (CH₂)₁₋₆O, O(CH₂)₁₋₆, O(CH₂)₂₋₆O, O(CH₂)₂₋₃O (CH₂)₁₋₃, CR¹(OH), (CH₂)₁₋₃O(CH₂)₁₋₃, (CH₂)₁₋₃O(CH₂)₂₋₃O, NR⁵, (CH₂)₁₋₆NR⁵, NR⁵(CH₂)₁₋₆, (CH₂)₁₋₃NR⁵(CH₂)₁₋₃O (CH₂)₂₋₆NR⁵, O(CH₂)₂₋₃NR⁵(CH₂)₁₋₃, (CH₂)₁₋₃NR⁵(CH₂)₂₋₃O, NR⁵(CH₂)₂₋₆O, NR⁵(CH₂)₂₋₃O(CH₂)₁₋₃, CONR⁵, NR⁵CO, S(O)_n, S(O)_nCH₂, CH₂S(O)_n, SO₂NR⁵ or NR⁵SO₂; n is 0, 1 or 2; R¹ represents a hydrogen atom or a C₁-C₆-alkyl group; one of R² and R³ represents a halogen, cyano, nitro, amino, hydroxyl, or a group selected from (i) C₁-C₆-alkyl optionally substituted by at least one C₃-C₆-cycloalkyl, (ii) C₃-C₈-cycloalkyl, (iii) C₁-C₆-alkyloxy optionally substituted by at least one C₃-C₆-cycloalkyl, and (iv) C₃-C₈-cycloalkyloxy, each of these groups being optionally substituted by one or more fluorine atoms, and the other of R² and R³ represents a hydrogen or halogen atom; either R⁴ represents a 3- to 9-membered saturated or unsaturated aliphatic heterocyclic ring system containing one or two nitrogen atoms and optionally an oxygen atom, the heterocyclic ring system being optionally substituted by one or more substituents independently selected from fluorine atoms, hydroxyl, carboxyl, cyano, C₁-C₆-alkyl, C₁-C₆-hydroxyalkyl, -NR⁶R⁷, -(CH₂)_rNR⁶R⁷ and CONR⁶R⁷, r is 1, 2, 3, 4, 5 or 6; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl

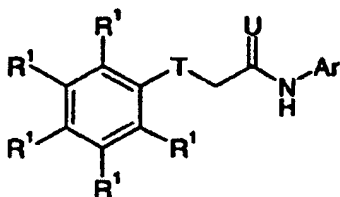
group; R⁶ and R⁷ each independently represent a hydrogen atom or a C₁-C₆-alkyl, C₂-C₆-hydroxyalkyl or C₃-C₈-cycloalkyl group, or R⁶ and R⁷ together with the nitrogen atom to which they are attached form a 3- to 8-membered saturated heterocyclic ring; with the provisos that, (a) when A represents C(O)NH and R⁴ represents an unsubstituted saturated heterocyclic ring system containing one nitrogen atom, then X is other than a bond, and (b) when A represents C(O)NH and X represents a group (CH₂)₁₋₆ or O(CH₂)₁₋₆, then R⁴ does not represent a bond, and (c) when A represents NHC(O) and R⁴ represents an unsubstituted 3- to 8-membered saturated aliphatic heterocyclic ring system containing one nitrogen atom, then X is other than a bond, and (d) when A represents NHC(O) and X represents O(CH₂)₁₋₆, NH(CH₂)₁₋₆ or SCH₂, then R⁴ does not represent an unsubstituted 1-piperidinyl or unsubstituted 1-pyrrolidinyl group, and (e) when A represents NHC(O) and X represents O(CH₂)₂₋₃NH(CH₂)₂, then R⁴ does not represent an imidazolyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0127] A compound of general formula:

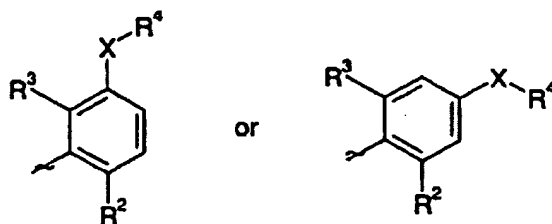


X represents a nitrogen atom or a group C(R⁵); Y represents an oxygen or sulphur atom or a group NR⁶; either R¹ and R² each independently represent a hydrogen atom or a C₁-C₄-alkyl group but do not both simultaneously represent a hydrogen atom, or R¹ and R² together represent a group -CH₂ZCH₂-; Z represents a bond, an oxygen or sulphur atom or a group CH₂ or NR⁷; m is 0 or 1; R³ represents a 5- to 10-membered unsaturated ring system which may comprise from 1 to 4 ring heteroatoms independently selected from nitrogen, oxygen and sulphur, the ring system being optionally substituted by one or more substituents independently selected from halogen, nitro, cyano, NR⁸R⁹, C₁-C₄-alkyl-C(O)NH-, NHR¹²C(O)-, C₁-C₄-alkyl-SO₂-, C₁-C₄-alkyl-SO₂NH-, C₁-C₄-alkyl-NHSO₂-, C₁-C₄-alkoxy, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms; R⁴ represents a phenyl or pyridinyl group, each of which is substituted in an ortho position with a substituent selected from halogen, C₁-C₄-alkoxy, C₁-C₄-alkylthio, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms, the phenyl or pyridinyl group being optionally further substituted by one or more substituents independently selected from halogen, cyano, hydroxyl, C₁-C₄-alkylthio, C₁-C₄-alkyl-NH-, NHR¹³-C₁-C₄-alkyl-, C₁-C₄-alkyl-SO₂-, C₁-C₄-alkyl-SO₂NH-, C₁-C₄-alkyl-NHSO₂-, C₁-C₄-alkyl-C(O)NH-, C₁-C₄-alkyl-NHC(O)-, -D-G, C₁-C₄-alkoxy optionally substituted by -NR¹⁴R¹⁵ or by R¹⁶, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms or by one or more hydroxyl groups, or R⁴ represents a 9- or 10-membered unsaturated bicyclic ring system which may comprise from 1 to 4 ring heteroatoms independently selected from nitrogen, oxygen and sulphur, the bicyclic ring system being optionally substituted by one or more substituents independently selected from halogen, oxo, C₁-C₄-alkyl, C₁-C₄-alkoxy, C₁-C₄-alkylthio and -NR¹⁰R¹¹; D represents an oxygen atom or a group (CH₂)_{sub.n} or CH₂NH; n is 1, 2 or 3; G represents a piperazinyl, morpholinyl or 2,5-diazabicyclo[2.2.1]heptyl group, or G represents a piperidinyl group optionally substituted by amino; R⁵ represents a hydrogen atom, or a hydroxyl or C₁-C₄-alkoxy group; R⁶ represents a hydrogen atom, or a cyano, nitro, hydroxyl, C₁-C₄-alkyl or C₁-C₄-alkoxy group; R⁷, R⁸ and R⁹ each independently represent a hydrogen atom or a C₁-C₄-alkyl group; R¹⁰ and R¹¹ each independently represent a hydrogen atom or a C₁-C₄-alkyl group, or R¹⁰ and R¹¹ together with the nitrogen atom to which they are attached form a 5- or 6-membered saturated heterocyclic ring comprising one or two ring nitrogen atoms; R¹² represents a hydrogen atom, or a C₁-C₄-alkyl group optionally substituted by amino; R¹³ represents a hydrogen atom, or a C₁-C₄-alkyl group optionally substituted by hydroxyl; R¹⁴ and R¹⁵ each independently represent a hydrogen atom or a C₁-C₄-alkyl group optionally substituted by hydroxyl, or R¹⁴ and R¹⁵ together with the nitrogen atom to which they are attached form a 5- or 6-membered saturated heterocyclic ring comprising one or two ring nitrogen atoms; and R¹⁶ represents a 1-(C₁-C₄-alkyl)-piperidinyl group; with the proviso that when m is 0, X is N and Y is O, then R⁴ does not represent 2-benzothiazolyl; or a pharmaceutically acceptable salt or solvate thereof.

[0128] A compound of general formula:

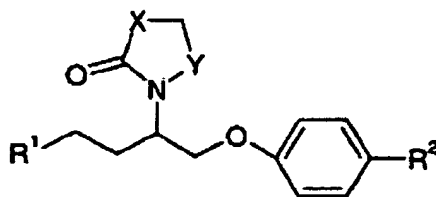


wherein: each R¹ independently represents a hydrogen or halogen atom, or a trifluoromethyl, cyano, nitro, C₁-C₆-alkyl or C₁-C₆-alkoxy group; T represents an oxygen atom or a group NH; U represents an oxygen or sulphur atom or a group NH; Ar represents a group:



X represents a bond, an oxygen atom or a group CO, CH₂, CH₂O, O(CH₂)_m, CH₂OCH₂, NR⁵, CH₂NR⁵, NR⁵CH₂, CH₂NR⁵CH₂, CONR⁵, S(O)_n or SO₂NR⁵, m is 1, 2 or 3; 15 n is 0, 1 or 2; one of R² and R³ represents a halogen, cyano, nitro, amino, hydroxyl, or a group selected from C₁-C₆-alkyl optionally substituted by at least one C₃-C₈-cycloalkyl, C₃-C₈-cycloalkyl, C₁-C₆-alkyloxy optionally substituted by at least one C₃-C₈-cycloalkyl, C₃-C₈-cycloalkyloxy, S(O)_pC₁-C₆-alkyl or S(O)_qC₃-C₈-cycloalkyl, each of these groups being optionally substituted by one or more fluorine atoms, and the other of R² and R³ represents a hydrogen or halogen atom or a methyl group; p is 0, 1 or 2; q is 0, 1 or 2; R⁴ represents di(C₁-₂alkyl)N(CH₂)_t, where t is 0, 1 or 2 or imidazolyl, or R⁴ represents a 3- to 9-membered saturated heterocyclic ring system containing one or two nitrogen atoms, the heterocyclic ring system being optionally substituted by one or more substituents independently selected from fluorine atoms, hydroxyl, C₁-C₆-alkyl, acetyl, hydroxyC₁-C₆-alkyl, -NR⁶R⁷, -(CH₂)_rNR⁶R⁷, -CONR⁶R⁷ and pyrimidinyl, or R⁴ represents a 3- to 8-membered saturated carbocyclic ring system substituted by one or more substituents independently selected from -NR⁶R⁷, -(CH₂)_rNR⁶R⁷, -CONR⁶R⁷ the ring system being optionally further substituted by one or more substituents independently selected from fluorine atoms, hydroxyl and C₁-C₆-alkyl; r is 1, 2, 3, 4, 5 or 6; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; and R⁶ and R⁷ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group, or R⁶ and R⁷ together with the nitrogen atom to which they are attached form a 3- to 8-membered saturated heterocyclic ring, provided that when R³ represents a cyano group, then X is other than a bond; or a pharmaceutically acceptable salt or solvate thereof.

[0129] A compound of general formula:



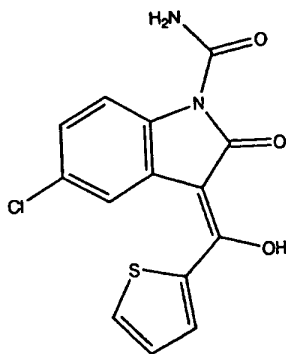
wherein X represents an oxygen or sulphur atom or a group NH, CH₂, CH₂CH₂ or OCH₂; Y represents a group CH₂ or C=O; R¹ represents a pyridyl or pyrimidinyl group; R² represents a phenyl, pyridyl or pyrimidinyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or an amino, cyano, hydroxyl, nitro, C₁-C₆-alkyl, halo-C₁-C₆-alkyl, C₁-C₆-alkoxy, C₁-C₆-alkylthio, (di)C₁-C₆-alkylamino, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphonyl, C₁-C₆-alkylsulphonyl, -NR³SO₂R⁴ or -SO₂NR⁵R⁶ group, or a group -Z-(CH₂)_p-Z-(CH₂)_q-H wherein each Z independently represents a nitrogen or oxygen atom, p is an integer from 2 to 5 and q is 0 or an integer from 1 to 5; R³ and R⁴ each independently represent a hydrogen atom or

a C₁-C₆-alkyl group; and R⁵ and R⁶ each independently represent a hydrogen atom or a C₁-C₆-alkyl group, or together with the nitrogen atom to which they are attached form a pyrrolidinyl or piperidinyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0130] An additional embodiment of the invention provides a method for treating affective disorders by administering an agent modulating the activity of P2X7R, such as an antagonist of the P2X7R. The term "antagonist" means an agent or drug or a compound that opposes the physiological effects of another. Examples of P2X7R antagonists include, but are not restricted to, adamantane derivatives, isoquinolines and their derivatives, substituted phenyl compounds, piperidine derivatives, piperazine derivatives. P2X7R antagonists are described in the art and include the compounds found in Chen et al., Bioconjugate Chem. 13 (2002), 1100-1111; WO 99/29660; WO 99/29661; WO 99/296896; WO 00/61569; WO 01/42194; WO 01/44170; WO 01/44213; WO 00/71529; WO 01/46200. P2X7R activity can also be modulated by RNA-based interference mechanisms and methods such as, but not limited to, small interference RNA (siRNA) molecules, and long double-stranded RNA (dsRNA).

[0131] Since it was unexpectedly found that agonists of P2X7R improve the symptoms of mice selected for anxiety and depressive behaviour, the present invention relates in a further embodiment to a method for treating affective disorders such as anxiety and depressive behaviour by administering an agent modulating the activity of P2X7R such as an agonist of the P2X7R. What is even more striking is the finding of the present application shown in Example 10 that antagonists of P2X7R have no antidepressive effects although this is being taught by the prior art, for example, WO 03/042190, WO 03/042191, WO 03/049353 or US 2004/0029841. WO 03/042190, WO 03/042191, WO 03/049353 or US 2004/0029841 describe compositions of P2X7R antagonists and methods of treating P2X7 mediated diseases by administering these compounds. However, while the prior art may make a link between P2X7R and, e.g., treating depression, it is generally implied that antagonists of P2X7R have to be used in the treatment of, e.g., depression. Thus, the finding of the present invention that antagonists have no antidepressive effects, but rather agonists of P2X7R have an antidepressive effect could not have been expected and is, thus, even more surprising. The present application, therefore, provides, inter alia, the basis for the development of effective medicaments having therapeutic benefits against, e.g., depression. In particular, said medicaments comprising an agonist of P2X7R are effective in treating affective disorders, in particular for treating those disorders mentioned herein, and in particular for treating depression. Examples of P2X7R agonists include but are not restricted to ATP, ATP-4, and BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)). Preferably, the P2X7R agonist to be used for treating affective disorders is BzATP. More preferably, BzATP is used to treat depression or anxiety as demonstrated in Example 9 hereinbelow.

[0132] The present application provides another unexpected finding in that the chemical compound called tenidap or a derivative thereof also functions as a modulator of P2X7R which can thus be used for treating affective disorders. So far, various medical applications are described for tenidap or a derivative thereof. However, the use of tenidap or a derivative thereof for treating affective disorders is neither known nor suggested in the prior art. Accordingly, the present application relates to the use of tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides for the preparation of a pharmaceutical composition for treating an affective disorder. Of course, also a method of treatment of an affective disorder comprising administering a therapeutically effective amount of tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides to a subject suffering from said disorder is envisaged. The composition of tenidap (5-chloro-2,3-dihydro-2-oxo-3-(2-thienylcarbonyl)-indole-1-carboxamide, i.e. C₁₅H₁₁ClN₂O₂S)) having the following structural formula



and other 3-substituted-2-oxindole-1-carboxamides and their use as antiinflammatory and analgesic agents, and as inhibitors of both the cyclooxygenase (Cox) and lipoxygenase (5-LPO) enzymes was first disclosed in US 4,556,672. Of course, various modifications of, e.g., side groups or atoms which are well known in the art can be made to the

composition of tenidap.

Derivatives of tenidap or 3-substituted-2-oxindole derivatives are described, for example, in US 4,556,672; US 4,658,037; US 4,721,712; US 5,290,802; US 5,118,703; US 5,270,331; US 5,298,522; US 5,086,186; US 5,449,788 and US 5,795,902. Various processes for the synthesis of tenidap and other 3-substituted-2-oxindole-1-carboxamides are well known in the art, see for example US 4,652,658; US 4,665,194; US 4,952,703; EP-B1 155 828, WO 90/04393, WO 94/07488, WO 94/17061, WO 95/20574; WO 97/36895; van Deurzen et al., *J. Mol. Catal. B-Enzym.*, 2 (1996), 33-42; Porcs-Makkay and Simig, *Org. Process. Res. Dev.*, 4 (2000), 10-16; Kumar et al., *Org. Process. Res. Dev.*, 5 (2001), 61-64. The anhydrous crystalline form of the sodium salt of tenidap is described in US 5,036,099 and WO 88/05656. Injectable composition and pharmaceutical composition for rectal administration of tenidap are mentioned in EP-B1 508 311 and EP-B1 508 310, respectively. It is also described in the prior art that tenidap or a derivative thereof can be administered in combination with tetracycline (US 5,308,839) or methotrexate (WO 96/35419) for the treatment of rheumatoid arthritis. Inhibition of the photodecomposition of tenidap and other 3-substituted-2-oxindole-1-carboxamides is disclosed in WO 96/33701.

Further applications of tenidap or a derivative thereof and other 3-substituted-2-oxindole-1-carboxamides have been described for the inhibition of interleukin-1 biosynthesis in mammals and for the treatment interleukin-1 mediated disorders (US 4,861,794); for the inhibition of elastase release from neutrophils (US 5,006,547); for the suppression of T-cell function in mammals and to treat T-cell mediated autoimmune disorders of the systemic or organ specific type (US 4,853,409; Dolhain et al., *Scand. J. Immunol.* 42(1995), 686-693). Tenidap is also used for the treatment of Alzheimer's disease (WO 96/31209; US 5,545,656).

Tenidap or a derivative thereof or its pharmaceutically base salts have also been shown to inhibit activation of collagenase, treat collagenase mediated disorders and diseases, and inhibit the activity of myeloperoxidase in mammals (US 5,008,283). Tenidap can reduce total serum cholesterol, LDL cholesterol and triglycerides (US 5,122,534), and can be used for the treatment of ischemia induced myocardial injury and cytokine mediated myocardial injury (EP-B1 679 396). However, none of the aforementioned documents discloses a use of tenidap or derivatives thereof or 3-substituted-2-oxindole-1-carboxamides thereof for treating, for example, affective disorders such as depression.

[0133] Sanz et al., *Eur. J. Pharmacol.* 355 (1998), 235-244 suggest that tenidap can enhance the activity of the P2X7 receptor. It is suggested that tenidap may act by increasing ATP levels or improving the effect of ATP on P2X7. ATP is the natural ligand of P2X7R. Accordingly, tenidap or a derivative thereof is a modulator of P2X7R as is described herein since a modulator is either directly or indirectly modulating the activity or expression of P2X7R. By making use of the teaching of the present invention that modulators of P2X7R are useful for treating affective disorders, it is envisaged that tenidap or a derivative thereof is used as a modulator of P2X7R activity for the preparation of a pharmaceutical composition for the treatment of an affective disorder, examples of which are described herein. The preparation of pharmaceutical compositions, the modes of administration etc. are described supra and infra and apply to the use of tenidap or a derivative thereof for the preparation of a pharmaceutical composition, mutatis mutandis. Moreover, also the embodiments relating to the uses of and methods for treating affective disorders described herein apply to the use of tenidap or a derivative thereof for treating affective disorders or the corresponding method of treatment, mutatis mutandis.

[0134] The present application moreover envisages that modulators of P2X7R activity can be used in any combinations thereof for treating an affective disorder. For example, BzATP and tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides may be used together, e.g., simultaneously or by successive administration for treating an affective disorder.

[0135] In a preferred embodiment the pharmaceutical composition described herein optionally comprises further molecules which have cell protective properties capable of altering the characteristics of the components of the invention thereby, for example, modulating, preferably blocking possible undesired, adverse or negative side effects of these components. One such possible undesired, adverse or negative side effect is the formation of pores in the cell membrane of treated cells which ultimately leads to apoptosis. Accordingly, said further molecules belong to the class of beta-adrenergic receptor modulators including agonists or antagonists having membrane-stabilizing properties. Beta-adrenergic receptor modulators including agonists and antagonists are compounds which decrease or increase the positive chronotropic, positive inotropic, bronchodilator and vasodilator responses caused by beta-adrenergic receptor agonists or antagonists. The magnitude of this decreased or increased response is proportional to the existing sympathetic tone and the concentration of beta-adrenergic receptor blocking agent which reaches the receptor sites. A beta-adrenergic receptor modulator in the context of the present invention is thus an antagonist or agonist. The activity of a beta-adrenergic receptor antagonist or agonist can be determined as is well known in the art. The activity of beta-adrenergic receptors can be determined by measuring the accumulation of cyclic adenosine mono-phosphate (cAMP) in Chinese hamster ovary (CHO) cells. CHO cells can be uniquely transfected with the cDNA coding for the human beta 1-, beta2-, or beta3-adrenergic receptor under the control of the CMV promoter or any other suitable promoter element. Transfection of the cells is performed using standard cell transfection methods, see for example, Joyner, "Gene Targeting: A Practical Approach", Oxford University Press, New York, 1993. Cells overexpressing one of the

beta-adrenergic gene are then grown to confluence in Ham's F12 media (Gibco BRL) containing 10% fetal bovine serum, 500 mg/ml Geneticin, 100 U/ml penicillin, 100 mg/ml streptomycin and 250 ng/ml fungizone according to the procedure described in American Type Culture Collection Catalogue of Cell Lines and Hybridomas, Seventh Edition, 1992, p. 36, ATCC CCL 61 CHO-K1. Beta-adrenergic modulator compounds can be prepared as 10 mM stock solutions in DMSO (0.1% DMSO, final concentration), diluted in Ham's F12 media and added to the cells at 10^{-10} to 10^{-5} M along with 10^{-3} M isobutylmethylxanthine to inhibit phosphodiesterase activity. The media and cells are then incubated for 5 minutes at 37°C. At the end of this period, the media is aspirated and the cells lysed in 0.01 N HCl. The cellular content of cAMP can then be determined by radioimmunoassay (RIA) using a kit from New England Nuclear (Burlington, Mass.). There is a direct correlation between the cellular content of cAMP and the activation/inhibition of the beta-adrenergic receptor. Other methods for determining the activity of a beta-adrenergic receptors are well described in the art, see for example, Vansal and Feller, J. Recept. Signal. Transduct. Res. 19 (1999) 853-863; Durocher et al., Anal. Biochem. 284 (2000) 316-326.

[0136] Examples of compounds which fit the definition of a beta-adrenergic receptor modulating agent include but are not limited to known beta-adrenergic receptor antagonist such as timolol, sotalol, esmolol, catechol, propranolol, betaxolol, penbutolol, metoprolol, acebutolol, atenolol, metoprolol, pindolol, and bisoprolol, and their salts, hydrates, solvates and any crystal forms in which they may occur. Further examples of beta-adrenergic receptor blocking agents are described in US 5,776,930. Preferred examples of beta-adrenergic receptor antagonists are DL-propranolol, D-propranolol and labetalol. DL-propranolol and labetalol are are beta-adrenergic receptor antagonists with membrane-stabilizing properties, while D-propranolol is an optical isomer with poor beta-adrenergic blocking activity. The optional addition of beta-adrenergic receptor antagonists or agonists to the pharmaceutical composition of the present invention for treating an affective disorder may be useful in the context of administering P2X7R agonists. This is because the prior art suggests that the activation of P2X7R by agonists may result in cell death by triggering the formation of pores within the cell membrane. However, as is demonstrated in Example 9 of the present application the pore-forming activity effect described for P2X7R agonists by the prior art was only observed for very few cells. Recently, Alzola et al., Cell Signal. 13 (2001), 465-473 have shown that concentrations of 10 to 300 μ M DL-propranolol, D-propranolol or labetalol can inhibit the pore-forming activity of P2X7R without affecting the opening of the cation channel activity of P2X7R. From FR 2768626 it is also known that beta-adrenergic modulators, e.g. agonists are useful as apoptosis inhibiting agents. Accordingly, in a preferred embodiment of the present invention, beta-adrenergic receptor modulators including antagonists or agonists are administered in combination with P2X7R agonists for the treatment of affective disorders. Said beta-adrenergic receptor antagonists or agonists are preferably administered in a concentration of 10 to 300 μ M.

[0137] Dosage, pharmaceutical preparation and delivery of P2X7R modulating agent for use in accordance with the present invention may be formulated in conventional manner according to methods found in the art, using one or more physiological carriers or excipient, see, for example Ansel et al., "Pharmaceutical Dosage Forms and Drug Delivery Systems", 7th edition, Lippincott Williams & Wilkins Publishers, 1999. Thus, the P2X7R modulating agent and its physiologically acceptable salts and solvates may be formulated for administration by inhalation, insufflation (either through the mouth, or nose), oral, buccal, parenteral, or rectal administration.

[0138] For oral administration, the pharmaceutical composition of the P2X7 modulating agent may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutical acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone, hydroxypropyl methylcellulose), fillers (e.g., lactose, microcrystalline cellulose, calcium hydrogen phosphate), lubricants (e.g., magnesium stearate, talc, silica), disintegrants (e.g., potato starch, sodium starch glycolate), or wetting agents (e.g., sodium lauryl sulphate). Liquid preparations for oral administration may take the form of, for example, solutions, syrups, or suspensions, or may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparation may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol, syrup, cellulose derivatives, hydrogenated edible fats), emulsifying agents (e.g., lecithin, acacia), non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol, fractionated vegetable oils), preservatives (e.g., methyl or propyl-p-hydroxycarbonates, soric acids). The preparations may also contain buffer salts, flavouring, coloring and sweetening agents as deemed appropriate. Preparations for oral administration may be suitably formulated to give controlled release of the agent modulating P2X7R activity.

[0139] For administration by inhalation, the agent modulating P2X7R activity for use according to the present invention is conveniently delivered in the form of an aerosol spray presentation from a pressurised pack or a nebulizer, with the use of a suitable propellant (e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas). In the case of a pressurised aerosol, the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, for example, gelatine, for use in an inhaler or insufflator may be formulated containing a powder mix of the P2X7R activity modulating agent and a suitable powder base such as lactose or starch.

[0140] An agent modulating P2X7R activity may be formulated for parenteral administration by injection, for example, by bolus injection or continuous infusion. Site of injections include intra-venous, intra-peritoneal or sub-cutaneous.

Formulations for injection may be presented in units dosage form (e.g., in phial, in multi-dose container), and with an added preservative. The agent modulating P2X7R activity may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing, or dispersing agents. Alternatively, the agent may be in powder form for constitution with a suitable vehicle (e.g., sterile pyrogen-free water) before use.

[0141] An agent modulating P2X7R activity may, if desired, be presented in a pack, or dispenser device which may contain one or more unit dosage forms containing the said agent. The pack may for example comprise metal or plastic foil, such as blister pack. The pack or dispenser device may be accompanied with instruction for administration.

[0142] In a more preferred embodiment the aforementioned methods or uses are envisaged to treat affective disorders selected from the group consisting of major depression, generalized anxiety disorder and bipolar disorder.

[0143] In a particularly preferred embodiment said major depression is selected from the group consisting of major depression, dysthymia, atypical depression, premenstrual dysphoric disorder and seasonal affective disorder.

[0144] In another particularly preferred embodiment said generalized anxiety disorder is selected from the group consisting of panic disorder, phobias, agoraphobia, social phobia, specific phobia, obsessive-compulsive disorder, post-traumatic stress disorder, separation anxiety disorder, mania, hypomania and cyclothymic disorder.

[0145] A still also particularly preferred embodiment is that said bipolar disorder is bipolar disorder type I or bipolar disorder type II.

[0146] Additionally, the present invention relates to a kit comprising the nucleic acid molecule, the vector, the host, the polypeptide, the antibody or the aptamer, the primer or pair of primers of the invention or the molecule as identified or characterized in a method herein below of the present invention.

Advantageously, the kit of the present invention further comprises, optionally (a) reaction buffer(s), storage solutions and/or remaining reagents or materials required for the conduct of scientific or diagnostic assays or the like. Furthermore, parts of the kit of the invention can be packaged individually in vials or bottles or in combination in containers or multicontainer units.

The kit of the present invention may be advantageously used, inter alia, for carrying out the method of producing a polypeptide of the invention, the method(s) of identification and/or characterization of molecules specifically interacting with P2X7R ATP-gated ion channels as described herein below and/or it could be employed in a variety of applications referred herein, e.g., as diagnostic kits, as research tools or therapeutic tools. Additionally, the kit of the invention may contain means for detection suitable for scientific, medical and/or diagnostic purposes. The manufacture of the kits follows preferably standard procedures which are known to the person skilled in the art.

[0147] Furthermore, the present invention relates to a method for identifying compounds or mixtures of compounds which are capable of specifically interacting with a polypeptide of the present invention, comprising the steps of (a) contacting a polypeptide of the present invention with a candidate compound or mixture of compounds to be tested; and (b) determining whether said is capable of specifically interacting with said polypeptide. The polypeptide may be provided directly or by expression of a corresponding nucleic acid molecule or vector of the invention, e.g., in vitro or in a suitable host cell.

[0148] Additionally, the present invention relates to a method for the characterization of compounds which are capable of altering characteristics of the polypeptides of the present invention, comprising the steps of (a) contacting a polypeptide of the invention with said compound; and (b) determining whether the compound alters a characteristic of said polypeptide.

[0149] The term "altering characteristic of the polypeptide of the present invention" means that the functional characteristics to the polypeptides of the present invention in comparison to functional characteristics which they had before being contacted with the compounds identified by the above-described method: as described hereinabove are altered; i.e. changed.

[0150] Said identification and/or characterization of which are capable of interacting with or altering characteristics of the polypeptide of this invention, may be, inter alia, achieved by transfecting an appropriate host with a nucleic acid molecule of invention. Said hosts comprise, but are not limited to, HEK 293 cells or are injected into frog oocytes, preferably a *Xenopus* oocyte for functional expression (Goldin, *Methods Enzymol.* 207 (1992), 266). Expressed P2X7R ATP-gated channels can be examined using standard two-electrode voltage clamp techniques (Stuhmer, *Methods Enzymol.* 207 (1992), 319; Kohler, *Science* 273 (1996), 1709). After expression of a P2X7R ATP-gated ion channel as defined herein, membrane currents may be deduced in the absence and/or presence of the molecule to be identified and/or characterized. Methods for the deduction of membrane currents are well known in the art and comprise, e.g., patch clamp methods as described in Hamill, *Pflüger's Arch.* 391 (1981), 85-100 or two-electrode voltage clamp in oocytes, as described in Methfessel, *Pflügers Archive* 407 (1986), 577-588. In accordance with the present invention the term "interacting with the polypeptides of the present invention" means that the polypeptides of the present invention interact directly and/or indirectly with compounds identified by the method described above. Furthermore, the present invention relates to a method of screening for molecules which are capable of interacting with the polypeptide of this invention, comprising the steps of (a) contacting a polypeptide of the invention with a molecule; and (b) measuring

and/or detecting a response; and (c) comparing said response to a standard response as measured in the absence of said candidate molecule.

[0151] The present invention also relates to a method for identifying a compound which is capable of enhancing or reducing the expression of the P2X7R gene comprising the steps of contacting a cell which expresses the P2X7R gene from its natural promoter or a reporter gene driven by the P2X7R promoter and determining whether the expression of the gene is increased or reduced when compared to conditions in which the compound is not present.

Potential candidate molecules or candidate mixtures of molecules may be, inter alia, substances, compounds or compositions which are of chemical or biological origin, which are naturally occurring and/or which are synthetically, combinatorially and/or chemically produced or compounds or compositions described hereinabove. Thus, candidate molecules may be proteins, protein-fragments, peptides, amino acids and/or derivatives thereof or other compounds, such as ions, which bind to and/or interact with wild-type P2X7R ATP-gated ion channels. Such binding and/or interacting candidate compounds may be found employing, inter alia, yeast two-hybrid systems or modified yeast two-hybrid systems as described, for example in Fields, Nature 340 (1989), 245-246; Gyuris, Cell 75 (1993), 791-801; or Zervos, Cell 72 (1993), 223-232.

[0152] Furthermore, potential candidate molecules may be contacted with a cell, such as an oocyte or a HEK 293 cell, which expresses a polypeptide of the invention or with a membrane patch comprising a polypeptide of the invention and a corresponding response (inter alia, a dose-response response, a current-response, or single current channel response) may be measured in order to elucidate any effect said candidate molecule causes.

[0153] Within the scope of the present invention are also methods for identifying, characterizing and for screening of molecules which are capable of interacting with the P2X7R ATP-gated ion channels according to the invention which comprise so-called high-throughput screening methods and similar approaches which are known in the art (Spencer, Biotechnol. Bioeng. 61 (1998), 61-67; Oldenburg, Annu. Rev. Med. Chem. 33 (1998), 301-311) carried out using 96-well, 384-well, 1536-well (and other) commercially available plates. Further methods to be employed in accordance with the present invention comprise, but are not limited to, homogenous fluorescence readouts in high-throughput screenings (as described, inter alia, in Pope, Drug Discovery Today 4 (1999), 350-362). The method of the present invention for identification, characterization and/or screening of molecules capable of interacting with P2X7R ATP-gated ion channels can, inter alia, employ hosts as defined herein which express the polypeptide of the present invention. Cell-based assays, instrumentation for said assays and/or measurements are well-known in the art and described, inter alia, in Gonzalez, Drug Discovery Today 4 (1999), 431-439 or Ramm, Drug Discovery Today 4 (1999), 401-410. It is also envisaged that the high throughput screens described herein are conducted by using, for example cRNA, i.e. synthetic RNA from a cDNA construct) that can be introduced in host cells, such as *Xenopus* oocytes using routine methods in the art. As an example, direct nucleic acid injection can be employed, such as the Eppendorf microinjection system (Micromanipulator 5171 and Transjector 5242). The injected/transformed cells can be analyzed for ion currents about 4 hours later using patch-clamp techniques which are commonly practiced in the art.

[0154] Additionally, the present invention relates to a method for the production of a pharmaceutical composition comprising the steps of a method of the invention for identifying, characterizing and/or screening of molecules which are capable of interacting with and/or altering the characteristics of a P2X7R ATP-gated ion channel of the invention and further comprising a step, wherein a derivative of said identified, characterized and/or screened molecule is generated. Such a derivative may be generated by, inter alia, peptidomimetics.

[0155] The invention furthermore relates to a method for the production of a pharmaceutical composition comprising the steps of a method of the invention for identifying, characterizing, screening and/or derivatizing of molecules which are capable of interacting with and/or altering the characteristics of a P2X7R ATP-gated ion channel and formulating the molecules identified, characterized, screened and/or derivatized in pharmaceutically acceptable form. In a more preferred embodiment the present invention relates to a method wherein said molecule(s) comprise(s) (a) neuroprotective, (a) nootropic and/or (a) antiepileptic molecule(s).

[0156] Yet another embodiment of the invention is the use of a P2X7R polypeptide, in particular those according to the present invention, to identify biological, chemical, or pharmacological agents that can have an antidepressive effect. The term 'agent' refers to a chemical compound or composition capable of inducing a desired therapeutic or prophylactic effect when properly administered to a subject or cell. For example, the present invention allows the generation of cells expressing P2X7R for the identification and characterization of agents which modulate ionic influx and efflux. For example, HEK293 cells, or other cell lines (e.g., HCN-1A, HCN-2, HIT-T15, RIN-m5F, betaTC3, PC12, HT22, SH-SY5Y, Neuro2A or CA77), can be stably transfected with cDNA encoding the human P2X7R and plated in 12, 96 and 384 well plates. Said cells are cultured in appropriate medium. Examples of such medium are well known in the art, see, for example Freshney, "Culture of Animal Cells: A Manual of Basic Technique, 4th edition, Wiley-Liss Publishing, 2000.

[0157] Said cells can then be pre-incubated with said agents for 15 min prior to stimulation with 3 mM ATP for 10 minutes. Reactions are then terminated by rapid aspiration of the extracellular medium in each well. The cells in each well are subsequently extracted overnight with 1 ml 10% HN03. Potassium (K⁺) content in the extracts can be determined by atomic absorbance spectrophotometry. Agent function is then measured by the percent inhibition or stimu-

lation of the K⁺ release triggered by 3 mM ATP and compared to K⁺ release in the absence of the agents. P2X7R activity can also be monitored according to the movement of calcium (Ca²⁺; see Denyer et al., Drug Discov. Today 7 (1998), 323-332; González et al., Drug Discov. Today 9 (1999), 431-439; Helmchen and Waters, Eur. J. Pharmacol. 447 (2002), 119-129). Agents can also be verified in the absence of ATP.

[0158] P2X7R activity can also be monitored according to secretion of neurotransmitters such as glutamate and GABA. Neurotransmitter levels in treated cells can be quantified by suitable methods, e.g., Enzyme Linked Immunoabsorbent Assay (ELISA), Radio Immuno Assay (RIA), High Performance Liquid Chromatography (HPLC). Using these methods, a large number of compounds can be screened for increase in neurotransmitter (for example, glutamate) secretion. The release of glutamate can be measured for example by Fluorometric glutamate release assays (e.g.,

[0159] In a further aspect the present invention uses the P2X7R polypeptides disclosed herein or polypeptides of the present invention in a method for identifying compounds or agents having agonist activity to said P2X7R polypeptides or to the polypeptides of the present invention. Agents and compounds are defined and described hereinabove and hereinbelow. In particular, cells that express the P2X7 gene are contacted with candidate agents, molecules or compounds as described hereinabove and either calcium influx or ethidium bromide entry is measured by methods known in the art, described hereinabove and in particular described in Example 8 hereinbelow. The cells used in the method for identifying agonists to P2X7R are preferably cells of a hippocampal cell line. Hippocampal cell lines are prepared by methods known in the art, for example, described in EP 0 773 287 or EP 0 773 292. Non limiting examples of hippocampal cell lines are rat H19-7 hippocampal cells (ATCC-2526) described in Eves et al. Proc. Natl. Acad. Sci. USA 89 (1992), 4373-4377, mouse HN9.10 hippocampal cells described in Lee et al. J. Neurosci. 10 (1992), 1779-1787 or rat Hi5B hippocampal cells described in Renfranz et al., Cell 66 (1991), 713-729. Preferably, the hippocampal cells used in accordance with the aforementioned method are cells of the HT-series (see Davis and Maher (1994), Brain Res. 652, 169-173), Morimoto and Koshland (1990), Neuron 5, 875-880). It is also preferred that the hippocampal cells express the endogenous P2X7R gene. However, it is also envisaged that such cells may be genetically modified by introducing an exogenous P2X7R gene using methods commonly known in the art. More preferably, HT-22 cells are used for identifying agonists to the P2X7R polypeptides described herein or to the polypeptides of the present invention and HT-39 cells are used as a negative control as described in Example 8 hereinbelow.

[0160] In another embodiment, cells are transfected with nucleic acid constructs encoding a reporter gene regulated by the P2X7R promoter (see above), an increase or decrease in the expression of the reporter gene in response to biological or pharmaceutical agents can be analyzed using methods that detect levels or status of protein or mRNA present in the corresponding cell or detect biological activities of the reporter gene. Suitable reporter molecules or labels, which may be used, include radionucleotides, enzymes, fluorescent, chemiluminescent or chromogenic agents as well as substrates, co-factors, inhibitors, magnetic particles, and the like. Designing such drug screening assays are well known in the art; see Harvey ed., 'Advances in drug discovery techniques', John Wiley and Sons, 1998; Vogel and Vogel eds., 'Drug discovery and evaluation: Pharmaceutical assays', Springer-Verlag Berlin, 1997). For example, drug screening in animal models, in vitro tests using animal cells, or in vivo tests involving toxicology tests in animals. An in vitro model can be used for screening libraries of compounds in any of a variety of drug screening techniques.

[0161] Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 Daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise carbocyclic or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups.

[0162] Candidate agents are also found among biomolecules including peptides, amino acids, saccharides, fatty acids, steroids, purines, pyrimidines, nucleic acids and derivatives, structural analogs or combinations thereof. Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, etc. to produce structural analogs.

[0163] Another technique for drug screening, which may be used, provides for high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO 84/03564. In this method, as applied to the proteins of the invention large numbers of different small test compounds, e.g. aptamers, peptides, low-molecular weight compounds etc., are provided or synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with the proteins or fragments thereof, and washed.

Bound proteins are then detected by methods well known in the art. Purified proteins can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support. In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding the protein specifically compete with a test compound for binding the protein. In this manner, the antibodies can be used to detect the presence of any peptide, which shares one or more antigenic determinants with the protein.

[0164] The present invention further particularly provides a method, wherein the pharmaceutical composition to be produced further comprises neuroprotective substances, nootropic substances, brilliant blue, piperidine or derivatives thereof, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate or 3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate. It is also envisaged that the pharmaceutical compositions to be produced further comprise antidepressants such as fluoxetine, paroxetine, sertraline, fluvoxamine, mirtazapine, reoxetine, nefazodone or lithium carbonate.

[0165] In a preferred embodiment of the present invention, the compounds of the aforementioned methods comprise antagonist(s), partial agonist(s), partial agonist(s) and/or agonist(s) for an altered ATP-gated ion channel P2X7R.

[0166] In accordance with the present invention, the term "antagonist" denotes molecules/substances, which are capable of inhibiting and/or reducing an agonistic effect. The term "antagonist" comprises competitive, non-competitive, functional and chemical antagonists as described, inter alia, in Mutschler, "Arzneimittelwirkungen" (1986), Wissenschaftliche Verlagsgesellschaft mbH, Stuttgart, Germany. The term "partial antagonist" in accordance with the present invention means a molecule/substance that is capable of incompletely blocking the action of agonists through, inter alia, a non-competitive mechanism.

In the context of the present invention, an antagonist is preferably a drug that does not provoke a response itself, but blocks agonist-mediated responses. It is a chemical entity that opposes the receptor-associated responses normally induced by another bioactive agent. For the P2X7R, the antagonists have an IC50 between 10 nanomolar and 300 micromolar.

[0167] As "agonist", in accordance with this invention, molecules/substances are denoted which have an affinity as well as an intrinsic activity. Mostly, said intrinsic activity (α) is defined as being proportional to the quotient of the effect, triggered by said agonist (EA) and the effect which can be maximally obtained in a given biological system (Emax): therefore, the intrinsic activity can be defined as

$$\alpha \sim \frac{E_A}{E_{\max}}$$

[0168] The highest relative intrinsic activity results from EA/Emax=1. Agonists with an intrinsic activity of 1 are full agonists, whereas substances/molecules with an intrinsic activity of >0 and <1 are partial agonists. Partial agonists show a dualistic effect, i.e. they comprise agonistic as well as antagonistic effects.

Preferably, in the context of the present invention, an agonist (or full agonist) is an endogenous substance or a drug that can interact with a receptor and initiate a maximal or complete physiological or a pharmacological response characteristic of that receptor. ATP, the natural ligand for the P2X7R, is an agonist with an EC50 of 300 micromolar while the synthetic P2X7R agonist Bz-ATP has an EC50 of 8 micromolar. Thus, agonists of P2X7R have an EC50 equal or below 300 micromolar. The EC50 is defined as the concentration of agonist that provokes a response half way between the baseline response and maximum response on a dose response curve where the X-axis plots concentration of an agonist and the Y-axis plots ion current. An inverse agonist (also called negative antagonist) is a drug which acts at the same receptor as that of an agonist, yet produces an opposite effect. A partial agonist is an endogenous substance or a drug that also provokes physiological or a pharmacological response but, the maximum response is less than the maximum response to a full agonist, regardless of the amount of drug applied. In the case of P2X7R, partial agonists have EC50s higher than 300 micromolar.

[0169] The person skilled in the art can, therefore, easily employ the compounds and the methods of this invention in order to elucidate the agonistic and/or antagonistic effects and/or characteristics of a compound/molecule/substance to be identified and/or characterized in accordance with any of the above described methods. Preferably, an identified antagonist of the ATP-gated ion channel P2X7R comprising the mutation(s) and/or deletion(s) described hereinabove may be useful to reestablish the properties normally shown by wild-type P2X7R ATP-gated ion channels. An identified agonist of the ATP-gated ion channel P2X7R comprising the mutation(s) and/or deletion(s) described hereinabove may be useful to reestablish the lost functionality of the P2X7R ATP-gated ion channel.

[0170] The Figures show:

Figure 1a. Genomic map of the region on the human chromosome 12 associated to bipolar affective disorder. Genes found between markers NBG11 and NBG2 are depicted.

Figure 1b. Graphic illustrating the multipoint analysis using ASPEX on independent sib-pairs.

Figure 1c. Graphic illustrating the multipoint analysis using ASPEX on all sib-pairs

Figure 1d. Graphic illustrating the ASPEX sib_phase by considering only independent sib-pairs

Figure 1e. Graphic illustrating the ASPEX sib_phase by considering all sib-pairs

Figure 1f. Effect of the P2XR7v13A polymorphism on basal cortisol levels before and after administration of dexamethasone (DST test). Individuals were subjected to the test within the first ten days of admission. Individuals with the AG and GG genotypes have significantly lower cortisol levels pre- and post-dexamethasone administration.

Figure 1g. Effect of the P2XR7v13A polymorphism on cortisol response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. At admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the GG genotype have lower cortisol levels in response to the Dex/CRH test at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 1h. Effect of the P2XR7v13A polymorphism on ACTH response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the GG genotype have lower ACTH levels in response to the Dex/CRH test, at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 1i. Duration of antidepressant treatment until remission. Depression is diagnosed according to the Hamilton Depression Rating Scale (HAM-D; Hamilton, Br. J. Soc. Clin. Psychol. 6 (1967) 278-296). A HAM-D score of 10 or below is regarded as remission of the depressive symptoms.

Figure 1j. Effect of the P2XR7v13C polymorphism on basal cortisol levels before and after administration of dexamethasone (DST test). Individuals were subjected to the test within the first ten days of admission. Individuals with the CC genotypes have elevated cortisol levels post-dexamethasone administration.

Figure 1k. Effect of the P2XR7v13C polymorphism on cortisol response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the AC or CC genotype have elevated cortisol levels in response to the Dex/CRH test at admission, indicating an abnormal HPA axis.

Figure 1l. Effect of the P2XR7v13C polymorphism on ACTH response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the CC genotype have lower ACTH levels in response to the Dex/CRH test, at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 2. RT-PCR analysis of the complete coding sequence of P2X7R in different tissues

Figure 3. P2X7R expression in the olfactory bulb, hypothalamus and ependymal cells in the brain of a stress-free mouse. Magnification 100X.

Figure 4. P2X7R expression in the hippocampus/dentate gyrus and subcommissural organ in the brain of a stress-free mouse. Magnification 100X.

Figure 5. Floating behaviour in the forced swim test. Passive stress coping behaviour decreased after long-term treatment with the antidepressant paroxetine (Par28: treated with paroxetine for 28 days, per os). Basal n=8; vehicle n=8; Par28 n=8.

Figure 6. Comparative analysis of P2X7R expression in the olfactory bulb of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 100X.

Figure 7. Comparative analysis of P2X7R expression in the hypothalamus of stress-free, treated-treated and antidepressant-treated mice. Magnification 100X.

Figure 8. Comparative analysis of P2X7R expression in ependymal cells of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 100X.

Figure 9. Comparative analysis of P2X7R expression in the hippocampus of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 25X.

Figure 10. P2X7R expression in the hippocampus of a vehicle treated mouse. Magnification 25X.

Figure 11. P2X7R expression in the hippocampus of a mouse treated with the antidepressant paroxetine. Magnification 25X.

Figure 12. Detailed expression of P2X7R in the dentate gyrus of a mouse treated with the antidepressant paroxetine. Magnification 400x.

Figure 13. Comparative analysis of P2X7R expression and apoptotic cells in the hippocampus of a mouse treated with the antidepressant paroxetine. Magnification 100X.

Figure 14. Floating behaviour in the forced swim test. Passive stress coping behaviour increased after acute intrahippocampal (bilateral, dentate gyrus) of siRNA targeting P2X7R. Vehicle n=7; control RNA n=10; P2X7R siRNA n=9.

Figure 15. Comparative analysis of P2X7R expression in the hippocampus of mice treated with vehicle, control RNA and of siRNA targeting P2X7R. Magnification 100X upper row, 25X lower row.

Figure 16a, b, c, d, e. Three splicing variants caused by polymorphisms in the introns of P2X7R.

Figure 17. Expression of P2X7R in immortalized hippocampal cell lines.

Figure 18. Increase calcium influx in hippocampal cells treated with a P2X7R agonist compound (BzATP).

Figure 19a, b. Entry of ethidium bromide dye into hippocampal cells (a) treated with P2X7R agonist compound (BzATP) or (b) pre-treated with a P2X7R antagonist compound.

Figure 19c. Agonist action of BzATP and tenidap on P2X7R activity. The calcium channel activity of human P2X7R was measured under basal conditions for four seconds to 10 seconds. A. Negative control consisting of cells loaded with 10 μ M Fluo-4-AM without further treatment. B. Cells treated with 20 μ M BzATP after four seconds of basal measurement. C. Cells treated with 50 μ M tenidap after four seconds of basal measurement.

Figure 20. Effect of intrahippocampal injection of a P2X7R agonist compound (BzATP) on behaviour in the forced swim test.

Figure 21. Open field test measuring locomotor activity of mice treated with a P2X7R agonist compound (BzATP).

Figure 22. Comparative analysis of apoptotic cells in the hippocampus of a mouse treated with control vehicle solution or a P2X7R agonist compound (BzATP).

Figure 23. Effect of intrahippocampal injection of the P2X7R antagonist KN-62 and oATP on behaviour during the forced swim test

Figure 24. Open field test measuring locomotor activity of mice treated with the P2X7R antagonist KN-62 and oATP.

[0171] A better understanding of the present invention and of its many advantages will be had from the following examples, offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

EXAMPLE 1

Linkage analysis of Bipolar Affective Disorder in a homogeneous human population

[0172] 41 families of different sizes containing a total of 485 sampled individuals from the region of Saguenay/Lac St-Jean were used in the linkage analysis. Individuals were distributed according to their diagnoses as follows: 105 individuals afflicted with Bipolar Disorder type I (BPI) or schizoaffective disorder bipolar type; 42 individuals diagnosed with Bipolar Disorder type II (BP II); 54 individuals with recurrent major depression; and 57 individuals with single episode major depression. The remaining 227 individual were unaffected and normal. For the purpose of the calculation, the following classification was used: individuals diagnosed with either BPI, schizoaffective disorder, bipolar type, BP II and recurrent major depression were considered as affected (n=201); individuals with a single major depression episode were scored as unknown phenotype (n=57); and all others diagnoses as unaffected (n=227).

[0173] Blood samples from each individual were collected in 10-ml K3 EDTA Vacutainer tube (Becton-Dickinson) and genomic DNA was isolated by Puregene DNA Isolation kit (Gentra Systems). Blood was poured into 50 ml conical tube and diluted with four volume of Red Blood Cell Lysis Solution. After an incubation of 10 minutes at room temperature, the tube was centrifuged for 10 minutes at 2,000 g and supernatant was removed leaving behind cell pellet and 200-400 µl of the residual liquid. Cells were resuspended by vortexing the tube and 9 ml of Cell Lysis Solution were added with up and down pipetting. 40 µl of RNase A Solution (20 mg/ml) were added and the sample was mixed by inverting the tube several times. Sample was incubated at 37°C for 15 minutes and cooled to room temperature. 3 ml of Protein Precipitation Solution were added to cell lysate. Tube was vigorously vortexed for 30 seconds and centrifuged at 2,000 g for 10 minutes. Supernatant was poured into a new tube containing 9 ml of 100% isopropanol. Sample was mixed by inverting gently several times. Tube was centrifuged at 2,000 g for 5 minutes. The DNA white pellet was washed with 10 ml 70% ethanol and the tube was centrifuged at 2,000 g for 3 minutes. Ethanol was poured off and pellet allowed to partially air dry. DNA was solubilized in 500 µl of DNA Hydration Solution. Final concentration was adjusted to 300-400 µg/ml.

[0174] A fluorescent-based method was used for the genotyping of microsatellite markers. Briefly, the region encompassing each repeated sequence was amplified by PCR using an unlabeled primer and a fluorescent-labeled primer (Applied biosystems inc, CA, USA). The marker-associated dyes and the corresponding PCR product length are listed in table 2. The PCR reaction was performed using 10ng of DNA sample, 0,2 unit of Taq platinum DNA polymerase (Invitrogene, CA, USA), 20 mM Tris-Cl (pH 8.4), 50 mM KCl, 1.5mM MgCl₂, 100µM of dNTP, and 1,5 µM of each primer in a final volume of 7 µl. The samples were incubated at 95°C for 3 minutes to activate the Taq platinum DNA polymerase, then 10 cycles of PCR amplification were performed as follows: 95°C for 15 seconds; 58°C for 15 seconds; 72°C for 30 seconds; after that 15 cycles were performed as follow: 89°C for 15 seconds; 58°C for 15 seconds; 72°C for 30 seconds. Finally, the samples were incubated at 72°C for 30 min. Following the PCR amplification samples were pooled according to their dye-labeled primer and their PCR product length (pool of four samples). Pooled sample were separated on an ABI 3100 DNA analyzer (Applied Biosystems inc, CA, USA). The resulting data were analysed using Genemapper2 (Applied Biosystems inc, CA, USA), and compiled in a 4D database (ACIUS) designed in a Macintosh environment as previously described (Morissette et al., Am. J. Med. Genet. (Neuropsychiatr. Genet.) 88 (1999), 567-587)

[0175] Markers used in the following linkage analysis are shown in table 2. Recombination fraction (q) between successive markers was computed according to the analyzed families.

Table 2.

Genomic markers used for the linkage analysis					
Locus	Associated dye	Allele length (bp)	Distance (g)	Cumulative distance (cM)	Heterozygosity (%)
D12S1619	VIC	170-210	0.0135	0.00	74.5
NBG11	VIC	204-218	0.006	1.37	65.5
D12S1666	FAM	241-281	0.001	1.97	66.9
NBG5	VIC	253-261	0.001	2.07	38.3
D12S1721	VIC	263-299	0.005	2.17	72.1
NBG8	VIC	166-188	0.011	2.67	73.3
NBG6	NED	182-218	0.0115	3.79	73.9

Table 2. (continued)

Genomic markers used for the linkage analysis					
Locus	Associated dye	Allele length (bp)	Distance (g)	Cumulative distance (cM)	Heterozygosity (%)
NBG9	VIC	156-180	0.0035	4.95	68.9
NBG10	FAM	174-186	0.001	5.30	49.7
NBG12	NED	165-207	0.009	5.40	64.2
NBG4	NED	171-199	0.001	6.31	66.4
NBG3	VIC	182-206	0.006	6.41	64.8
NBG2	VIC	171-199		7.01	54.2
- Haldane's map function was used for cumulative distance in cMorgans.					

[0176] For bipoint parametric analysis, MOD score analysis were used where parametric LOD score were maximized over genetic models.

[0177] The following results were obtained under MOD score analysis for recessive models.

Table 3.

MOD score analysis for recessive models			
Locus	Distance (g)	Cumulative distance (cM)	LOD score (q_{\max})
D12S1619	0.0135	0.00	3.46 (0.10)
NBG11	0.006	1.37	4.06 (0.04)
D12S1666	0.001	1.97	1.22 (0.14)
NBG5	0.001	2.07	0.66 (0.16)
D12S1721	0.005	2.17	2.82 (0.10)
NBG8	0.011	2.67	1.51 (0.00)
NBG6	0.0115	3.79	4.77 (0.06)
NBG9	0.0035	4.95	0.75 (0.22)
NBG10	0.001	5.30	0.74 (0.00)
NBG12	0.009	5.40	1.41 (0.16)
NBG4	0.001	6.31	3.56 (0.08)
NBG3	0.006	6.41	3.96 (0.08)
NBG2		7.01	2.59 (0.10)

[0178] Model-free LOD score studies using ANALYZE, sib_phase from the ASPEX V1.85 package (David Hinds and Neil Risch 1999; <ftp://lahmed.stanford.edu/pub/aspepx>, see also <http://watson.hgen.pitt.edu/docs/usage.html>) and SIMWALK2 (Sobel and Lange, Am J Hum Genet 58 (1996), 1323-1337) were performed to analyze the allele sharing among affected sib-pairs. The ANALYZE program weights sibships according to their size. The ASPEX sib_phase program uses allele frequencies to reconstruct missing information, and is tailored for data sets where parents are missing, but additional typed children may be used to reconstruct and phase the parents. SimWalk2 is a statistical genetics computer application for haplotype, parametric linkage, non-parametric linkage (NPL), identity by descent (IBD) and mistyping analyses on any size of pedigree. SimWalk2 uses Markov chain Monte Carlo (MCMC) and simulated annealing algorithms to perform these multipoint analyses.

[0179] ASPEX sib_phase was used with two computational strategies: First, by using strictly independent sib pairs; secondly, by using all affected sib-pair combinations. ASPEX was performed for bi-point and multipoint calculations.

[0180] The bi-point results observed with ANALYZE and ASPEX are shown in Table 4.

Table 4.

Bi-point results observed with ANALYZE and ASPEX					
Locus	Distance (q)	Cumulative distance (cM)	Sib-pair from ANALYZE LOD score	sib_phase LOD score indep. sib-pairs	sib_phase LOD score all sib-pairs
D12S1619	0.0135	0.00	2.31	2.55	3.14
NBG11	0.006	1.37	2.83	2.72	3.27
D12S1666	0.001	1.97	1.01	2.52	3.14
NBG5	0.001	2.07	0.50	2.52	3.13
D12S1721	0.005	2.17	1.57	2.51	3.12
NBG8	0.011	2.67	0.51	2.24	2.75
NBG6	0.0115	3.79	2.55	2.11	2.64
NBG9	0.0035	4.95	0.49	1.65	1.97
NBG10	0.001	5.30	0.77	1.45	2.10
NBG12	0.009	5.40	0.47	1.44	2.17
NBG4	0.001	6.31	1.21	1.29	3.07
NBG3	0.006	6.41	1.84	1.29	3.07
NBG2		7.01	1.24	1.22	3.00
SIMWALK2 computed four different statistics based on descent trees. These statistics measure the degree of clustering among the marker alleles descending from the founders.					

[0181] Statistic A is the number of different founder-alleles contributing alleles to the affected it is most powerful at detecting linkage to a recessive trait. Statistic B is the maximum number of alleles among the affected descended from any one founder-allele and most powerful at detecting linkage to a dominant trait. Statistic C is the 'entropy' of the marker alleles among the affected. Statistic D is the extent of allele sharing among all affected pairs as measured by their IBD kinship coefficient. Statistics C and D are more general statistics indicating whether a few founder-alleles are overly represented among the affected.

[0182] Table 5 shows the results observed with SIMWALK2. The authors signal that p-values should be generally conservative. They are expressed as $-\log(p\text{-values})$. For correspondence purpose, $-\log(0.05)=1.30$, $-\log(0.01)=2$, $-\log(0.001)=3$ etc.

Table 5.

SIMWALK2 analysis						
Locus	Distance (q)	Cumul. Distance (cM)	STAT(A) -Log(p-value)	STAT(B) -Log(p-value)	STAT(C) -Log(p-value)	STAT(D) -Log(p-value)
D12S1619	0.0135	0.00	1.4550	0.4103	1.1306	1.1310
NBG11	0.006	1.37	2.0157	1.4375	1.5955	1.9845
D12S1666	0.001	1.97	2.0236	0.9765	1.4727	1.4614
NBG5	0.001	2.07	1.7596	0.8558	1.3866	1.3602
D12S1721	0.005	2.17	1.6628	1.1692	1.4235	1.6384
NBG8	0.011	2.67	1.5374	0.6940	1.0623	1.1552
NBG6	0.0115	3.79	1.5896	0.4452	1.0935	1.1786
NBG9	0.0035	4.95	1.2677	0.3815	0.8412	0.9133
NBG10	0.001	5.30	1.1117	0.3642	0.6987	0.7554

Table 5. (continued)

SIMWALK2 analysis						
Locus	Distance (q)	Cumul. Distance (cM)	STAT(A) -Log(p-value)	STAT(B) -Log(p-value)	STAT(C) -Log(p-value)	STAT(D) -Log(p-value)
NBG12	0.009	5.40	1.0809	0.3485	0.6694	0.7179
NBG4	0.001	6.31	1.1024	0.4148	0.6368	0.8544
NBG3	0.006	6.41	1.1040	0.4146	0.6373	0.8559
NBG2		7.01	1.0963	0.5380	0.6587	0.9356

[0183] Multipoint result observed with ASPEX when only independent sib-pairs were used (Figure 1b). The maximum LOD score value was observed at NBG11.

[0184] Multipoint result observed with ASPEX when all sib-pairs were considered (Figure 1c). The maximum LOD score value was observed at NBG11 but a second peak appeared at NBG4 and NBG3.

[0185] Multipoint and bi-point LOD score values computed by ASPEX were similar. The second peak, observed when all sib-pairs are used, may be explained by the presence of a recombinant affected individual, with many affected sibs, sharing the chromosomal region telomeric to NBG12. This kind of individuals has a large impact on LOD score values when all sib-pairs are used instead of one sib-pair. This situation was observed in two sibships.

[0186] Strata analysis was subsequently performed. Although HOMOG did not detect evidence for heterogeneity, a homogeneity test was constructed based on allele sharing found in selected chromosomal regions. Only 20 of the 41 families were used for this analysis since the others were not genotyped in all these regions. For each marker within the selected regions, the proportion of alleles shared IBD by affected sib-pairs was estimated with ASPEX (sib_phase). For each region retained, the proportion of shared alleles was used as variable for a Principal Component Analysis and the first principal component as an index of linkage. Correlation analysis was done on these indexes to detect heterogeneity (correlation < 0) or epistasis (correlation > 0). Fisher algorithm was used to classify into two groups of families as linked or unlinked to a particular locus. A negative correlation was observed between the chromosome 12 region and the chromosome 15 area ($r=-0.51$; $p=0.023$). Cluster analysis suggested that 11 families out of 20 were linked to chromosome 12. This sub-sample was called the strata.

[0187] This strata included 11 families (266 sampled individuals) that include 52 BPI or schizoaffective disorder, bipolar type, 20 BPII and 28 recurrent major depression

[0188] The following MOD score values illustrated in Table 6 were obtained under recessive models.

Table 6.

MOD scores under recessive models			
Locus	Distance (q)	Cumulative distance (cM)	LOD score (q_{max})
D12S1619	0.0135	0.00	4.03 (0.08)
NBG11	0.006	1.37	4.98 (0.00)
D12S1666	0.001	1.97	1.49 (0.12)
NBG5	0.001	2.07	0.79 (0.14)
D12S1721	0.005	2.17	4.23 (0.06)
NBG8	0.011	2.67	2.79 (0.00)
NBG6	0.0115	3.79	5.06 (0.06)
NBG9	0.0035	4.95	1.57 (0.14)
NBG10	0.001	5.30	1.73 (0.00)
NBG12	0.009	5.40	1.65 (0.12)
NBG4	0.001	6.31	4.60 (0.08)
NBG3	0.006	6.41	4.84 (0.06)
NBG2		7.01	2.80 (0.06)

[0189] Model-free LOD score results obtained with ANALYZE and ASPEX applied to the strata are shown in Table 7.

Table 7.

Model-free LOD score obtained with ANALYZE and ASPEX					
Locus	Distance (q)	Cumulative distance (cM)	ANALYZE LOD score	sib_phase LOD score independent sib-pairs	sib_phase LOD score all sib-pairs
D12S1619	0.0135	0.00	4.54	5.29	7.65
NBG 11	0.006	1.37	4.29	5.34	7.70
D12S1666	0.001	1.97	2.77	5.36	7.74
NBG5	0.001	2.07	0.67	5.36	7.74
D12S1721	0.005	2.17	4.48	5.35	7.74
NBG8	0.011	2.67	2.97	4.87	7.00
NBG6	0.0115	3.79	4.05	4.59	6.76
NBG9	0.0035	4.95	2.03	3.72	5.41
NBG10	0.001	5.30	2.00	3.42	5.89
NBG12	0.009	5.40	0.89	3.44	6.11
NBG4	0.001	6.31	2.84	3.71	9.00
NBG3	0.006	6.41	3.89	3.71	9.01
NBG2		7.01	1.91	3.52	8.73

[0190] Model-free results observed with SIMWALK2 are illustrated in Table 8.

Table 8.

Model-free LOD score obtained with SIMWALK2						
Locus	Distance (q)	Cumulative Distance (cM)	STAT(A) -Log(p-value)	STAT(B) -Log(p-value)	STAT(C) -Log(p-value)	STAT(D) -Log(p-value)
D12S1619	0.0135	0,00	2,5963	0,9565	3,2156	2,3584
NBG11	0.006	1,37	3,0698	1,7400	3,7747	3,0103
D12S1666	0.001	1,97	2,9340	1,6546	3,5812	2,7223
NBG5	0.001	2,07	2,9781	1,2722	3,6505	2,7846
D12S1721	0.005	2,17	2,9680	1,2630	3,6844	2,7752
NBG8	0.011	2,67	3,0954	1,0804	3,4399	2,5654
NBG6	0.0115	3,79	3,1632	1,0672	3,2670	2,5956
NBG9	0.0035	4,95	2,2106	1,0137	2,7765	2,4456
NBG10	0.001	5,30	2,5513	1,0251	2,7625	2,1914
NBG12	0.009	5,40	2,4893	0,9868	2,6841	2,0920
NBG4	0.001	6,31	2,9028	1,1312	3,4063	2,8156
NBG3	0.006	6,41	2,9070	1,1326	3,4637	2,8300
NBG2		7,01	2,8430	1,1108	3,3135	2,7978

[0191] Multipoint results on the strata with ASPEX sib_phase by considering only independent sib-pairs (Figure 1b) or all sib-pairs (Figure 1c) are shown in Figures 1d and 1e. As previously reported a second peak appeared when all

sib-pairs were observed.

A confidence interval was calculated. GENEFINDER (Liang et al., Am. J. Hum. Genet. 66 (2000), 1631-1641) was used to estimate the location of the susceptibility gene (say t). The method is based on the IBD (Identity by Descent) sharing of affected sib-pairs for multiple markers. For the purpose of our analysis, pedigrees were divided into sibship.

- 5 56 nuclear families and 183 sib-pairs were used. Liang KY, Huang CY, Beaty TH (2000) A unified sampling approach for multipoint analysis of qualitative and quantitative traits in sib pairs. Am J Hum Genet 66:1631-1641
- [0192] The GENEFINDER results points to localization of a susceptibility gene for affective disorders at 3.19 ± 0.446 cM telomeric to the marker D12S1721 (D12S1721 is approximately located at 136.82 cM on the sex-averaged Marshfield chromosome 12 map).

95%	C.I.: [2.32, 4.06];
99%	C. I.: [2.03, 4.35]
99.9%	C. I.: [1.71, 4.67]

- 15 [0193] From the strata, 24 nuclei, and 107 sib-pairs were obtained, and the location of the susceptibility gene was estimated at 3.07 ± 0.57 (see map above). The following confidence interval (C.I.) was obtained:

95%	C.I.: [1.95, 4.19];
99%	C. I.: [1.59, 4.55]
99.9%	C. I.: [1.18, 4.96]

- 20 [0194] An association study using the NBG microsatellite markers was done with CLUMP (Sham & Curtis, Ann. Hum. Genet. 59 (1995), 97-105). Samples were distributed as follow: 83 male/case; 124 female/case; 95 male/control; and 101 female/control. One thousand simulations were used to estimate p-values. The observed results are summarized in Table 9.

Table 9.

Association study using the NBG microsatellite						
Locus	Sample		T1statistic (p-value)	T2statistic (p-value)	T3statistic (p-value)	T4statistic (p-value)
	Case	Control				
NBG11	204	129	0.226	0.562	0.410	0.421
NBG5	206	194	0.972	0.980	0.948	0.971
NBG8	206	194	0.983	1.000	0.994	0.978
NBG6	206	194	0.147	0.074	0.759	0.485
NBG9	206	190	0.512	0.940	0.786	0.583
NBG10	206	190	0.594	0.480	0.403	0.709
NBG12	206	190	0.002	0.019	0.003	0.117

T1 statistic is the usual chi-squared statistic on the raw contingency table

T2 statistic is the usual chi-squared statistic apply on he contingency table obtained after collapsing columns with small expected values together

T3 statistic is the largest chi-squared statistic got by comparing one column of the original table against the total of the others columns

T4 statistic is the largest chi-squared statistic got by comparing any combination of alleles against the rest.

[0195] Only the NBG12 marker gave significant association at the 1% level. For the others markers, there was no single alleles that seems to be associated with bipolar disorder. It seems that no founder-alleles was overly represented among the affected. There is no significant result for association of genotypes with the NBG markers.

[0196] Further microsatellite marker based association studies using CLUMP was performed on samples containing additional control and case individuals. One thousand simulations were used to estimate p-values.

Table 9a.

Empirical p-values observed with CLUMP for statistics T1 and T3 for allelic and genotypic analyses of microsatellite markers						
Name	Effective		Alleles		Genotypes	
	case	controls	T1 (p-value)	T3 (p-value)	T1 (p-value)	T3 (p-value)
NBG11	204	98	0.250	0.421	0.680	0.553
D12S1666	208	175	0.366	0.543	0.393	0.476
NBG5	213	179	0.969	0.934	0.997	1.000
D12S1721	210	176	0.693	0.463	0.805	0.838
NBG8	213	179	0.754	0.921	0.973	0.929
NBG6	213	179	0.008	0.356	0.172	0.449
NBG9	213	175	0.759	0.768	0.690	0.606
NBG10	213	175	0.521	0.178	0.122	0.173
D12S1349	212	180	0.887	0.864	0.782	0.816
NBG12	213	175	0.002	<10 ⁻³	0.018	0.552
NBG4	207	178	0.418	0.506	0.813	0.545
NBG3	209	175	0.171	0.829	0.601	0.897
D12S378	211	180	0.171	0.405	0.540	0.560
NBG2	210	170	0.896	0.749	0.210	0.613
D12S1614	210	179	0.803	0.692	0.710	0.831
D12S342	211	180	0.394	0.740	0.445	0.622
D12S340	209	179	0.890	0.869	0.895	0.838
D12S1639	209	180	0.087	0.170	0.652	0.295
D12S1634	211	181	0.361	0.248	0.505	0.590
D12S2075	203	181	0.023	0.157	0.085	0.451

[0197] HWE hypothesis was satisfied at the 5% level for each microsatellite marker after application of the conservative Bonferroni corrections for multiple testing (Bland & Altman, Brit. J. Med. 310 (1995) 170). Table 9a lists empirical p-values observed with CLUMP for allele and genotype association analyses. Empirical p-values less than 0.005 were observed at marker NBG12 for T1 and T3 statistics under allelic association analysis. T1 statistic suggested allelic association between bipolar affective disorders and NBG6 (empirical p-value=0.008). Moreover, a barely significant empirical p-value of 0.023 was observed at the most distal marker D12S2075.

[0198] In conclusion, the parametric and model-free multipoint results suggest to investigate genes located between D12S1619 and D12S1666. Moreover, according to GENEFINDER results, genes situated centromeric to NBG9 should be considered for association and linkage disequilibrium analysis. Moreover, positive association was seen with the NBG6 marker, which is located in intron 9 of the P2X7R gene.

EXAMPLE 2

Physical mapping and Mutation analysis of chromosome 12 associating the P2X7R to Bipolar Affective Disorders

[0199] The most conservative prediction for the disease-associated region is included between markers NBG11 and NBG2 (see Figure 1a). This region was delimited according to linkage and association analysis described in Example 1, using genethon markers and NBG markers. The approximate length of this region is 5,2 Mb. Two major gaps (between FLJ10701 and FLJ32372, and between FLJ1466 and MONDOA) were included in this region. At least 73 genes were listed in this area, where 48 are known genes and 25 are unknown but associated to mRNA and/or EST clusters based

on the last genome assembly available at UCSC (November 2002). Predicted genes were not listed. However, the estimation of CI 99% (confidence interval) using GENEFINDER has limited the most interesting region between markers D12S1666 and NBG9. This genomic region covers 1,6 Mb and includes at least 28 genes, and has no major gap. Thus, the term fBAD (familial Bipolar Affective Disorders) region was used to describe the genomic segment between D12S1666 and NBG9. Genes found within this region include CaMKK2, CABP, P2X7, P2X4, PIN, PLA2, G1B, CIT, PXN, Rab35, and APC5. However, given the present art, it would not have been obvious to an ordinary person skilled in the art to select P2X7R as the gene associated with affective diseases. Other genes from the ones listed above would be obvious.

[0200] For example, the CaMKK2 gene (also known as Ca²⁺/Calmodulin-dependent protein kinase kinase beta, or CaMKKb) is a serine/threonine protein kinase involved in Ca²⁺ dependent signalling pathways. CaMKK2 can activate in vitro the downstream kinases CaMKIV and CaMKI, which modulate gene transcription through phosphorylation of transcription factors (e.g., CREB, SRF, MEF2; Corcoran and Means, J. Biol. Chem. 276 (2001), 2975-2978; Soderling, Trends Biochem. Sci. 24 (1999), 232-236). Its role in the Ca²⁺ cascade is not critical. Some studies suggest that CaMKs could be activated without the CaMKs phosphorylation (Matsushita and Nairn, J. Biol. Chem. 274 (1998), 10086-10093). However, CaMKK phosphorylation step would contribute to amplification of the Ca²⁺ signal since CaMKK is more sensitive to activation by Ca²⁺/Calmodulin, therefore CaMKK would be an important mediator when the levels of intracellular Ca²⁺ are low (Anderson et al., J. Biol. Chem. 273 (1998), 31880-31889).

[0201] CaMKK2 is an obvious target for depression since prior art suggest that cAMP-dependent signaling pathways (mediated by PKA activation) is affected in brain from patients with Bipolar Affective Disorders (Field et al., J. Neurochem. 73 (1997), 1704-1710; Rahman et al., J. Neurochem. 68 (1997), 297-304; Takahashi et al., J. Neurosci. 19 (1999), 610-618). According to a study using lymphoblastic cell lines, Bipolar disorder could be related to a elevated intracellular calcium levels (Yoon et al., Mol. Psychiatry 6 (2001), 678-683). Moreover, some groups found relations between antidepressant drugs and CaMK activation (Budziszewska et al., Br. J. Pharmacol. 130 (2000), 1385-1393; Consogno et al., Neuropsychopharmacology 24 (2001), 21-30; Mori et al., Neuropharmacology 40 (2001), 448-456; Zanotti et al., Neuropharmacology 37 (1998), 1081-1089). Furthermore, inhibition of CaMKK by PKA-mediated phosphorylation suggest a close relationship between both pathways (Matsushita et al., J. Biol. Chem. 273 (1999), 21473-21481). These observations would suggest to a person skilled in the art that CaMKK2 is the gene responsible for bipolar affective disease.

[0202] Another obvious candidate for affective disorders would have been the CABP1 gene which generates four neuronal Ca²⁺-binding protein by alternative usage of the 9 coding exons, which are L-CABP, S-CABP, calbrain, and caldendrin (Haeseleer et al., J. Biol. Chem. 275 (2000), 1247-1260). Their expression is almost totally restricted to brain tissues. A functional study on calbrain reveals its negative effect on Ca²⁺/Calmodulin-dependent CaMKII activity by competitively interacts with the CaM-binding domain of CaMKII (Yamaguchi et al., J. Biol. Chem. 274 (1999), 3610-3616). One would expect similar roles in Ca²⁺ signaling for other CABP1 alternative products. Participation of CABP1 gene in Ca²⁺-dependent signaling pathways would make it obvious to one skilled in the art to select this gene as a candidate for bipolar affective disorder. However, all CABP1 exons were analyzed for the presence of mutations, and surprisingly only two mutations were detected in noncoding regions.

[0203] The PIN gene (Protein inhibitor of NOS (Nitric oxide synthase)) is another obvious candidate responsible for bipolar affective disorder. Nitric oxide (NO) in the brain, may be involved in apoptosis, synaptogenesis, and neuronal development. Because NO cannot be stored in vesicles like other neurotransmitters, its release is regulated by the activity of NOS (Nitric oxide synthase). PIN is a direct inhibitor of NOS by binding and destabilizing the active homodimer complex of NOS (Jaffrey et al., Science 274 (1996), 774-777). PIN is highly conserved throughout the evolution and is expressed in many cell types. A recent clinical study evaluating plasma nitrate levels in depressive states suggests that NO production is increased in depression (Suzuki et al., J. Affect. Disord. 63 (2001), 221-224) and may result from a deficiency in NOS inhibition. Moreover in a mouse model, NO synthase antagonists have been linked to antidepressant properties (Harkin et al., 1999; Karolewicz et al., Eur. J. Pharmacol. 372 (1999), 215-220). Thus, PIN would be an obvious However, due to the pleiotropic action of NO, a deficiency in PIN function would generate many unrelated disorders throughout the body. Thus, without the information presented in the disclosure herein, a person of ordinary skills in the art would have predicted PIN and not P2X7R as the gene associated with affective disorders.

[0204] The human phospholipase A2 group IB (PLA2G1B) catalyses the release of fatty acids from glycerol-3-phosphocholines. Phospholipase A2 genes (PLA2) are expressed in many tissues. Some studies have demonstrated associations between excessive PLA2 activity in brain and affective disorders (Chang et al., Neurochem. Res. 23 (1998), 887-892; Hibbeln et al., Biol. Psychiatry 25 (1989), 945-961). Moreover, other genetic studies have found associations between PLA2G1B gene and bipolar affective disorder (Dawson et al., Psychiatr. Genet. 5 (1995), 177-180). Thus, PLA2G1B represent a likely candidate for affective disorders. However in the present example, only a single silent mutation was found within exon 3 of the PLA2G1B gene.

[0205] The human citron kinase gene, Rho-associated protein (CIT) is a 183 kDa protein which associates to the GTPase Rho. CIT shares strong similarity with ROCK and ROK proteins which are other Rho-associated kinases

(Madaule et al., Nature 394 (1998), 491-494). Rho GTPases are involved in many processes such as cytoskeletal organization, membrane trafficking, cell growth, and transcriptional activation (Van Aelst and D'Souza-Schorey, Genes Dev. 11 (1997), 2295-2322). Studies on brain variants of Citron-K (without the kinase domain) reveal the association with postsynaptic density proteins (PSD-95), suggesting a role in either synapse organization or function (Zhang et al., J. Neurosci. 19 (1999), 96-108; Furuyashiki et al., J. Neurosci. 19 (1999), 109-118).

[0206] The human paxillin (PXN) gene encodes for a 68 kDa protein found in focal adhesions. It is within focal adhesions where adhesion molecules dynamically interact with the cytoskeleton (Salgia et al., J. Biol. Chem. 270 (1995), 5039-5047). The signaling pathways that regulate these dynamic interactions begin to be elucidated. Many observations suggest that paxillin is involved in transducing signals from growth factor receptors to focal adhesions.

The paxillin is expressed in many tissues including brain.

[0207] However as set forth below, the gene causative for affective diseases is identified as being the P2X7 receptor (P2X7R).

[0208] Mutations were searched in coding sequences and exon-intron boundaries of the above mentioned genes since such mutations are more likely to give a functionally significant Single Nucleotide Polymorphisms (SNP). The starting sample was composed of 16 unrelated affected individuals from the Saguenay/Lac St-Jean region, which gives an 80% power to detect polymorphisms with a frequency of 0.05. To identify polymorphisms, targeted sequences were first amplified by PCR. Then, PCR products are purified on Whatman GF/C membranes (VWR, Montreal, Canada), and quantified using the PicoGreen dsDNA quantitation assay (Molecular probes, Oregon, USA). 4 ng of purified PCR products are sequenced using the DYEnamic ET terminator cycle sequencing kit (Amersham Biosciences, Baie D'Urfé, Canada). The sequencing products are resolved on an ABI PRISM 3730XL DNA analyzer, and an ABI PRISM 3700 DNA analyzer. The PCR products are sequenced in both directions. The SNPs identified in studied genes are listed in Table 10.

Table 10.

Mutation analysis between markers D12S1666 and NBG9				
Genes	Positions	Variations	Alleles	Modifications
Rab35	Exon06	RABE06A	486G-A	Silent Asn162
Rab35	Intron04	RABI04A	51C-T	unknown
Rab35	Intron03	RABI03A	33G-A	unknown
Rab35	Intron02	RABI02B	85G-A	unknown
Rab35	Intron02	RABI02A	76C-G	unknown
PXN	Exon1	PXNE11A	1527C-T	Silent Thr509
PXN	Exon06	PXNE06A	750C-T	Silent Ser250
PXN	Exon02	PXNE02A	217G-A	Gly73Ser
PLA2G1B	Exon03	PLA2G1BE03A	294C-T	Silent Ser98
PIN	5'UTR01	PINUTR01A	-49T-G	unknown
PIN	5'UTR01	PINUTR01B	-80T-C	unknown
PIN	Intron02	PINI02A	26C-T	unknown
PIN	Intron02	PINI02B	50C-T	unknown
CaBP	Intron04	CaBPI04A	35C-T	unknown
CaBP	exon01	CaBPE01A	-23A-G	unknown
OASL	Exon02	OASLE02A	213G-T	Silent Gly72
OASL	Exon02	OASLE02B	408C-T	Silent Leu136
OASL	Exon05	OASLE05A	1042G-A	Va1348Met
OASL	Exon06	OASLE06A	1509G-A	Silent Ser503
P2X7R	5'UTR	P2XR7UTR5L	362T-C	unknown
P2X7R	5'UTR	P2XR7UTR5M	532T-G	unknown
P2X7R	5'UTR	P2XR7UTR5K	1100A-G	unknown
P2X7R	5'UTR	P2XR7UTR5J	1122A-G	unknown
P2X7R	5'UTR	P2XR7UTR5I	1171C-G	unknown
P2X7R	5'UTR	P2XR7UTR5F	1351T-C	unknown
P2X7R	5'UTR	P2XR7UTR5N	1702G-A	unknown

Table 10. (continued)

Mutation analysis between markers D12S1666 and NBG9				
Genes	Positions	Variations	Alleles	Modifications
P2X7R	5'UTR	P2XR7UTR5G	1731T-G	unknown
P2X7R	5'UTR	P2XR7UTR5H	1860C-T	unknown
P2X7R	5'UTR	P2XR7UTR5A	2162C-A	unknown
P2X7R	5'UTR	P2XR7UTR5B	2238C-T	unknown
P2X7R	5'UTR	P2XR7UTR5D	2373A-G	unknown
P2X7R	5'UTR	P2XR7UTR5E	2569G-A	unknown
P2X7R	5'UTR	P2XR7UTR5C	2702G-A	unknown
P2X7R	Intron01	P2XR7I01C	3166G-C	unknown
P2X7R	Intron01	P2XR7I01A	24778C-T	unknown
P2X7R	Intron01	P2XR7I01B	24830C-T	unknown
P2X7R	Exon02	P2XR7v02A	24942T-C	Val176Ala
P2X7R	Exon03	P2XR7E03A	26188C-T	Arg117Trp
P2X7R	Intron03	P2XR7I03A	26308A-G	unknown
P2X7R	Intron03	P2XR7I03B	26422G-A	unknown
P2X7R	Intron04	P2XR7I04A	32394G-A	unknown
P2X7R	Intron04	P2XR7v05B	32434T-C	unknown
P2X7R	Exon05	P2XR7E05D	32493G-A	Gly150Arg
P2X7R	Exon05	P2XR7v05A	32507C-T	Tyr155His
P2X7R	Exon05	P2XR7E05C	32783C-T	Silent Cys168
P2X7R	Intron05	P2XR7I05C	32783A-C	unknown
P2X7R	Intron05	P2XR7I05D	35309T-C	unknown
P2X7R	Intron05	P2XR7I05B	35374C-T	unknown
P2X7R	Intron05	P2XR7I05A	35378A-C	unknown
P2X7R	Exon06	P2XR7E06A	35438G-A	Glu186Lys
P2X7R	Exon06	P2XR7E06B	35454T-C	Leu191Pro
P2X7R	Intron06	P2XR7I06C	35549T-C	unknown
P2X7R	Intron06	P2XR7I06G	35641G-C	unknown
P2X7R	Intron06	P2XR7I06D	35725A-C	unknown
P2X7R	Intron06	P2XR7I06F	36001T-G	unknown
P2X7R	Intron06	P2XR7I06E	36064A-T	unknown
P2X7R	Intron06	P2XR7I06A	36091De1GTTT	unknown
P2X7R	Intron06	P2XR7I06B	36108C-G	unknown
P2X7R	Intron07	P2XR7I07A	36374C-T	unknown
P2X7R	Intron07	P2XR7I07B	36378G-A	unknown
P2X7R	Intron07	P2XR7I07C	36387T-A	unknown
P2X7R	Intron07	P2XR7I07D	36398G-C	unknown
P2X7R	Intron07	P2XR7I07E	37439C-T	unknown
P2X7R	Intron07	P2XR7I07F	37513T-C	unknown
P2X7R	Exon08	P2XR7E08C	37604C-T	Arg270Cys
P2X7R	Exon08	P2XR7v08A	37605G-A	Arg270His
P2X7R	Exon08	P2XR7v08B	37623G-A	Arg276His
P2X7R	Exon08	P2XR7E08D	37633C-T	Silent Asp279
P2X7R	Intron09	P2XR7v11A	47214C-T	unknown
P2X7R	Exon11	P2XR7v11B	47383G-A	Ala348Thr
P2X7R	Exon11	P2XR7v11C	47411C-G	Thr357Ser
P2X7R	Intron11	P2XR7I11D	47563T-C	unknown
P2X7R	Intron12	P2XR7I12A	54307C-T	unknown
P2X7R	Intron12	P2XR7I12B	54308G-A	unknown

Table 10. (continued)

Mutation analysis between markers D12S1666 and NBG9				
Genes	Positions	Variations	Alleles	Modifications
P2X7R	Exon13	P2XR7v13F	54399C-T	Ala433Val
P2X7R	Exon13	P2XR7v13A	54480A-G	Gln460Arg
P2X7R	Exon13	P2XR7v13B	54523C-T	Silent Pro474
P2X7R	Exon13	P2XR7v13G	54562DelCCCTGAGAG	Del of 7aa 488 to 494
			CCACAGGTGCCT	PESHRL
P2X7R	Exon13	P2XR7v13C	54588A-C	Glu496A1a
P2X7R	Exon13	P2XR7v13H	54664C-G	Silent His521
P2X7R	Exon13	P2XR7E13D	54703G-T	Silent Leu534
P2X7R	Exon13	P2XR7E13J	54804A-T	Ile568Asn
P2X7R	Exon13	P2XR7v13I	54834G-A	Arg578Gln
P2X7R	Exon13	P2XR7v13E	54847G-A	Silent Pro582
P2X7R	3'UTR	P2XR7UTR3A	55169C-A	unknown
P2X7R	3'UTR	P2XR7UTR3B	55170A-C	unknown
P2X7R	3'UTR	P2XR7UTR3C	55171A-C	unknown
P2X7R	3'UTR	P2XR7UTR3D	55917C-T	unknown
P2X7R	3'UTR	P2XR7UTR3E	54925G-A	unknown
P2X4R	5'UTR	P2XR4UTR5I	-1956G-A	unknown
P2X4R	5'UTR	P2XR4UTR5H	-1649G-A	unknown
P2X4R	5'UTR	P2XR4UTR5G	-800G-A	unknown
P2X4R	5'UTR	P2XR4UTR5A	-648C-A	unknown
P2X4R	5'UTR	P2XR4UTR5B	-537A-G	unknown
P2X4R	5'UTR	P2XR4UTR5C	-437A-G	unknown
P2X4R	5'UTR	P2XR4UTR5J	-206VNRG	unknown
P2X4R	5'UTR	P2XR4UTR5D	-211C-G	unknown
P2X4R	5'UTR	P2XR4UTR5F	-150VNRGGGCCCC	unknown
P2X4R	5'UTR	P2XR4UTR5E	-98G-T	unknown
P2X4R	Intron01	P2XR4I01A	31G-T	Silent mutation Ala87
P2X4R	Exon02	P2XR4E02A	262G-A	unknown
P2X4R	Intron02	P2XR4I02A	4600C-T	unknown
P2X4R	Intron03	P2XR4I03A	15G-A	unknown
P2X4R	Intron03	P2XR4I03B	72G-A	unknown
P2X4R	Exon04	P2XR4E04A	355G-A	Ile119Val
P2X4R	Exon04	P2XR4E04A	375G-A	Silent Val125
P2X4R	Intron04	P2XR4I04B	17T-C	unknown
P2X4R	Intron04	P2XR4I04A	32G-A	unknown
P2X4R	Exon05	P2XR4E05A	465T-C	Silent Ser155
P2X4R	Exon07	P2XR4E07A	724A-G	Ser242Gly
P2X4R	Intron08	P2XR4I08A	DelT	unknown
P2X4R	Exon09	P2XR4E09A	944A-G	Tyr315Cys
P2X4R	Intron10	P2XR4I10A	11G-T	unknown
P2X4R	Intron10	P2XR4I10B	G-C	unknown
P2X4R	Intron10	P2XR4I10C	A-G	unknown
P2X4R	Intron11	P2XR4I11B	C-G	unknown
P2X4R	Intron11	P2XR4I11C	T-A	unknown
P2X4R	Intron11	P2XR4I11A	374C-T	unknown
CaMKK2	3'UTR	CaMKK2UTR3bA	733C-T	unknown
CaMKK2	3'UTR	CaMKK2UTR3aB	390G-A	unknown
CaMKK2	3'UTR	CaMKK2UTR3aA	239G-A	unknown

Table 10. (continued)

Mutation analysis between markers D12S1666 and NBG9				
Genes	Positions	Variations	Alleles	Modifications
CaMKK2	Intron 15	CaMKK2I15B	325T-C	unknown
CaMKK2	Intron15	CaMKK2I15A	169G-A	unknown
CaMKK2	Intron14	CaMKK2I14A	224A-G	unknown
CaMKK2	Intron10	CaMKK2I10A	156DelGTGATCCGCCT G	unknown
CaMKK2	intron09	CaMKK2I09B	528A-G	unknown
CaMKK2	intron09	CaMKK2I09A	521A-G	unknown
CaMKK2	Exon09	SNP6f18v5	1095C-A	Silent Ile365
CaMKK2	Exon09	SNP6f18v4	1087C-T	Arg363Cys
CaMKK2	Exon05	CaMKKE05A	687C-T	Silent Pro229
CaMKK2	Intron03	CaMKK2I03A	10C-T	unknown
CaMKK2	Intron02	CaMKK2I02A	39C-T	unknown
CaMKK2	Intron01	CaMKK2I01B	2911G-C	unknown
CaMKK2	Intron01	CaMKK2I01 A	89C-A	unknown
CaMKK2	Exon01	SNP6f18v2	253A-T	Thr85Ser
CaMKK2	Exon01	SNP6f18v1	29G-A	Ser10Asn
CaMKK2	5'UTR01	CaMKK2UTR01B	253T-C	unknown
CaMKK2	5'UTR01	CaMKK2UTR01A	63C-A	unknown
APC5	Intron01	APC5I01A	10G-T	unknown
APC5	Intron01	APC5I01B	50A-T	unknown
APC5	Intron05	APC5I05A	73T-C	unknown
APC5	Intron06	APC5I06A	73T-G	unknown
APC5	Exon1	APC5E11A	1416C-T	Silent His472

[0209] Each SNP in genes Rab35, PXN, PLA2G1B, PIN, CaBP, OASL, P2X4R, CaMKK2 and APC5 was designated according to the gene where it was found, and its location in that gene (intronic or exonic regions). Each SNP in the P2X7R gene was designated according to their position on SEQ ID NO: 1. The allele describes the position and the variation observed. In coding regions, the position is relative to the start codon, whereas the intronic SNPs are positioned relative to the beginning of the corresponding intron (when known). Primers used for identifying the SNPs in the P2X7R and the location of each SNPs included in tables 2 and 12 are defined in table 1a and SEQ ID NOs 52 to 111.

[0210] Association studies using missense SNPs were performed. Missense SNPs or SNPs that could be close to the splice sites were used, because it is more likely that diseases would be associated to an improper function in proteins. Case group was composed by bipolar I individuals, schizoaffective bipolar type (182 subjects) and bipolar II diagnosed persons (31 subjects). Many controls from the Saguenay/Lac-St-Jean region, were sampled from Steinert, Glaucoma and Paget DNA banks. The control individuals were not diagnosed for affective disorders. According to the lifetime risks of bipolar disorders (1%), there is no need to screen controls for psychiatric disorders.

[0211] Direct sequencing of PCR products is by far the most accurate method of analysis and is the method of choice in view of our sequencing platform capacity. PCR products were analyzed by direct sequencing as described above. After sequencing analysis, individuals are automatically typed for the corresponding SNP using a home-developed program, GENO.pl. The results of SNP genotyping are compiled in a 4D database.

[0212] The association hypothesis was tested with CLUMP (Sham & Curtis 1995, Ann. Hum. Genet. 59:97-105). One thousand simulations were used to estimate p-values. Results are illustrated in table 11. The T1 statistic, which is the usual chi-squared statistic on the raw contingency table, was used to test for allelic association. Moreover, the largest chi-squared statistic got by comparing one column of the original table against the total of the other columns, called T3 statistic, was added to the previous one to test for potential genotype association since T1 statistic results may be biased when the contingency table contains cells with low values.

Table 11. Association hypothesis using CLUMP

gene	SNPs	Effective		Allele Analysis p-value (T1)	Genotype Analysis	
		Cases	Controls		p-value (T2)	p-value (T3)
P2X7R	P2XR7v11B	208	211	0.795	0.036	0.028
	P2XR7v13A	212	214	0.344	0.250	0.186
	P2XR7v13E	212	211	0.780	0.017	0.017
CAMKK2	SNP6f18v5	206	135	1.00	1.00	1.00
	SNP6f18v4	206	135	0.816	0.962	0.841
	SNP6f18v2	205	135	0.057	0.110	0.095
	SNP6f18v1	206	135	0.512	0.532	0.385

[0213] The association studies using SNPs in P2X7, P2X4, and CaMKK2 reveal associations significant at level of about 5% or less. Three genotype associations in P2X7 were observed. However, SNPs P2XR7v11B and P2XR7v13E are closely linked together based on a contingency table. There is also an allele association at level of 5,7% for

SNP6f18v2 in CaMKK2. The information associated to each relevant SNP can be found in Tables 10 and 12.

[0214] Further association studies using CLUMP were performed on samples that contain more case and control individuals. One thousand simulations were used to estimate p-values.

Table 11a.

Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs									
Gene	Marker (marker rank)	Allele Frequencies	Effective		Alleles Alleles			Genotypes	
			case	controls	T1 p-value	OR	OR 95% CI	T1 p-value	T3 p-value
P2XR7	P2XR7UTR5F (1)	C (0.18); T (0.82)	212	208	0.280	1.21	0.86- 1.71	0.067	0.069
	P2XR7UTR5G (2)	G (0.09); T (0.91)	211	204	0.481	1.19	0.76- 1.87	0.261	0.231
	P2XR7UTR5H (3)	C (0.95); T (0.05)	210	202	0.549	1.19	0.67- 2.13	0.768	0.582
	P2XR7UTR5A (4)	A (0.05); C (0.95)	210	207	0.526	1.26	0.68- 2.34	0.754	0.517
	P2XR7UTR5B (5)	C (0.78); T (0.22)	211	207	0.629	1.09	0.79- 1.50	0.104	0.128
	P2XR7UTR5D (6)	A (0.96); G (0.04)	211	205	0.268	1.43	0.77-2.65	0.598	0.240
	P2XR7UTR5E (7)	A (0.04); G (0.96)	211	210	0.658	1.23	0.65-2.33	0.139	0.234
	P2XR7UTR5C (8)	A (0.22); G (0.78)	208	210	0.889	1.04	0.75-1.44	0.168	0.293
	P2XR7I01B (9)	C (0.98); T (0.02)	210	207	0.352	1.71	0.67-4.39	0.348	0.348
	P2XR7v02A (10)	C (0.05); T (0.95)	211	208	0.189	1.49	0.84-2.64	0.397	0.167
	P2XR7I04A (11)	A (0.01); G (0.99)	211	211	0.344	0.25	0.03-2.23	0.356	0.356

Table 11a. (continued)

Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs									
Gene	Marker (marker rank)	Allele Frequencies	Effective		Alleles Alleles			Genotypes	
			case	controls	T1 p-value	OR	OR 95% CI	T1 p-value	T3 p-value
	P2XR7v05B (12)	C (0.75); T (0.25)	212	211	0.854	1.03	0.76-1.41	0.234	0.335
	P2XR7E05D (13)	A (0.01); G (0.99)	211	211	0.726	1.51	0.42-5.38	0.735	0.735
	P2XR7v05A (14)	C (0.48); T (0.52)	211	209	0.638	1.07	0.82-1.40	0.895	0.895
	P2XR7E05C (15)	C (0.97); T (0.03)	210	211	0.195	0.45	0.16-1.31	0.349	0.276
	P2XR7I07E (16)	C (0.64); T (0.36)	208	214	0.394	0.87	0.66-1.16	0.057	0.064
	P2XR7v08A (17)	A (0.24); G (0.76)	210	212	0.221	1.22	0.90-1.67	0.433	0.496
	P2XR7v08B (18)	A (0.05); G (0.95)	210	213	0.386	0.71	0.36-1.41	0.520	0.662
	P2XR7V11A (19)	C (0.88); T (0.12)	213	149	0.394	0.80	0.50-1.29	0.387	0.463
	P2XR7v11 B (20)	A (0.36); G (0.64)	208	211	0.795	1.04	0.79-1.38	0.036	0.028
	P2XR7v11C (21)	C (0.89); G (0.11)	211	212	0.409	0.82	0.52-1.28	0.303	0.661
	P2XR7v13F (22)	C (0.99); T (0.01)	196	207	0.030	3.24	1.04-10.12	0.039	0.039
	P2XR7v13A (23)	A (0.84); G (0.16)	212	214	0.344	1.21	0.85-1.72	0.250	0.186

Table 11a. (continued)

Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs									
Gene	Marker (marker rank)	Allele Frequencies	Effective		Alleles Alleles			Genotypes	
			case	controls	T1 p-value	OR	OR 95% CI	T1 p-value	T3 p-value
	P2XR7v13B (24)	C (0.89); T (0.11)	207	212	0.494	0.83	0.53-1.31	0.315	0.699
	P2XR7v13C (25)	A (0.77); C(0.23)	211	213	0.731	0.95	0.68-1.31	0.557	0.616
	P2XR7V13H (26)	C (0.98); G (0.02)	211	213	0.238	1.75	0.68-4.49	0.236	0.236
	P2XR7E13D (27)	G (0.89); T (0.11)	211	213	0.435	0.82	0.53-1.28	0.268	0.680
	P2XR7E13J (28)	A (0.03); T (0.97)	204	199	0.179	0.48	0.16-1.42	0.329	0.329
	P2XR7v13E (29)	A (0.36); G (0.64)	212	213	0.841	1.04	0.79-1.37	0.026	0.025
	P2XR7UTR3E (30)	A (0.04); G (0.96)	205	197	1.000	0.96	0.45-2.04	1.000	1.000
	P2XR7UTR3A (31)	A (0.47); C (0.53)	208	209	0.932	0.99	0.75-1.30	0.264	0.239
	P2XR7UTR3B (32)	A (0.92); C (0.08)	208	210	0.174	0.65	0.38-1.14	0.151	0.303
	P2XR7UTR3C (33)	A (0.95); C (0.05)	208	210	0.395	0.71	0.36-1.40	0.508	0.667
P2XR4	UTR5A	A (0.18); C (0.82)	212	210	0.285	0.82	0.57-1.18	0.514	0.484

Table 11a. (continued)

Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs									
Gene	Marker (marker rank)	Allele Frequencies	Effective		Alleles Alleles			Genotypes	
			case	controls	T1 p-value	OR	OR 95% CI	T1 p-value	T3 p-value
	UTR5B	A (0.69); G (0.31)	212	210	0.670	0.93	0.70-1.25	0.833	0.833
	106A	C (0.84); T (0.16)	207	192	0.212	0.78	0.53-1.16	0.398	0.217
	E07A	A (0.84); G (0.16)	212	208	0.294	0.81	0.55-1.19	0.536	0.479
	UTR3A	C (0.74); G (0.26)	211	203	0.015	1.50	1.11-2.02	0.021	0.014
	UTR3B	A (0.97); T (0.03)	211	209	0.653	0.81	0.33-1.97	0.649	0.649
	UTR3C	C (0.03); G (0.97)	211	209	0.653	0.81	0.33-1.97	0.672	0.672
CAMK K2	E09B	A (0.03); C (0.97)	208	214	0.830	0.85	0.36-2.00	0.829	0.829
	E09A	C (0.83); T (0.17)	208	214	0.202	0.78	0.54-1.14	0.446	0.473
	E01B	A (0.35); T (0.65)	207	214	0.048	1.33	1.01-1.76	0.126	0.218
	E01A	C (0.93); T (0.07)	208	214	0.189	1.44	0.86-2.39	0.439	0.237

[0215] Thirty-three SNPs in P2X7R, seven SNPs in P2X4R, and four SNPs in CAMKK2, with minor allele frequency higher or equal to 1% were genotyped (Table 11a). The genotype distributions of these SNPs did not deviate significantly from HWE. At the 5% level, statistically significant increases of minor allele frequency were observed in the bipolar affective disorder group at p2XR7v13F (p-value=0.030, OR=3.24, 95% CI=1.04-10.12), P2XR4UTR3A (p-value=0.015, OR=1.50, 95% CI=1.11-2.02) and CAMKK2E01B (p-value=0.048, OR=1.33, 95% CI=1.01-1.76). The distribution of genotypes at SNPs P2XR7v13F and P2XR4UTR3A also differed significantly at this level for T1 and T3 statistics, with an increase of heterozygotes in the case sample. One SNP from exon 11 of P2X7R, P2XR7v11B, and another from exon 13, P2XR7v13E, displayed difference in genotype distributions with minimum p-value of 0.028 and 0.025 observed both with T3 statistic. Again, increase in heterozygote frequency of 12% and 13% were respectively observed in the bipolar sample at these polymorphisms.

[0216] Significant haplotypic association tests led to p-values less than 0.5% for different SNP groups overlapping the P2X7R gene (Table 11b). Considering the SNPs collection ranging from SNP32507 to SNP54847 (table 11c) as an example for haplotype distribution, we observed the largest difference of frequencies between cases and controls with the haplotype no 1 (table 11d). The haplotype no 2 is another example of haplotype that is more frequently observed in cases group. On the other hand, the frequency for haplotype no 3 is slightly increased in control sample (difference of frequencies = 0.091). Table 11e presents the peptidic products derived from the nucleotidic haplotypes shown in table 11d.

Table 11b.

Haplotypes showing allelic association significant at the 0.5% level for T1 or T3 statistics.							
Haplotype (marker ranks ¹)	#SNPs	Distance ²	Haplotype effective		T1 statistic	T3 statistic	#haplotype ³
		(bp)	case	control	(p- value)	(p- value)	
P2XR7101 B- P2XR7v13A (9-23)	15	29618	361	257	0.0003	0.0252	20
P2XR7v02A- P2XR7v13B (10-24)	15	29550	361	260	0.00008	0.0294	20
P2XR7104A- P2XR7v13C (11-25)	15	22164	360	264	0.0003	0.0323	19
P2XR7v05B- P2XR7v13H (12-26)	15	22200	361	265	0.0004	0.0065	18
P2XR7E05D- P2XR7E13D (13-27)	15	22180	365	268	0.0035	0.0287	16
P2XR7v05A- P2XR7E13J (14-28)	15	22267	352	246	0.0007	0.0163	15
P2XR7E05C- P2XR7v13E (15-29)	15	22269	353	250	0.0012	0.0200	10
P2XR7107E- P2XR7UTR3E (16-30)	15	17452	355	247	0.0020	0.0192	11

The marker ranks of SNPs in the haplotype indicated in table 11b refer to those genotyped in table 11a

²Distance between the two most distal SNPs of the haplotype

³Number of haplotypes with frequencies > 1 % in case or control groups.

Table 11c.

Position and Allele for haplotype-forming SNPs. Haplotypes are described in table 11d.		
SEQ ID NO	Polymorphism	Position
1	C-T	32507
1	C-T	32548

Table 11c. (continued)

Position and Allele for haplotype-forming SNPs. Haplotypes are described in table 11d.		
SEQ ID NO	Polymorphism	Position
1	C-T	37439
1	G-A	37605
1	G-A	37623
1	C-T	47214
1	G-A	47383
1	C-G	47411
1	C-T	54399
1	A-G	54480
1	C-T	54523
1	A-C	54588
1	C-T	54664
1	G-T	54703
1	T-A	54804
1	G-A	54847

Table 11d.

haplotypes with significant difference of frequencies between affected and control individuals.										
Haplotype	32507	32548	37439	37605	37623	47214	47383	47411	54399	54480
No 1	C	C	C	A	G	C	G	C	C	A
No 2	C	C	C	G	G	C	G	C	C	A
No 3	C	C	T	G	G	C	A	C	C	A

Haplotype	54523	54588	54664	54703	54804	54847	F _{affected}	F _{controls}
No 1	C	A	C	G	T	G	0.20	0.13
No 2	C	C	C	G	T	G	0.05	0.01
No 3	C	A	C	G	T	A	0.11	0.20

Table 11e.

Corresponding amino acids for cSNPs described in table 11c. They are positioned according to SEQ ID NO3.							
Position in SEQ ID NO3	155	168	270	276	348	357	433
Haplotype 1	Y	C	H	R	A	T	A
Haplotype 2	Y	C	R	R	A	T	A
Haplotype 3	Y	C	R	R	T	T	A

Position in SEQ ID NO3	460	474	496	521	534	568	582
Haplotype 1	Q	P	E	H	L	I	P
Haplotype 2	Q	P	A	H	L	I	P
Haplotype 3	Q	P	E	H	L	I	P

EXAMPLE 3**Polymorphisms found in the P2X7R in individuals suffering from depression**

[0217] Association studies using SNPs in the P2X7R gene was performed in a case/control sample (535 individuals) from a German population. The case group was composed of 36 individuals diagnosed with bipolar type I or type II, and 279 individuals diagnosed with unipolar disorders (i.e. depression) representing 133 affected males and 182 affected females. Among controls, we count The remaining 220 control individuals were normal (i.e. diagnosed as non depressive), and comprising 81 males, 182 females and 14 of unknown gender. The same sexual distribution was noted in both groups.

[0218] SNPs were identified in this sample by using a subgroup of 24 affected individuals. SNPs in the P2X7R gene detected in the German population were similar if not identical to the SNPs seen in the Saguenay/Lac-St-Jean population (see table 12). Other rare missense SNPs were also noted in the German population, such as Arg117Trp (P2XR7E03A), Glu186Lys (P2XR7E06A), Leu191Pro (P2XR7E06B), Ile568Asn (P2XR7E13J). These amino acids are quite conserved between ortholog P2X7 genes. It is possible that the Ile568Asn (P2XR7E13J) mutation may be involved in the surface expression of P2X7.

Table 12.

Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2XR7R gene						
Associated exons or Introns	Variation (SNP or others)	Allele	Position*	Modification	Frequency (Canada)	Frequency (Germany)
5'UTR	P2XR7UTR5L	T-C	362	unknown	0,13	0,08
5'UTR	P2XR7UTR5M	T-G	532	unknown	0,16	0,1
5'UTR	P2XR7UTR5K	A-G	1100	unknown	0,13	0,13
5'UTR	P2XR7UTR5J	A-G	1122	unknown	0,13	0,13
5'UTR	P2XR7UTR5I	C-G	1171	unknown	0,06	0,02
5'UTR	P2XR7UTR5F	T-C	1351	unknown	0,3	0,12
5'UTR	P2XR7UTR5N	G-A	1702	unknown	-	0,02
5'UTR	P2XR7UTR5G	T-G	1731	unknown	0,17	0,15
5'UTR	P2XR7UTR5H	C-T	1860	unknown	0,07	0,15
5'UTR	P2XR7UTR5A	C-A	2162	unknown	0,07	0,12
5'UTR	P2XR7UTR5B	C-T	2238	unknown	0,3	0,27
5'UTR	P2XR7UTR5D	A-G	2373	unknown	0,07	0,12
5'UTR	P2XR7UTR5E	G-A	2569	unknown	0,1	0,02
5'UTR	P2XR7UTR5C	G-A	2702	unknown	0,31	0,27
Intron01	P2XR7I01C	G-C	3166	unknown	0,03	-
Intron01	P2XR7I01A	C-T	24778	unknown	0,03	-
Intron01	P2XR7I01B	C-T	24830	unknown	0,03	RARE
Exon02	P2XR7v02A	T-C	24942	Val76Ala	0,06	0,08
Exon03	P2XR7E03A	C-T	26188	Arg117Trp	-	RARE
Intron03	P2XR7I03A	A-G	26308	unknown	0,7	0,44
Intron03	P2XR7I03B	G-A	26422	unknown	0,18	0,12
Intron04	P2XR7I04A	G-A	32394	unknown	0,03	0,01

35 30 25 20 15 10 5

Table 12. (continued)

Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2X7R gene						
Associated exons or Introns	Variation (SNP or others)	Allele	Position*	Modification	Frequency (Canada)	Frequency (Germany)
Intron04	P2XR7v05B	T-C	32434	unknown	0,33	0,29
Exon05	P2XR7E05D	G-A	32493	Gly150Arg	RARE	0,02
Exon05	P2XR7E05E	G-A	32506	Silent Val154	-	RARE
Exon05	P2XR7v05A	C-T	32507	Tyr155His	0,33	0,44
Exon05	P2XR7E05C	C-T	32548	Silent Cys168	RARE	0,02
Intron05	P2XR7I05C	A-C	32783	unknown	0,25	-
Intron05	P2XR7I05D	T-C	35309	unknown	ND	0,35
Intron05	P2XR7I05B	C-T	35374	unknown	0,7	0,67
Intron05	P2XR7I05A	A-C	35378	unknown	0,7	0,65
Exon06	P2XR7E06A	G-A	35438	Glu186Lys	-	0,02
Exon06	P2XR7E06B	T-C	35454	Leu191Pro	-	0,02
Intron06	P2XR7I06C	T-C	35549	unknown	0,04	0,08
Intron06	P2XR7I06G	G-C	35641	unknown	-	0,02
Intron06	P2XR7I06D	A-C	35725	unknown	0,21	0,27
Intron06	P2XR7I06F	T-G	36001	unknown	0,17	0,3
Intron06	P2XR7I06E	A-T	36064	unknown	0,11	0,1
Intron06	P2XR7I06A	DelGTTT	36091-36094	unknown	0,14	0,3
Intron06	P2XR7I06B	C-G	36108	unknown	0,14	0,29
Intron07	P2XR7I07A	C-T	36374	unknown	0,07	-
Intron07	P2XR7I07B	G-A	36378	unknown	0,21	0,28
Intron07	P2XR7I07C	T-A	36387	unknown	0,21	0,28
Intron07	P2XR7I07D	G-C	36398	unknown	0,42	0,4
Intron07	P2XR7I07E	C-T	37439	unknown	0,41	-

55 50 45 40 35 30 25 20 15 10 5

Table 12. (continued)

Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2X7R gene						
Associated exons or introns	Variation (SNP or others)	Allele	Position*	Modification	Frequency (Canada)	Frequency (Germany)
Intron07	P2XR7I07F	T-C	37513	unknown	-	RARE
Exon08	P2XR7E08C	C-T	37604	Arg270Cys	RARE	-
Exon08	P2XR7v08A	G-A	37605	Arg270His	0,46	0,24
Exon08	P2XR7v08B	G-A	37623	Arg276His	0,03	0,02
Exon08	P2XR7E08D	C-T	37633	Silent Asp279	RARE	-
Intron09	P2XR7v11A	C-T	47214	unknown	0,08	0,03
Exon11	P2XR7v11B	G-A	47383	Ala348Thr	0,5	0,44
Exon11	P2XR7v11C	C-G	47411	Thr357Ser	0,08	0,07
Intron11	P2XR7I11D	T-C	47563	unknown	0,43	0,44
Intron12	P2XR7I12A	C-T	54307	unknown	0,32	-
Intron12	P2XR7I12B	G-A	54308	unknown	0,03	-
Exon13	P2XR7v13F	C-T	54399	Ala433Val	0,13	-
Exon13	P2XR7v13A	A-G	54480	Gln460Arg	0,13	0,17
Exon13	P2XR7v13B	C-T	54523	Silent Pro474	0,1	0,07
Exon13	P2XR7v13G	DelCCCTGAGA GCCACAGG TGCCT	54562-54582	Del of 7aa 488 to 494 (PESHRCL)	RARE	-
Exon13	P2XR7v13C	A-C	54588	Glu496Ala	0,13	0,06
Exon13	P2XR7v13H	C-G	54664	His521Gln	0,03	-
Exon13	P2XR7E13D	G-T	54703	Silent Leu534	0,1	0,02
Exon13	P2XR7E13J	A-T	54804	Ile568Asn	-	0,01
Exon13	P2XR7v13I	G-A	54834	Arg578Gln	-	RARE
Exon13	P2XR7v13E	G-A	54847	Silent Pro582	0,4	0,45
3'UTR	P2XR7UTR3A	C-A	55169	unknown	0,48	0,37

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55 50 45 40 35 30 25 20 15 10 5

Table 12. (continued)

Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2X7R gene						
Associated exons or Introns	Variation (SNP or others)	Allele	Position*	Modification	Frequency (Canada)	Frequency (Germany)
3'UTR	P2XR7UTR3B	A-C	55170	unknown	0,09	0,1
3'UTR	P2XR7UTR3C	A-C	55171	unknown	0,05	0,06
3'UTR	P2XR7UTR3D	C-T	55917	unknown	0,001	-
3'UTR	P2XR7UTR3E	G-A	54925	unknown	-	0,01

[0219] The position and numbering of the polymorphism corresponds to the human P2X7R gene as defined in SEQ ID NO: 1. To identify the genomic organization of the P2X7R gene, BAC clones were firstly organized using known polymorphic markers, sequence tag sites (STSs), BAC-end sequences and expressed sequence tags (ESTs). Unorientated and unordered DNA regions were reassembled into a sequences using Phrap and reordered the pieces using P2X7R exons as scaffolds. No complete gene organization for P2X7R has been done. There is only a partial gene structure from exon6 to 13, NT_037809. Therefore, this genomic sequence encompassing the P2X7R gene as depicted in SEQ ID NO: 1 could contain some sequence errors, specifically in intronic regions. Primers used for SNP amplification and sequencing are shown in Table 1a and depicted in SEQ ID NOs: 52 to 111.

[0220] Statistical analysis was performed according to the CLUMP method (Sham & Curtis 1995, Ann. Hum. Genet. 59:97-105). Table 13 resumes the allelic and genotypic association studies for SNPs in P2X7 gene.

Table 13. Allelic and genotypic association studies using CLUMP

Locus	Allele Frequencies*	Effective		Allele Analysis p-value (T1)	Genotype Analysis	
		Cases	Controls		p-value (T1)	p-value (T3)
P2XR7UTR5F	2(0.23); 4(0.77)	311	217	0.109	0.319	0.339
P2XR7UTR5N	1(0.001); 3(0.999)**	314	218	0.038	0.048	0.048
P2XR7UTR5G	2(0.001); 3(0.105); 4(0.894)	314	218	0.993	0.714	0.761
P2XR7UTR5H	2(0.92); 4(0.08)	312	215	0.743	0.884	0.754
P2XR7UTR5A	1(0.08); 2(0.92)	312	219	0.557	0.786	0.678
P2XR7UTR5B	2(0.73); 4(0.27)	310	218	0.485	0.761	0.814
P2XR7UTR5D	1(0.92); 3(0.08)	311	217	0.555	0.787	0.691
P2XR7v02A	2(0.09); 4(0.91)	313	218	0.501	0.729	0.591
P2XR7i04A	1(0.04); 3(0.96)	314	220	0.604	0.433	0.348
P2XR7v05B	2(0.69); 4(0.31)	314	220	0.133	0.270	0.325
P2XR7E05D	1(0.03); 3(0.97)	314	220	0.842	0.827	0.827
P2XR7E05E	1(0.006); 3(0.994)**	314	220	0.048	0.045	0.045
P2XR7v05A	2(0.60); 4(0.40)	314	220	0.038	0.144	0.219
P2XR7E05C	2(0.98); 4(0.02)	314	220	1.000	1.000	1.000
P2XR7i07F	2(0.002); 4(0.98)	315	219	1.000	1.000	1.000
P2XR7v08A	1(0.23); 3(0.77)	315	219	0.454	0.673	0.634
P2XR7v08B	1(0.02); 3(0.98)	315	219	0.636	0.638	0.638
P2XR7v11A	2(0.95); 4(0.05)	311	218	0.348	0.391	0.436
P2XR7v11B	1(0.45); 3(0.55)	312	218	0.605	0.803	0.790
P2XR7v11C	2(0.93); 3(0.07)	312	218	0.793	0.256	0.924
P2XR7i11D	2(0.45); 4(0.55)	312	219	0.665	0.735	0.740
P2XR7v13A	1(0.87); 3(0.13)	305	215	0.017	<0.001	<0.001
P2XR7v13B	2(0.93); 4(0.07)	305	216	1.000	0.228	0.677
P2XR7V13C	1(0.91); 2(0.09)	305	216	0.151	0.006	0.008
P2XR7E13D	3(0.94); 4(0.06)	315	219	0.402	0.429	0.474
P2XR7E13J	1(0.01); 4(0.99)	315	219	0.618	0.603	0.603
P2XR7E13I	1(0.004); 3(0.996)	315	219	0.999	1.000	1.000
P2XR7v13E	1(0.46); 3(0.54)	314	219	0.699	0.866	0.845
P2XR7UTR3A	1(0.518); 2(0.482)	314	219	0.617	0.850	0.875
P2XR7UTR3B	1(0.966); 2(0.034)	313	219	0.522	0.850	0.643
P2XR7UTR3C	1(0.979); 2(0.021)	313	219	0.636	0.505	0.382
P2XR7UTR3E	1(0.02); 3(0.98)	315	219	0.147	0.161	0.161

* The column Allele Frequencies presents the allele for each SNP (A=1, C=2, G=3, T=4) and their respective frequency.

** For this SNP we observed a zero cell in both (allele and genotype) 2X2 contingency tables. p-value <0.045 was observed exact Fisher test.

[0221] For the SNP analysis, the Hardy-Weinberg (HW) equilibrium was controlled in the control samples. The Hardy-Weinberg principle (HWP) may be stated as follow: In a large, randomly mating population, in which there is no migration, or selection against a particular genotype and the mutation rate remains constant, the proportions of the various genotypes will remain unchanged from one generation to another. Take a two allele system with alleles A and a. If the proportion of A in the population is represented as p and the proportion of a as q, then p plus q represent the sum total of alleles at this locus, that is $p+q=1$. The HWP is useful to evaluate some population problems like marital assortment, Inbreeding, population stratification, admixture, decreased viability of a particular genotype. The SNP P2XR7v13A did not respect the Hardy-Weinberg equilibrium.

[0222] The association hypothesis was also tested using an allele positivity table known to be suitable for the detection of susceptibility alleles showing a dominant mode of inheritance (Ohashi and Tokunaga, J. Hum. Genet. 44 (1999), 246-248; Ohashi et al., Ann. Hum. Genet. 65 (2001), 197-206). Similar results were obtained using this method as those obtained using the allele frequency tables, with the exception of P2XR7v05A where the p-values were 0.253. Thus, P2XR7v05A presented a less significant association in this analysis. This difference can be attributed to the mode of inheritance.

[0223] The proportion of unipolar individuals in analysis of the German population is quite important since the American Psychiatric Association (Diagnostic and Statistical Manual of Mental Disorders-4th Edition Text Revision (DMS-IV-TR), American Psychiatric Press, 2000) has reported an increase in susceptibility for unipolar disorders in female groups. To determine whether the sexual variable could influence the association analysis, additional association studies were performed by controlling the sexual parameter. Normal individuals in the German population without gender information were omitted from the study. Then, a logistic regression model was derived by including the sex as factor. In order to obtain a model that is as stable as possible, the regression model was minimised by using the difference between loglikelihood's for models with or without interaction (Hosmer, and Lemeshow, "Applied logistic regression", John Wiley and Sons, 1989). The strategy used for handling the zero cells from contingency tables was to eliminate associated category completely. Calculations were done with SAS v8.0 SAS is a statistical software package that allows the user to manipulate and analyze data in many different ways. Because of its capabilities, this software package is used in many disciplines, including medical sciences, biological sciences, and social sciences.

[0224] The introduction of a sexual parameter did not perturb the association already observed in previous analysis. Moreover, this analysis model revealed additional results: a potential allele association with P2XR7v05B ($p=0.064$), and a genotypic association for P2XR7v08A ($p=0.042$) was observed.

[0225] Association studies using pooled samples was performed by merging individuals from the samples of the Saguenay/Lac St-Jean with those of the German population. Results are illustrated in table 14. The aim of this analysis is to highlight common features between both populations. However, according to differences between both samples (mainly the phenotype of affected individuals i.e. bipolar disorder in the Saguenay/Lac St-Jean samples, versus mostly unipolar disorder in the German population) some parameters were controlled, including sex and ethnicity. The modelling strategy for logistic regressions was described above.

Table 14.

Association studies using pooled samples from both populations				
Locus	Allele analysis		Genotype analysis	
	p-value for SNP	p-value for sex	p-value for SNP	p-value for sex
P2XR7v02A	0.8254	0.0085	0.8650	0.4531
P2XR7v05B	0.1751	0.3714	0.2034	0.5110
P2XR7v05A	0.3808	0.0266	0.0885	0.1392
P2XR7v08A	0.0452	0.0041	0.1021	0.3452
P2XR7v08B	0.3471	0.0040	0.3413	0.3617
P2XR7v11A	0.3559	0.0136	0.5888	0.4404
P2XR7v11 B	0.5902	0.0093	0.3897	0.4302
P2XR7v11C	0.3731	0.0094	0.7648	0.4615
P2XR7v13A	0.0047	0.0209	<0.0001	0.4814
P2XR7v13B	0.5129	0.2352	0.9584	0.4092
P2XR7v13C	0.2466	0.0284	0.2225	0.4228

Table 14. (continued)

Association studies using pooled samples from both populations				
Locus	Allele analysis		Genotype analysis	
	p-value for SNP	p-value for sex	p-value for SNP	p-value for sex
P2XR7v13E	0.8168	0.0159	0.3713	0.4990

[0226] An allelic and genotypic association was observed for the P2XR7v13A locus ($p=0.0047$) which was stronger than in the separate analyses. A significant allelic association was also noted for the P2XR7v08A locus ($p=0.0452$). In addition, the present analysis also demonstrate the potential relationship between SNP P2XR7v05A and the origin with a p -value= 0.0515 (not shown in the table) which is in agreement with previous association analysis done in both samples separately (see Table 13).

[0227] The haplotype analysis was performed using the German population. The PHASE program (Stephens et al., Am. J. Hum. Genet. 68 (2001), 978-989) was used to estimate SNPs haplotypes within exons of the P2X7R gene. Haplotypes were created for each exon having more than one associated SNP (see Table 15 for exon-associated SNPs). Case groups varied from 218-220 individuals, whereas control groups varied between 312-316 individuals. Association hypothesis was tested with the CLUMP method since many haplotypes were created for each exon. T1 and T3 statistic tests performed as described above. T2 and T4 statistics were also calculated owing to the presence of small effective cells in the contingency tables. T2 statistic is the usual chi-squared statistic applied on the contingency table obtained after collapsing columns with small expected values. T4 statistic is the largest chi-squared statistic obtained by comparing one column of the original table against the total of the other columns. One thousand simulations were used to estimate p -values. The resulting data was analyzed with the logistic regression model (describe above) using SAS V8.0 in order to consider the sexual parameter (for these tests the sample was reduced by 14 normal individuals). However, this analysis method is limited by the reliability of reconstructed haplotypes.

Table 15.

Exon-associated SNPs	
Exons	Associated SNPs
5	P2XR7E05D P2XR7E05E P2XR7v05A P2XR7E05C
8	P2XR7v08A P2XR7v08B
11	P2XRv11B P2XRv11C
13	P2XR7v13A P2XR7v13B P2XR7v13C P2XR7E13D P2XR7E13J P2XR7v13I P2XR7v13E

Table 16.

Genotypic association with haplotypes in exon 13 of P2X7R						
Exon (haplotype)	Allele analysis			Genotype analysis		
	Clump*	p-value(sex)	p-value(haplo)	Clump	p-value(sex)	p-value(haplo)
5(5)	T1:0.032 T2:0.068 T3:0.054 T4:0.059	0.3133	0.1947	T1:0.193 T2:0.159 T3:0.099 T4:0.304	0.460	0.5355
8(3)	T1:0.551 T2:0.585 T3:0.646 T4:0.646	0.3813	0.3064	T1:0.812 T2:0.689 T3:0.644 T4:0.756	0.5428	0.6652
11(3)	T1:0.750 T2:0.786 T3:0.726 T4:0.726	0.0886	0.7396	T1:0.625 T2:0.919 T3:0.929 T4:0.921	0.2305	0.9494
13(15**)	T1:0.088 T2:0.079 T3:0.147 T4:0.072	0.1871	0.1264	T1:0.001 T2:0.002 T3:0.057 T4:<0.001	0.4610	0.019

*T1 test should not be considered because of contingency tables with zero cells.

**Among these 15 haplotypes, we observed 8 haplotypes where case cells have less than 3 individuals.

[0228] Table 16 illustrates a genotypic association with haplotypes in exon 13 of the P2X7R genes. Interestingly, many haplotypes for the exon 13 were observed. The differences between statistics in exon 13 (T3 less significant) can be explained by the involvement of more than one genotype of haplotypes in the disease. A potential allelic association was also noted with haplotypes in exon 5 of the P2X7R gene.

[0229] The following are clinical results illustrating the functional consequences of polymorphisms in P2X7R.

The development and course of depression is causally linked to impairments in the central regulation of the hypothalamic-pituitary-adrenocortical (HPA) axis. Abnormalities in the HPA axis can be measured using the dexamethasone-suppression test (DST) or the combined dexamethasone/corticotropin-releasing hormone (Dex/CRH) test. Changes in cortisol and/or adrenocorticotrophic hormone (ACTH) measurements during the DST or Dex/CRH test are indicative of HPA dysfunction in depressed patients (Heuser et al, J. Psychiat. Res. 28 (1994) 341-356; Rybakowski and Twardowska, J. Psychiat. Res. 33 (1999) 363-370; Zobel et al, J. Psychiat. Res. 35 (2001) 83-94; Künzel et al, Neuropsychopharmacology 28 (2003) 2169-2178). In order to demonstrate that P2X7R SNPs associated with affective disorders also correlate with changes in the HPA axis, cortisol and ACTH levels in response to the DST and Dex/CRH test were measured for the P2XR7v13A and P2XR7v13C SNPs. P2XR7v13A consist of an A to G nucleotide change resulting in a Gln460Arg modification in the P2X7R protein. The P2XR7v13C SNP corresponds to an A to C nucleotide change resulting in a Glu496Ala modification that has been shown to drastically reduce protein activity (Wiley et al, Drug Dev. Res. 53 (2001) 72-76).

[0230] Methods and conditions for performing the DST and Dex/CRH test are well known in the art, see for example Heuser et al, J. Psychiat. Res. 28 (1994) 341-356; Künzel et al, Neuropsychopharmacology 28 (2003) 2169-2178. Briefly, individuals were pre-treated at 23:00 with an oral administration of 1.5 mg dexamethasone. For the DST test, a blood sample was drawn at 8:00 prior to dexamethasone administration (i.e. pre-dexamethasone) and at 8:00 the morning following dexamethasone administration (i.e. post-dexamethasone). For the Dex/CRH test, a venous catheter was inserted at 14:30 the day following dexamethasone administration and blood was collected at 15:00, 15:30, 15:45, 16:00, and 16:15 into tubes containing EDTA and trasylol (Bayer Inc., Germany). At 15:02, 100 mg of human CRH (Ferring Inc., Germany) was administered intravenously. Measurement of plasma cortisol concentrations was done using a commercial radioimmunoassay kit (ICN Biomedicals, USA) while plasma ACTH concentrations was measured using a commercial immunometric assay (Nichols Institute, USA). Both assays were performed according to the manufacturer specifications.

[0231] For the P2XR7v13A SNP, a decrease in basal cortisol levels was seen at admission in individuals with an AG or GG allele when compared to individuals with the AA allele (Figure 1f). During the Dex/CRH test, a reduction in cortisol and ATCH response was measured in individuals with the GG allele when compared to individuals with an AA or AG allele (Figures 1g and 1h).

[0232] Furthermore, response to antidepressant treatment was delayed in GG individuals (figure 1i).

[0233] For the P2XR7v13C SNP, an increase in basal cortisol levels was measured post-dexamethasone administration (Figure 1j). During the Dex/CRH test, individuals with the CC allele displayed elevated cortisol response (Figure 1k), but reduced ATCH response (Figure 1l) when compared to AA and AC individuals. These results are indicative of dysregulation of the HPA axis.

[0234] Thus, SNPs in P2XR7R correlate with dysfunction in the HPA axis and demonstrate the functional and clinical consequences of polymorphisms in P2XR7R.

EXAMPLE 4

P2XR7R gene structure and mRNA expression and transcript sequence

[0235] A 1700 bp nucleotide sequence corresponding to the human P2XR7R promoter was analyzed by using MatInspector V2.2 and Transfac 4.0 algorithms. This analysis showed that the P2XR7R gene does not contain a standard TATA box, but has SP1 sites that can make up for transcriptional initiation. Besides the SP1 sequences, there are binding sites for the transcription factors GATA, Oct and Ikarus. These sites are thought to provide tissue specificity. Interestingly, the P2XR7R promoter has binding sites that suggest responsiveness to different cytokines such as AP-1, NFAT and CEBPB.

[0236] P2XR7R possesses 13 exons and 12 introns (Buell et al., Receptors Channels 5 (1998), 347), providing a basis for alternative splicing that would yield in theory different transcripts and produce different isoforms with possible different functions. No alternatively spliced variant was clearly identified. However, experiments of EST clustering allowed the description of three splicing variants. One is defined by the lack of the exon 5. This P2XR7v02 variant corresponds to the clone IMAGE: 3628076 isolated from brain-derived cell lines. The P2XR7v02 lacking the exon 5 produces a frame shift, thus generating a shorter polypeptide. The second splicing variant, P2XR7v03, is characterized by the presence of the short intron 10 into the mRNA. This variant is supported by two high quality sequences, the cDNA clone BRAMY2008977 (AC number: AK090866) from human amygdala and the EST clone dbEST:7339877 derived from an unknown human tumor. The last variant, P2XR7v04, is defined by the lack of the first exon that suggests an alternative promoter usage closed to the exon 2. A high quality EST clone dbEST:4782844 derived from a head and neck tumor supports this variant. These variants are shown in Figures 16a to 16e.

P2X7 variants.

5	P2X7v01	MPACCS	SDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS	SYVCFALVSDKLYQRKEPVISS
	P2X7v04	MPPVD-----	-----AFPCLPFS---	FALVSDKLYQRKEPVISS
	P2X7v02	MPACCS	SDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS	SYVCFALVSDKLYQRKEPVISS
	P2X7v03	MPACCS	SDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS	SYVCFALVSDKLYQRKEPVISS
1.....10.....20.....30.....40.....50				
10	P2X7v01	VHTKVKGIAEVKKEIVENG	VKKLVHSVFDTADYTFPLQGN	SFFVMTNFLKTEGQEQR
	P2X7v04	VHTKVKGIAEVKKEIVENG	VKKLVHSVFDTADYTFPLQGN	SFFVMTNFLKTEGQEQR
	P2X7v02	VHTKVKGIAEVKKEIVENG	VKKLVHSVFDTADYTFPLQGN	SFFVMTNFLKTEGQEQR
	P2X7v03	VHTKVKGIAEVKKEIVENG	VKKLVHSVFDTADYTFPLQGN	SFFVMTNFLKTEGQEQR
61.....70.....80.....90.....100.....110				
15	P2X7v01	EYPT	RRTLCS	SDRGCKKGWMDPQSKGIQTGR
	P2X7v04	EYPT	RRTLCS	SDRGCKKGWMDPQSKGIQTGR
	P2X7v02	EYPT	RRTLCS	SDRGCKKGWMDPQSKGLLS-----
	P2X7v03	EYPT	RRTLCS	SDRGCKKGWMDPQSKGIQTGR
121.....130.....140.....150.....160.....170				
20	P2X7v01	LLNSAENFTVLIKNNIDF	PGHNYTTRNILPGLNITCTF	HKTNPQCFIFRLGDI
	P2X7v04	LLNSAENFTVLIKNNIDF	PGHNYTTRNILPGLNITCTF	HKTNPQCFIFRLGDI
	P2X7v02	LLNSAENFTVLIKNNIDF	PGHNYTTRNILPGLNITCTF	HKTNPQCFIFRLGDI
	P2X7v03	LLNSAENFTVLIKNNIDF	PGHNYTTRNILPGLNITCTF	HKTNPQCFIFRLGDI
181.....190.....200.....210.....220.....230				
25	P2X7v01	NFSDVAIQGGIMGIEIY	WDCNLD	RFHCHPKYSFRRLDDKT
	P2X7v04	NFSDVAIQGGIMGIEIY	WDCNLD	RFHCHPKYSFRRLDDKT
	P2X7v02	NFSDVAIQGGIMGIEIY	WDCNLD	RFHCHPKYSFRRLDDKT
	P2X7v03	NFSDVAIQGGIMGIEIY	WDCNLD	RFHCHPKYSFRRLDDKT
241.....250.....260.....270.....280.....290				
30	P2X7v01	ENNVEKRTLIKVF	GIRFDILVFGTGGKFDIIQL	VVYIGSTLSYFGLAAV
	P2X7v04	ENNVEKRTLIKVF	GIRFDILVFGTGGKFDIIQL	VVYIGSTLSYFGLAAV
	P2X7v02	ENNVEKRTLIKVF	GIRFDILVFGTGGKFDIIQL	VVYIGSTLSYFGLAAV
	P2X7v03	ENNVEKRTLIKVF	GIRFDILVFGTGGKFDIIQL	VVYIGSTLSYFGLV
301.....310.....320.....330.....340.....350				
35	P2X7v01	NCCRSHIYPWCKCCQ	PCVNVNEYYYRKKCESI	VEPKPTLKYVSFVDESH
	P2X7v04	NCCRSHIYPWCKCCQ	PCVNVNEYYYRKKCESI	VEPKPTLKYVSFVDESH
	P2X7v02	NCCRSHIYPWCKCCQ	PCVNVNEYYYRKKCESI	VEPKPTLKYVSFVDESH
	P2X7v03	NCCRSHIYPWCKCCQ	PCVNVNEYYYRKKCESI	VEPKPTLKYVSFVDESH
361.....370.....380.....390.....400.....410				
40	P2X7v01	LQDVKGQEVPRPAM	DFTDLSRLPLALHDT	PPIPGQPEEIQLLRKEAT
	P2X7v04	LQDVKGQEVPRPAM	DFTDLSRLPLALHDT	PPIPGQPEEIQLLRKEAT
	P2X7v02	LQDVKGQEVPRPAM	DFTDLSRLPLALHDT	PPIPGQPEEIQLLRKEAT
	P2X7v03	LQDVKGQEVPRPAM	DFTDLSRLPLALHDT	PPIPGQPEEIQLLRKEAT
421.....430.....440.....450.....460.....470				
45	P2X7v01	SCLPSQLPESHRCLEEL	CCRKKPGACIT	TSELFRKLVL
	P2X7v04	SCLPSQLPESHRCLEEL	CCRKKPGACIT	TSELFRKLVL
	P2X7v02	SCLPSQLPESHRCLEEL	CCRKKPGACIT	TSELFRKLVL
	P2X7v03	SCLPSQLPESHRCLEEL	CCRKKPGACIT	TSELFRKLVL
481.....490.....500.....510.....520.....530				
50	P2X7v01	TNSRLRHCA	YRCYATWRFSGQDMAD	FAILPSCCRWRIRKEFPK
	P2X7v04	TNSRLRHCA	YRCYATWRFSGQDMAD	FAILPSCCRWRIRKEFPK
	P2X7v02	TNSRLRHCA	YRCYATWRFSGQDMAD	FAILPSCCRWRIRKEFPK
	P2X7v03	TNSRLRHCA	YRCYATWRFSGQDMAD	FAILPSCCRWRIRKEFPK
541.....550.....560.....570.....580.....590				

[0237] Therefore the transcriptional and translational start sequences of the human P2X7R were analyzed using Blast, Genescan and HMMgene computer software. This analysis indicated that P2X7R possesses with high probability only one translation start site. Most P2X7R expression sequence tags (ESTs; Unique cluster Hs. 193470) having a reliable 5' end showed identical transcriptional start site. None of the ESTs showed any indication of alternative splicing. Therefore, in silico analysis suggests that there is a low probability to find different transcripts produced by alternative splicing or alternative promoter usage.

[0238] The above mentioned in silico data were confirmed by RT-PCR analysis spanning the whole predicted human

P2X7R coding sequence using 14 and 19 bases (5'-ATGCCGGCTTGCTG-3'; 5'-GTAGGGATACTTGAAGCCA-3') oligonucleotides corresponding to the beginning and end of the coding sequence, respectively. Total RNA from whole brain, different dissected brain areas, thymus, spleen and kidney were isolated and analyzed for P2X7R expression. RT-PCR reactions were performed using the C. Therm One Step polymerase system (Roche Applied Science) and a protocol for touch down PCR with hot start. Briefly, Reverse Transcription was performed at 52°C according to the manufacturer's conditions. PCR reactions were executed with an annealing temperatures of 64°C for the first five cycles and of 54°C for the next 30 cycles.

[0239] A single specific band of the size of 1785 bp corresponding to the complete coding sequence of P2X7R was detected. P2X7R mRNA was detected in the whole brain, hippocampus, cerebellum, leukocytes and thymus but not in cerebral cortex, hypothalamus, spleen and kidney (Figure 2). All PCR products were cloned using the pGEM-T-Easy plasmid (Promega), selected in Top-10 bacteria (Invitrogen) by blue-white selection and tested by EcoRI digestion. Clones having fragments of the expected size were amplified and purified for sequencing. The sequence confirmed the identity of the 1785 bp clones as the complete coding sequence of wild-type P2X7R. Therefore, in all the tissues tested, wild-type P2X7R is expressed as a single transcript which includes the complete coding sequence. The presence of tissue specific isoforms is unlikely. These studies provide useful information about the P2X7R mRNA expression and transcript processing. This information can be used to synthesize riboprobes for in situ hybridization, Northern and Southern blot as well as engineering cells for the overexpression of P2X7R.

EXAMPLE 5

P2X7R expression in the mouse brain

[0240] The expression of P2X7R was further studied by immunohistochemistry of serial sections of complete mouse brains using a polyclonal antibody directed against an internal peptide of P2X7R (Santa Cruz Biotechnology). The brains from stress-free mice were shock frozen, cut into 16 µm slices and fixed with paraformaldehyde for 5 minutes. The sections were blocked for 30 minutes at room temperature with 1:10 horse serum. All antibodies were diluted in TBST buffer (Tris-buffered saline with 0.05% Tween-20). The first antibody was used in a dilution 1:200 and incubated overnight. All washes were performed with TBST buffer. As a secondary antibody, an anti-goat IgG biotinylated (Vector Laboratories) was used and detection was performed using the streptavidin-biotin-horse-radish peroxidase complex (Vector Laboratories) in combination with diaminobenzidine. Slides were counterstained with toluidine blue using standard procedures. The same procedure in the absence of the primary antibody was performed as a negative control. As a positive control to test the Preservation of the tissue was verified with an antibody specific for the protein Patched1 (Santa Cruz Biotechnology). Patched1 was used as positive control since it stains all relevant brain structures and is not affected by stress or antidepressants. Very specific staining pattern was detected, consistent with the specific subcellular localization of P2X7R in brain cells. Negative controls were completely devoid of signal. Positive control with Patched1 showed identical signal intensity and distribution in all samples, indicating that all tissues were equally well preserved and processed.

[0241] Proceeding from frontal to caudal, P2X7R protein was observed in the glomerular layer of the olfactory bulb at low levels (Figure 3). P2X7R was also present at very low levels in a restricted area of the periventricular hypothalamic nucleus (figure 3). Ependymal cells surrounding the lateral ventricles also showed a faint staining (Figure 3). A stronger signal was detected in restricted areas of the hippocampus, where the signal was present in single cells of the polymorph layer, the lacunosum moleculare and the oriens layer (Figure 4). In more posterior areas of the hippocampus, the signal was present in the molecular layer, stratum radiatum and near the CA3. In a further caudal position, P2X7R was expressed in the subcomisural organ (Figure 4). Therefore, the basal P2X7R expression in the brain of stress-free mice is restricted to areas that had been previously associated with depression, stress, learning and memory.

EXAMPLE 6

P2X7R is modulated in mice treated with an antidepressant

[0242] Further validation of role of P2X7R in affective disorders was performed by examining its expression pattern in response to stress and treatment with antidepressant drugs. A treatment schedule which has been proven to produce antidepressant effects on the behavioural level was administered to mice which were characterized as antidepressant responsive by using a variety of behavioural paradigms suitable to detect anxiolytic and antidepressant effects of classical antidepressants like the selective serotonin reuptake inhibitor paroxetine. Paroxetine was delivered by gavage to naive male mice over a time period of 28 days at a dosage of 10 mg/kg bodyweight twice per day. In parallel, a control group of mice was given vehicle solution (i.e. without paroxetine) using the same treatment regiment while a

second control group of mice was left undisturbed and stress-free (i.e. untreated) during the same period of the experiments. At the end of the long-term treatment, part of the mice of each experimental group were tested in the dark/light box (test of anxiety behaviour) and in the Porsolt's forced swim test (test of depressive-like behaviour) to confirm the effectiveness of the treatment (Figure 5). Passive stress coping behaviour decreased after long-term treatment with the antidepressant paroxetine. The other part of the experimental groups (i.e. mice without test experience) were decapitated, brains rapidly removed and frozen at -80°C until usage.

[0243] The expression of P2X7R in the brains of mice under stress-free conditions, and mice under mild stress produced by the vehicle application, and mice under paroxetine treatment was evaluated using three different brains from each group. Serial slides from each group of animals were analyzed in parallel by immunohistochemistry using the same materials in order to produce completely comparable results. No significant change in P2X7R expression in the olfactory bulb was seen in response to stress or to paroxetine treatment (Figure 6). However, in the periventricular nucleus of the hypothalamus, paroxetine produced a slight inhibition of P2X7R expression (Figure 7). No significant change was observed in the ependymal cells from different brain areas (Figure 8). The most dramatic changes were observed in the hippocampus, where P2X7R was strongly inhibited by stressful handling whereas paroxetine treatment produced a marked stimulation above basal levels (Figures 9, 10 and 11). This effect was observed all along the hippocampus but was more evident in the polymorph layer near the dentate gyrus. In the subcommissural organ, P2X7R expression remained unchanged by the different treatments. Therefore, P2X7R expression is strongly regulated in two specific brain areas involved in depression and stress. Other brain areas, which showed low levels of P2X7R and are not directly involved in depression, did not show changes.

[0244] In the samples from mice treated with paroxetine and showing a strong P2X7R expression, it was possible to analyze the distribution of P2X7R in more detail (Figures 10 and 11). The P2X7R protein was not only present in cell bodies but also was clearly detected in projections innervating the granular layer of the dentate gyrus (Figure 12). This subcellular localization of P2X7R is consistent with a role in neurotransmitter release and long term potentiation.

[0245] Since some reports (Muria et al., *Biochem. J.* 288 (1992), 897-901; Ferrari et al., *FEBS Lett.* 447 (1999), 71-75) suggest that chronic and high dose stimulation of P2X7R may cause apoptosis in some cell types, the hippocampus of the above described animals were analyzed for the co-localization of apoptotic cells and P2X7R expressing cells, in consecutive sections, using TUNNEL staining and immunohistochemistry. In correlative sections, only few apoptotic cells were detected and they were present along the granular layers of the hippocampus where no P2X7R expression was observed (Figure 13). No significant differences in the numbers of apoptotic cells were observed between the different treatment conditions. Therefore, the location and number of apoptotic cells did not correlate with the location and number of cells expressing P2X7R and rules out an involvement of P2X7R in the induction of apoptosis in the hippocampus.

[0246] Thus, P2X7R expression is considerably restricted to specific brain areas involved in depression. Moreover, P2X7R expression is inhibited by stress and strongly stimulated by antidepressant treatment in these specific areas. Therefore, P2X7R fulfils all criteria required for the actions of antidepressants according to the highest standards in the field of depression research. In addition, these results suggest that modulation of function of P2X7R is associated with chronic stress, which serves as a model for several aspects of affective disorders.

EXAMPLE 7

The behavioural effect of P2X7R inhibition in mice

[0247] To demonstrate that P2X7R inhibition acts as a causative agent for affective disorders, P2X7R function was specifically inhibited in distinct regions of the brain without affecting any other brain function. This was achieved by delivering double stranded small interference RNA molecules (siRNA) into restricted areas of the brain.

[0248] According to the observed expression pattern of P2X7R in the hippocampus (Figures 9, 10, and 11) and the known involvement of the hippocampus in depression, the dentate gyrus (hippocampus) was selected as target region for siRNA application. Male, naive mice were bilaterally implanted with a guide cannulae (23 gauge, length 8 mm) by means of a stereotactic instrument. The coordinates, in relation to bregma, were -2.0 mm posterior, ± 1.0 mm lateral, and -1.0 mm ventral. Following a recovery period of 5 days, the mice were divided into three experimental groups: vehicle (veh), control double stranded RNA (control), and P2X7R specific double stranded siRNA (siRNA). Sequences used for P2X7R siRNA are 5'-GUGGGUCUUGCACAUGAUCTT-3' and 5'-GAUCAUGUGCAAGACCCACTT-3'. Both sequences were annealed and injected together as a double stranded RNA. On day 6 after surgery, mice were slightly anaesthetized with Isoflurane and injections of siRNA were carried out. The concentration of the control and siRNA was 0.1 nmol/ μ l, and a volume of 1 μ l per side was infused using specifically adapted injection systems (30 gauge, length 9 mm). The anaesthesia for the infusion was of short duration and the mice were awake immediately or few seconds after the manipulation.

[0249] Once delivered into the brain the siRNA molecules specific for P2X7R were taken up by brain cells and spe-

cifically induce the degradation of the complementary P2X7R mRNA with high efficiency. As a result, P2X7R function was specifically inhibited for a short period without affecting any other brain function. In this regard, injection of vehicle or control siRNA did not result in any obvious changes in normal behaviour, i.e., food and water intake, or motor behaviour in the home cage.

[0250] The effects of P2X7R inhibition on depressive-like behaviour was assessed 24 hours and 48 hours after infusion of siRNA, control or vehicle according to the standard test paradigm, the Porsolt's forced swim test (Porsolt et al., Arch. Int. Pharmacodyn. 229 (1977), 327-336; Porsolt, Rev. Neurosci. 11 (2000), 53-58). The parameter used to evaluate depressive-like behaviour is the time the animal is floating in the water, a behaviour which is associated with behavioural despair as the animal does not make any effort to actively cope with the stressful situation. Compared to vehicle application, no influence of control double stranded RNA (5'-CAACUUCUUCUUCUACGCGTT-3') on floating behaviour (passive stress coping) was detected. In contrast, compared to controls, mice infused with P2X7R specific siRNA showed a significant increase in passive behaviour, which is construed as depressive-like behaviour (Figure 14). This interpretation becomes moreover evident when the effects of antidepressants on passive stress coping behaviour in the forced swim test are visualized (Figure 5). Passive stress coping behaviour increased after acute intrahippocampal injection (bilateral, dentate gyrus) of siRNA targeting P2X7R. The Porsolt's forced swim test is a standard test used to assess the effectiveness of antidepressants and it has been proven by many studies that the test is selectively sensitive for these effects, given that the right animal model is used. The paradigm has been widely used to test pharmaceutical compounds and to validate animal models of depression, which show an increase in passive behaviour as do the mice where P2X7R has been inhibited (siRNA).

[0251] At the end of the experiment, the mice were sacrificed and the brains were examined to confirm the location and efficiency of the siRNA injections. For this purpose the brains were cut into sections and the slides were stained by immunohistochemistry using the above mentioned protocols. Brains from mice injected with the specific double stranded siRNA, with control double stranded RNA and with vehicle were examined in parallel. Under these conditions, the specific siRNA directed against P2X7R injected near the dentate gyrus induced on average an 80% inhibition of P2X7R protein expression as compared to the samples from mice injected with vehicle or with control double stranded RNA. Both the number of cells expressing P2X7R as well as the intensity of the expression were strongly reduced (Figure 15). The injections with siRNA did not produce any sign of local inflammation or infiltration at the hippocampus. Thus, P2X7R expression is specifically and locally inhibited by siRNA application in vivo. This inhibition produced behavioural changes indicating a causative role for P2X7R in affective disorders. These results in combination with those mentioned above support and confirm the observation of mutations in P2X7R being associated with affective diseases in humans and that modulation of P2X7R activity has antidepressive effects.

EXAMPLE 8

Drug screening assay

[0252] Methods for identifying P2X7R agonists were established using an immortalised mouse hippocampal cell line expressing the endogenous P2X7 gene. Briefly, the expression of P2X7 was confirmed by culturing the cells at 37°C/5% CO₂ in DMEM with 10% foetal calf serum (Gibco). Upon reaching 80 % confluence, cells were collected in PBS and homogenized by repeated passage through a syringe (18G needle). The amount of total protein was measured by the Bradford assay (Sigma; diluted 1:5, O.D. measured at 595 nm) according to the manufacturer's recommendation. Protein homogenates were then mixed with an equal volume of loading buffer (50 mM Tris-Cl pH 6.8; 25% glycerol; 7,2 mM bromophenol blue; 2% SDS; 200 nM β-mercaptoethanol) and subsequently denatured in boiling water for 10 minutes. 20 mg of each sample were loaded onto a 10% polyacrylamide gel containing 0,4 % SDS. Electrophoresis and Western blot transfer were performed according to conventional protocols described, for example, in Sambrook, Russell "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, N.Y. (2001). Membranes were then blocked with 5 % dry milk and incubated with an antibody against P2X7R (1:1000 dilution; Santa Cruz Biotech) followed by incubation with a horse anti-goat peroxidase-coupled secondary antibody (1: 10000 dilution; Santa Cruz Biotech). Membranes were then incubated for 1 hour at 37°C in Lumi-Light Western Blotting Substrate (Roche Applied Science) followed by a 10 minute exposure on a BioMax MR Film (Kodak).

[0253] A 70 kD band corresponding to the expected size of the P2X7R protein was detected in HT-22 cells demonstrating expression of the endogenous mouse P2X7 gene (Figure 17). A second mouse hippocampal cell line (HT-39) did not express P2X7.

[0254] Since P2X7R is an ATP-gated ion channel which allows the entry of calcium and sodium ions into cells, a method for identifying P2X7R agonist was established by monitoring calcium influx into HT-22 cells. Cells were first loaded with the fluorescent dye Oregon green AM ester (Molecular Probes) for 30 minutes at room temperature, washed 2 times with DMEM/10% foetal calf serum to remove excess dye and cultured for 15 minutes in the presence of 100 μM 2'- and 2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (BzATP: C₂₄H₂₄N₅O₁₅P₃). BzATP is a known agonist

of P2X7R (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). Calcium movement into the cells was visualised under a fluorescent microscope with a fluorescein filter (wavelength 492/517 nm). Oregon green AM ester is a fluorescent dye that binds to intracellular calcium. Accordingly, an increase in green fluorescence was observed in cells treated with BzATP (Figure 18) signalling an activation of P2X7R which results in an influx of calcium

into the cells and an increase binding of Oregon green dye to intracellular calcium.
 [0255] Alternatively, Oregon green AM ester can be replaced by Fluo-3, fluo-4, fluo-5F, fluo-5N, fluo-4FF, Fluo-4 dextran, Fluo-3 AM, Fluo-4 AM, Fluo-5F AM, Fluo-5N AM and Fluo-4FF AM (Molecular Probes). Calcium influx in HT-22 cells can also be measured in 96-well and 384-well microplate using the Calcium Plus Assay Kit (Molecular Device) or FLIPR® Calcium Assay Kit for Fluorometric Imaging Plate Reader Systems (Molecular Device). HT-22 cells can be replaced by any cells expressing P2X7R, including cells that have been genetically modified by introducing an exogenous P2X7 gene.

[0256] The specificity of the P2X7R agonist on calcium influx was confirmed by pretreatment of HT-22 cells with 100 mM Oxidized ATP (oATP; Sigma) for 1 hour before the addition of BzATP. oATP is an irreversible inhibitor of the receptor (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203). Activation of P2X7R by the agonist was inhibited by oATP (Figure 18) as illustrated by the absence of green fluorescence in the cells.

[0257] Yet another method of measuring P2X7R activity involves the entry of ethidium bromide into P2X7R expressing cells. Activation of P2X7R by an agonist allows the entry of ethidium bromide which binds nuclear DNA and emits a fluorescence signal. Alternatively, the propidium dye YOPRO-1 can be substituted for ethidium bromide. An increase in fluorescence can be used as a measure of P2X7 receptor activation. Therefore, the assay can be used to test and quantify the effect of an agent or compound with agonist properties on P2X7R. In the present example, 10^3 HT-22 cells were seeded per well in a 96-well flat bottom microtitre plates and incubated at 37°C/5%CO₂ in DMEM medium containing 10% FCS until the cells attached to the culture surface. Once attached, cells were incubated for 60 minutes in DMEM medium containing 10%FCS, 10^{-4} M ethidium bromide and increasing concentrations of BzATP (1 µM, 10 µM, 100 µM, 500µM, 1 mM). The number of fluorescent cells which have integrated the ethidium bromide to the DNA can then be counted using a fluorescent microscope (Zeiss, Germany). Concentrations above 100µM BzATP increased the number of fluorescent nuclei signalling activation of P2X7R (Figure 19a). Alternatively, ethidium bromide fluorescence can be measured using a Perkin-Elmer fluorescent plate reader (excitation 520 nm, emission 595 nm, slit widths: Ex 15 nm, Em 20 nm). From the readings obtained, a pIC50 figure can be calculated for each candidate agent or compound. Accordingly, a P2X7R agonist is defined as an agent or a compound with an EC50 equal or below 300 micromolar, whereas the term EC 50 is defined as the concentration eliciting 50% of maximal response to an agonist (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). The specificity of an agonist for P2X7R can be evaluated by pre-incubation of the cells for 60 minutes with 100 µM o-ATP before adding the agonist and ethidium bromide dye. Under these conditions, activation of P2X7R by the agonist is inhibited by oATP resulting in a reduction in the number of fluorescent cells (Figure 19b).

[0258] Yet another method for identifying P2X7R agonists was devised by generating a immortalised mouse cell line that overexpresses the human P2X7R gene under the control of the human cytomegalovirus (CMV) early promoter/enhancer region. The human P2X7R cDNA was inserted into the pcDNA3.1 vector (Invitrogen) and transfected into the mouse hippocampal cell line HT-22 using Lipofectamine (Invitrogen) according to the manufacturer's specifications. One day after transfection, culture medium containing 500 µg/ml G418 was added to the cells. Resistant clones were separately isolated and cultured 14 days after applying the selection medium.

[0259] The agonistic activity of a compound was evaluated by measuring calcium entry in the cells that overexpress the human P2X7R. Cells were cultured in 96 well plates and incubated at 37°C with 5% CO₂ DMEM with 10% foetal calf serum (Gibco) until they reached confluence. Cells were then loaded for one hour with 10 µM of Fluo-4 AM (Molecular Probes). Fluo-4 AM is a fluorescent dye that binds to intracellular calcium. After loading, cells were washed once with a buffer containing 0.5 mM CaCl₂ and 20 mM Hepes and were treated with 20 µM BzATP or 50 µM tenidap. Agonist activity was detected by measuring an increase in calcium influx which results in increased binding to Fluo-4 AM and increased fluorescence. Changes in fluorescence signal are measured using a Fluostar Optima plate reader (BMG biotech). Both BzATP and tenidap produced a rapid increase in fluorescence intensity which declined slowly over time (Figure 19c). Thus, both compound stimulated the activity of P2X7R which results in an influx of ions into the cells.

EXAMPLE 9

Activation of P2X7R with agonists has antidepressive effects

[0260] To demonstrate that activation of P2X7R has therapeutic effects on affective disorders, the P2X7R agonist BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)) was administered to a selected DBA/2Ola mouse strain that displays characteristics of being highly anxious, responding to antidepressants, and showing

anxiolysis after subchronic antidepressant treatment (Lucki et al., *Psychopharmacology* 155 (2001), 315-322). BzATP is a compound with strong specificity to P2X7R (North and Surprenant, *Annu. Rev. Pharmacol. Toxicol.* 40 (2000), 563-580). In the present example, the P2X7R agonist was directly injected into the hippocampus of mice. However, a P2X7R agonist agent or compound could also be delivered orally, subcutaneously, intravenously, intra-arterial, intranasally, intramedullary, intrathecal, intraventricular, intranasally, intrabronchial, transdermally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly.

[0261] Four months old male mice were bilaterally implanted with guide cannulae (23 gauge, length 8 mm) by means of a stereotaxic instrument (David Kopf Instruments). The coordinates, in relation to bregma, were -2.0 mm posterior, ± 1.0 mm lateral, and -1.0 mm ventral. After surgery, the mice were allowed to recover for 10 to 12 days. Following this recovery period, mice were injected with 1 μ l vehicle solution (0.5% DMSO, Sigma) or 50 μ M BzATP (Sigma, prepared in 0.5% DMSO) in each side of the brain over a period of 60 seconds. Injections were performed using a 9 mm-30 gauge needle inserted into the guide cannulae and connected via tubing to a 10 μ l Hamilton syringe.

[0262] The behaviour of individual mice was assessed using the Porsolt's forced swim test 24 hours after injection of vehicle solution or BzATP. A pre-exposure of 5 minutes to the test was done 10-15 minutes after vehicle or BzATP injection. The forced swim test is a standard test that measures primary stress-induced reductions in avoidance or escape, termed behavioural despair. The test is used to determine the effectiveness of antidepressants, test new pharmaceutical compounds and validate animal models of depression (Porsolt et al., *Arch. Int. Pharmacodyn.* 229 (1977), 327-336; Porsolt, *Rev. Neurosci.* 11 (2000), 53-58; R  n  ric et al., *Behav. Brain Res.* 136 (2002), 521-532; Page et al., *Psychopharmacology* 165 (2003), 194-201; Kelliher et al., *Psychoneuroendocrinology* 28 (2003), 332-347). The test consists of placing a mouse for a period of 5 minutes into a glass cylinder containing water. Under such circumstances, the mouse cannot touch the bottom of the cylinder and is thus forced to swim. Time, latency and frequency of struggling versus floating are scored as behavioural parameters. Floating (i.e. movements made only for keeping balance and breath) is a passive behaviour associated with despair and represents a depressive-like symptom since the animal does not make any effort to actively cope with the stressful situation. Increased struggling (i.e. active attempts to escape) indicates active coping behaviour that can be interpreted as an improvement of depression-like symptoms. For example, treatment with serotonergic antidepressants reduce the total time spent floating (Borsini, *Neurosci. Biobehav. Rev.* 19 (1995), 377-395; Redrobe and Bourin, *Psychopharmacology* 138 (1998), 198-206, and in parallel increases the time of active behaviour (i.e. swimming or struggling; Lucki et al., *Psychopharmacology* 155 (2001), 315-322).

[0263] The P2X7R agonist BzATP was found to increase active escape attempts (i.e. increase in time and frequency of struggling, decrease in latency of struggling) while a decrease in passive behaviour (i.e. decrease in time and frequency of floating, increase in latency of floating) was measured when compared to control mice injected with vehicle solution (Figure 20). Observed results were verified statistically using Mann-Whitney U and one-way MANOVA tests. The differences in time struggling, latency of floating and frequency of floating were found to be statistically significant. While latency and frequency of struggling and time floating results were not supported statistically, they still represented a tendency towards improvement in stress coping behaviour. These results demonstrate that a P2X7R agonist can lead to improvements in depressive-like symptoms.

[0264] Since conclusions drawn from the forced swim test can be influenced by unspecific effects of an agent or compound on animal activity (i.e. increase in struggling behaviour can be the result of hyperactivity instead of increased active coping behaviour), the potential effect of BzATP on locomotor activity was assessed by the open field test (Crawley, "What's wrong with my mouse: Behavioral phenotyping of transgenic and knockout mice", Wiley-Liss (2000)). Locomotor activity in mice treated with control vehicle solution or 50 μ M BzATP was assessed 24 hours after injection by placing individual animal in a dark-grey wooden box (30x30x40 cm). Locomotor activity was monitored for a period of 30 minutes using a video camera. Overall distance travelled by the animals during the testing period was then analysed by means of VideoMot2 computer software (TSE GmbH, Bad Homburg). No difference in locomotor activity was measured between mice treated with control vehicle solution and BzATP (Figure 21). Therefore, the application of BzATP did not induce hyperactivity. These results confirm that activation of P2X7R by an agonist agent or compound leads to improvements in depressive-like symptoms and is not the result of an unspecific effect on animal activity per se.

[0265] Several reports suggest that activation of P2X7R can induce apoptosis and cell death in vitro (Di Virgilio et al., *Cell Death Differ.* 5 (1998), 191-199; Virginio et al., *J. Physiol.* 519 (1999), 335-346). To test whether P2X7R activation in the hippocampus resulted in cell death, apoptosis levels were quantified in the brain of the mice treated with BzATP. Mice were sacrificed at the end of the behavioural experiments, the brains were removed, shock frozen and sectioned into 16 μ m slices. Brain sections were then studied for apoptosis using the DeadEnd fluorometric TUNEL system according to the manufacturer's recommendation (Promega Corporation). The TUNEL system measures the fragmented DNA of apoptotic cells. Positive control for the assay are made by pre-treating brain sections for 10 minutes with 1 unit/ml of DNase I.

[0266] Very few apoptotic cells (i.e. less than one cell per brain section) were observed in brains of mice treated with control vehicle or the P2X7R agonist (Figure 22) when compared to positive control sections pre-treated with DNase.

Moreover, no significant differences in the numbers of apoptotic cells was observed between the control animals and mice treated with BzATP, indicating that activation of P2X7R did not result in cerebral cell death in vivo.

Example 10

P2X7R antagonists have no antidepressive effects

[0267] The P2X7R antagonists KN-62 (1-(N,O-bis[5-isoquinolinesulphonyl]-N-methyl-L-tyrosyl)-4-phenylpiperazine) and oxidized ATP (oATP) were administered to DBA/2O1a mice (Harlan Winkelmann, Germany) that exhibit the behavioural characteristic of being highly anxious. KN-62 has been shown to be a non competitive antagonist of P2X7R (Chessel et al., Brit. J. Pharmacol., 124 (1998), 1314-1320) while oATP acts as an irreversible inhibitor of P2X7R (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203).

[0268] In the present example, the P2X7R antagonists were directly injected into the dentate gyrus region of the hippocampus. Briefly, three months old male mice were bilaterally implanted with guide cannulae (23 gauge, length 8 mm) by means of a stereotactic instrument (David Kopf Instruments). The coordinates, in relation to bregma, were -1.5 mm posterior, ± 1.0 mm lateral, and -0.8 mm ventral. Mice were allowed to recover for 10 to 13 days after surgery. Following this recovery period, mice were injected with 1 μ l vehicle solution (0,01% DMSO, Sigma), or 100nM KN-62 (Sigma, prepared in 0,01% DMSO), or 10 μ M oATP (Sigma, prepared in PBS) in each side of the brain over a period of 60 seconds. All injections were performed using a 9 mm-31 gauge needle inserted into the guide cannulae and connected via tubing to a 10 μ l Hamilton syringe.

[0269] The behaviour of individual mice was assessed using the Porsolt's forced swim test 24 hours after injection of vehicle solution, KN-62, or oATP. A pre-exposure of 5 minutes to the test was performed 15-17 minutes after administration of vehicle, KN-62, or oATP. A description of the Porsolt's forced swim test is given in example 9. In the present example, no changes in active escape attempts (i.e. time, frequency, latency of struggling) or in passive behaviour (i.e. time, frequency, latency of floating) was measured between vehicle, KN-62 or oATP treated mice (figure 23). Observed results were verified statistically using one-way MANOVA test. The differences seen in the different parameters between vehicle, KN-62 or oATP treated mice were not supported statistically. These results demonstrate that P2X7R antagonists do not improve depressive-like symptoms and have no antidepressive action.

[0270] Since conclusions drawn from the forced swim test can be influenced by unspecific effects of an agent or compound on animal activity (i.e. increase in struggling behaviour can be the result of hyperactivity instead of increased active coping behaviour), the potential effect of the P2X7R antagonist oATP on locomotor activity was assessed by performing the open field test. Locomotor activity in mice treated with control vehicle solution, 10 μ M oATP, or 50 μ M oATP was assessed 15 minutes after injection by placing individual animal in a dark-grey wooden box (30x30x40 cm). Locomotor activity was monitored for a period of 30 minutes using a video camera. Overall distance travelled by the animals during the testing period was then analysed by means of VideoMot2 computer software (TSE GmbH, Bad Homburg). No difference in locomotor activity was measured between mice treated with control vehicle solution and oATP (Figure 24). Therefore, the application of a P2X7R antagonist did not induce hypo- or hyperactivity in the animals.

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Glu Gly Asn Gln Lys Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu
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Ala Val Glu Glu Ala Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn
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Phe Thr Val Leu Ile Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr
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Thr Thr Arg Asn Ile Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His
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	Gln	Leu	Val	Val	Tyr	Ile	Gly	Ser	Thr	Leu	Ser	Tyr	Phe	Gly	Leu	Ala	
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	Ala	Val	Phe	Ile	Asp	Phe	Leu	Ile	Asp	Thr	Tyr	Ser	Ser	Asn	Cys	Cys	
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	Arg	Ser	His	Ile	Tyr	Pro	Trp	Cys	Lys	Cys	Cys	Gln	Pro	Cys	Val	Val	
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	Pro	Thr	Leu	Lys	Tyr	Val	Ser	Phe	Val	Asp	Glu	Ser	His	Ile	Arg	Met	
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	Leu	Ala	Leu	His	Asp	Thr	Pro	Pro	Ile	Pro	Gly	Gln	Pro	Glu	Glu	Ile	
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	Gln	Leu	Leu	Arg	Lys	Glu	Ala	Thr	Pro	Arg	Ser	Arg	Asp	Ser	Pro	Val	
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	Trp	Cys	Gln	Cys	Gly	Ser	Cys	Leu	Pro	Ser	Gln	Leu	Pro	Glu	Ser	His	
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	Gln	Phe	Leu	Leu	Leu	Tyr	Gln	Glu	Pro	Leu	Leu	Ala	Leu	Asp	Val	Asp	
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	Ser	Thr	Asn	Ser	Arg	Leu	Arg	His	Cys	Ala	Tyr	Arg	Cys	Tyr	Ala	Thr	
		540				545				550						555	
	tgg	cgc	ttc	ggc	tcc	cag	gac	atg	gct	gac	ttt	gcc	atc	ctg	ccc	agc	1791
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5 tac agt ggc ttc aag agt cct tac tgaagccagg caccgtggct cacgtctgta 1893
Tyr Ser Gly Phe Lys Ser Pro Tyr 595

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30 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
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Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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45 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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50 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
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Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
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 5 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
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 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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 10 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys
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 275 280 285
 15 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
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 20 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
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 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
 325 330 335
 25 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
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 30 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
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 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
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Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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5 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
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Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
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30 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
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Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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35 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
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40 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
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Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
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45 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
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50 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
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Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
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5 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
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Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
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10 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
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Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
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15 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
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20 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
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Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
485 490 495

25 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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30 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
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Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
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35 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
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Ser Pro Tyr
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	Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile 195 200 205		
30	Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro 210 215 220		
35	Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp 225 230 235 240		
	Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile 245 250 255		
40	Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys 260 265 270		
	Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr 275 280 285		
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	Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu 305 310 315 320		
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	Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp 435 440 445		
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	Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly 465 470 475 480		
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	Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg 530 535 540		
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 10 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
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 35 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
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 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
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 40 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
 225 230 235 240
 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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 45 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
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 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 55 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
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Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
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5 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
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10 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
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15 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
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Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
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20 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
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Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
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25 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

30 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
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Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
485 490 495

35 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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40 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
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Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
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Ser Pro Tyr
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Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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15 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
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25 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
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35 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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Pro Arg Pro Ala Leu Leu Asn Ser Ala Lys Asn Phe Thr Val Leu Ile
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40 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
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Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
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Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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50 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
260 265 270

55 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

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5	Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu	305	310	315
	Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr		325	330
10	Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp		340	345
	Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr		355	360
15	Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr		370	375
	Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr		385	390
20	Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu		405	410
	Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro		420	425
25	Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp		435	440
	Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys		450	455
30	Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly		465	470
	Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu		485	490
35	Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu		500	505
	Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu		515	520
40	Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg		530	535
	Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser		545	550
45	Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg		565	570
	Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys		580	585
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Ser Pro Tyr
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15 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

20 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

25 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

30 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

35 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

40 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Pro Ile
180 185 190

45 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

50 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

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Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
 260 265 270
 5 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
 275 280 285
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 10 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
 305 310 315 320
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
 325 330 335
 15 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
 340 345 350
 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
 355 360 365
 20 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
 370 375 380
 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
 385 390 395 400
 25 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
 405 410 415
 30 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
 420 425 430
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
 435 440 445
 35 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
 450 455 460
 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
 465 470 475 480
 40 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
 485 490 495
 45 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
 515 520 525
 50 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
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 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
 545 550 555 560
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Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
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5 Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys
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Ser Pro Tyr
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Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

25 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

30 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
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35 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

40 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

45 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

50 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

55 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp

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	225		230		235		240
5	Asn Phe Ser Asp	Val Ala Ile Gln Gly	Gly Ile Met Gly Ile Glu Ile				
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		260		265		270	
10	Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr						
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	Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val						
		290		295		300	
15	Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu						
		305		310		315	
	Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr						
		325		330		335	
20	Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp						
		340		345		350	
	Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr						
		355		360		365	
25	Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr						
		370		375		380	
	Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr						
		385		390		395	
	Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu						
		405		410		415	
35	Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro						
		420		425		430	
	Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp						
		435		440		445	
40	Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys						
		450		455		460	
	Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly						
		465		470		475	
45	Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu						
		485		490		495	
	Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu						
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50	Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu						
		515		520		525	
55	Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg						

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	Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys 50 55 60		
30	Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val 65 70 75 80		
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	Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser 130 135 140		
45	Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys 145 150 155 160		
	Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala 165 170 175		
50	Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile 180 185 190		
55	Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile 195 200 205		

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5 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
 210 215 220
 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
 225 230 235 240
 10 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
 260 265 270
 15 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
 275 280 285
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 20 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
 305 310 315 320
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
 325 330 335
 25 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
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 30 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
 355 360 365
 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
 370 375 380
 35 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
 385 390 395 400
 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
 405 410 415
 40 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
 420 425 430
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
 435 440 445
 45 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
 450 455 460
 50 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
 465 470 475 480
 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
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 55 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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5 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
515 520 525

10 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
530 535 540

15 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
545 550 555 560

Gln Asp Met Ala Asp Phe Ala Asn Leu Pro Ser Cys Cys Arg Trp Arg
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20 Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys
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Ser Pro Tyr
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35 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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40 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

45 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

50 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
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55 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

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	Pro	Arg	Pro	Ala	Leu	Leu	Asn	Ser	Ala	Glu	Asn	Phe	Thr	Val	Leu	Ile
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			195					200					205			
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10	Gln	Cys	Pro	Ile	Phe	Arg	Leu	Gly	Asp	Ile	Phe	Arg	Glu	Thr	Gly	Asp
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	Asn	Phe	Ser	Asp	Val	Ala	Ile	Gln	Gly	Gly	Ile	Met	Gly	Ile	Glu	Ile
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			275					280					285			
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		290					295					300				
25	Glu	Lys	Arg	Thr	Leu	Ile	Lys	Val	Phe	Gly	Ile	Arg	Phe	Asp	Ile	Leu
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	Val	Phe	Gly	Thr	Gly	Gly	Lys	Phe	Asp	Ile	Ile	Gln	Leu	Val	Val	Tyr
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30	Ile	Gly	Ser	Thr	Leu	Ser	Tyr	Phe	Gly	Leu	Ala	Ala	Val	Phe	Ile	Asp
				340					345					350		
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35			355					360					365			
	Pro	Trp	Cys	Lys	Cys	Cys	Gln	Pro	Cys	Val	Val	Asn	Glu	Tyr	Tyr	Tyr
		370					375					380				
40	Arg	Lys	Lys	Cys	Glu	Ser	Ile	Val	Glu	Pro	Lys	Pro	Thr	Leu	Lys	Tyr
	385					390					395					400
	Val	Ser	Phe	Val	Asp	Glu	Ser	His	Ile	Arg	Met	Val	Asn	Gln	Gln	Leu
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45	Leu	Gly	Arg	Ser	Leu	Gln	Asp	Val	Lys	Gly	Gln	Glu	Val	Pro	Arg	Pro
				420					425					430		
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			435					440					445			
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55		465				470					475					480

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Ser Cys Leu Pro Ser Gln Leu Glu Glu Leu Cys Cys Arg Lys Lys Pro
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 5 Gly Ala Cys Ile Thr Thr Ser Glu Leu Phe Arg Lys Leu Val Leu Ser
 500 505 510
 Arg His Val Leu Gln Phe Leu Leu Leu Tyr Gln Glu Pro Leu Leu Ala
 515 520 525
 10 Leu Asp Val Asp Ser Thr Asn Ser Arg Leu Arg His Cys Ala Tyr Arg
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 Cys Tyr Ala Thr Trp Arg Phe Gly Ser Gln Asp Met Ala Asp Phe Ala
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 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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 40 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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 45 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
 100 105 110
 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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 50 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
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 55 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

5 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

10 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

15 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
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Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
260 265 270

20 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

25 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
290 295 300

Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
305 310 315 320

30 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
325 330 335

Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

35 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
355 360 365

Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
370 375 380

40 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
385 390 395 400

45 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
405 410 415

Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

50 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

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	485 490 495	
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10	Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu	
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	Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg	
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	Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg	
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Claims

1. A nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

(a) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 5'UTR region corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(b) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of the ATP-gated ion channel P2X7R, wherein in the exon as indicated in column "Exon" of the following Table A the amino acid residue as indicated in column "Amino acid residue" of Table A corresponding to the position as indicated in column "Position in wild-type" of Table A of the wild-type ATP-gated ion channel P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue

Table A

Exon	Amino acid residue	Position in wild-type
exon 3	R (Arg)	117
exon 5	G (Gly)	150
exon 6	E (Glu)	186
exon 6	L (Leu)	191
exon 8	R (Arg)	270
exon 13	I (Ile)	568
exon 13	R (Arg)	578

(c) a nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in exon 5 or 8 corresponding to position 32548 or position 37633 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide

(d) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted;

(e) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R, wherein in the intron as indicated in column "Intron" of the following Table B the nucleotide as indicated in column "Replaced nucleotide" of Table B corresponding to the position as indicated in column "Position in wild-type" of Table B of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1 is replaced by another nucleotide

Table B

Intron	Replaced nucleotide	Position in wild-type
intron 1	G	3166
intron 1	C	24778
intron 1	C	24830
intron 3	A	26308
intron 3	G	26422
intron 4	G	32394
intron 4	T	32434
intron 5	A	32783
intron 6	G	35641
intron 6	A	35725
intron 6	T	36001
intron 7	G	36378
intron 7	T	36387
intron 7	G	36398
intron 9	C	47214
intron 11	T	47563
intron 12	C	54307
intron 12	G	54308

(f) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 3'UTR region corresponding to position 54925, 55169, 55170, 55171 or 55917 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(g) a nucleotide sequence comprising at least 20 or 21 nucleotides and comprising the mutations or deletions as defined in any one of (a) to (f);

(h) a nucleic acid sequence comprising a nucleotide sequence as shown in any one of SEQ ID NOs: 13 to 51;

(i) a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NOs: 5 to 12;

(j) a nucleotide sequence which hybridizes to a nucleotide sequence defined in any one of (a) to (g) or to the nucleotide sequence of (h) and having a mutation as defined in any one of (a) to (f); and

(k) a nucleic acid sequence being degenerate as a result of the genetic code to the nucleic acid sequence as defined in (j).

2. The nucleic acid molecule of claim 1 derived from mouse, rat or human.
3. The nucleic acid molecule of claim 1 or 2 which is DNA, RNA, PNA or phosphorothioates.
4. A vector comprising the nucleic acid molecule of any one of claims 1 to 3.
5. The vector of claim 4 which is an expression vector, a gene targeting vector and/or a gene transfer vector.
6. A host transformed with a vector of claim 4 or 5 or transformed with the nucleic acid molecule of any one of claims 1 to 3.
7. The host of claim 6 which is a mammalian cell, an amphibian cell, a fish, an insect cell, a fungal cell, a plant cell

or a bacterial cell.

8. The host of claim 7, wherein said mammalian cell is selected from the group consisting of CHO cells, HEK293 cells, COS-7 cells or PC12 cells.

9. The host of claim 7, wherein said amphibian cell is an oocyte, preferably a *Xenopus* oocyte.

10. The host of claim 9, wherein said oocyte is a frog oocyte.

11. The host of claim 6 which is a non-human transgenic organism.

12. The host of claim 11, wherein said non-human organism is a mammal, amphibian, a fish, an insect, a fungus or a plant.

13. A method for producing the polypeptide encoded by a nucleic acid molecule of claims 1(b) or 1(d) comprising culturing/raising the host of any one of claims 6 to 11 and isolating the produced polypeptide.

14. A polypeptide encoded by the nucleic acid molecule of claim 1(b) or 1(d) or produced by the method of claim 13.

15. An antibody specifically directed to the polypeptide of claim 14, wherein said antibody specifically reacts with an epitope generated and/or formed by the mutation in the ATP-gated ion channel P2X7R selected from the group consisting of:

(i) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein the R (Arg), G (Gly), E (Glu), L (Leu), R (Arg), I (Ile) or R (Arg) residue corresponding to position 117, 150, 186, 191, 270, 568 or 578 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue; and

(ii) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted.

16. The antibody of claim 15 which is a monoclonal antibody.

17. An aptamer specifically binding to a nucleic acid molecule of any one of claims 1 to 3 or to the polypeptide of claim 14.

18. A primer or pair of primers capable of specifically amplifying a nucleic acid molecule as defined in any one of claims 1 to 3.

19. The primer or pair of primers of claim 18, which is selected from the group consisting of SEQ ID NOs.: 52 to 111.

20. A composition comprising the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16, the aptamer of claim 17 and/or the primer or pair of primers of claim 18 or 19.

21. The composition of claim 20 which is a diagnostic composition.

22. The diagnostic composition of claim 21, optionally further comprising suitable means for detection.

23. Use of the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16, the aptamer of claim 17 and/or the primer or pair of primers of claim 18 or 19 for the preparation of a diagnostic composition for the detection of an affective disorder.

24. A method of diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2XR7 protein expressed in the cells of said individual is non-functional, shows an altered ATP-gating in comparison to the wild-type P2XR7 protein or is over- or under-expressed in comparison to the P2XR7 protein level in an unaffected individual.

25. A method for diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R gene sequence or encoded protein thereof comprises a mutation in comparison to the wild-type P2X7R sequence.

26. The method of claim 25, wherein said mutation is a mutation as defined in claim 1 and/or a nucleotide replacement or deletion selected from the following Table C indicating in column "Region of P2X7R" the region of the P2X7R genomic nucleotide sequence in which the replacement or deletion occurs, in column "Nucleotide" of Table C the nucleotide which is replaced by another nucleotide or the nucleotides which are deleted and in column "Position in wild-type" of Table C the corresponding position in the nucleotide sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1

Table C

Region of P2X7R	Nucleotide	Position in wild-type
5'UTR	T	362
5'UTR	T	532
5'UTR	A	1100
5'UTR	A	1122
5'UTR	C	1171
5'UTR	T	1351
5'UTR	G	1702
5'UTR	T	1731
5'UTR	C	1860
5'UTR	C	2162
5'UTR	C	2238
5'UTR	A	2373
5'UTR	G	2569
5'UTR	G	2702
intron 1	G	3166
intron 1	C	24778
intron 1	C	24830
exon 2	T	24942
exon 3	C	26188
exon 3	A	26308
exon 3	G	26422
intron 4	G	32394
intron 4	T	32434
exon 5	G	32493
exon 5	G	32506
exon 5	C	32507
exon 5	C	32548
intron 5	A	32783
intron 5	T	35309
intron 5	C	35374

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Table C (continued)

	Region of P2X7R	Nucleotide	Position in wild-type
5	intron 5	A	35378
	exon 6	G	35438
	exon 6	T	35454
10	intron 6	T	35549
	intron 6	G	35641
	intron 6	A	35725
	intron 6	T	36001
15	intron 6	A	36064
	intron 6	deletion of GTTT	36091 to 36094
	intron 6	C	36108
20	intron 7	C	36374
	intron 7	G	36378
	intron 7	T	36387
	intron 7	G	36398
25	intron 7	C	37439
	intron 7	T	37513
	exon 8	C	37604
30	exon 8	G	37605
	exon 8	G	37623
	exon 8	C	37633
	intron 9	C	47214
35	exon 11	G	47383
	exon 11	C	47411
	intron 11	T	47563
40	intron 12	C	54307
	intron 12	G	54308
	exon 13	C	54399
	exon 13	A	54480
45	exon 13	C	54523
	exon 13	deletion of CCCTGAGAGCCACAGGTGCCT	54562 to 54582
	exon 13	A	54588
50	exon 13	C	54664
	exon 13	G	54703
	exon 13	A	54804
	exon 13	G	54834
55	exon 13	G	54847
	3'UTR	G	54925

Table C (continued)

Region of P2X7R	Nucleotide	Position in wild-type
3'UTR	C	55169
3'UTR	A	55170
3'UTR	A	55171
3'UTR	C	55917

27. The method of claim 26, wherein the occurrence of the mutation in the ATP-gated ion channel P2X7R gene is determined by PCR or immunological methods.

28. The composition of claim 20 which is a pharmaceutical composition.

29. The pharmaceutical composition of claim 28, optionally further comprising a pharmaceutically acceptable carrier.

30. A method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule as defined in any one of claims 1 to 3 or a therapeutically effective amount of the polypeptide of claim 14 to a subject suffering from said disorder.

31. Use of the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16 and/or the aptamer of claim 17 for the preparation of a pharmaceutical composition for the treatment of an affective disorder.

32. A pharmaceutical composition comprising a nucleic acid molecule comprising a nucleotide sequence which encodes a functional ATP-gated ion channel P2X7R and which is selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence as depicted in SEQ ID NO: 3 or 4;
- (b) a nucleotide sequence comprising the nucleotide sequence as depicted in SEQ ID NO: 1 or 2;
- (c) a nucleotide sequence which hybridizes to the nucleotide sequence of

- (a) or (b); and
- (d) a nucleotide sequence which is degenerated as a result of the genetic code to the nucleotide sequence of (c).

33. A pharmaceutical composition comprising a compound the administration of which to cells leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells or comprising a nucleic acid molecule the expression of which in cells or the administration of which to cells leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells.

34. A method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule as defined in claim 32 or 33 or a therapeutically effective amount of the polypeptide encoded thereof to a subject suffering from said disorder.

35. Use of the nucleic acid molecule as defined in claim 32 or 33 for the preparation of a pharmaceutical composition for treating an affective disorder.

36. Use of a modulator of P2X7R activity for the preparation of a pharmaceutical composition for treating an affective disorder.

37. The use of claim 36, wherein said modulator is an agonist.

38. The use of claim 37, wherein said agonist is selected from the group consisting of ATP, ATP-4 and BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)).

39. Use of tenidap ($C_{15}H_{11}ClN_2O_2S$) or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides for the preparation of a pharmaceutical composition for treating an affective disorder.
- 5 40. The use of any one of claims 35 to 39 or the method of claim 34, wherein said pharmaceutical composition optionally further comprises a β -adrenergic receptor modulator.
41. The use or the method of claim 40, wherein said β -adrenergic receptor modulator is a β -adrenergic receptor antagonist selected from the group consisting of DL-propanolol, D-propanolol and labetalol.
- 10 42. The use of any one of claims 23, 30 or 35 to 41 or the method of any one of claims 24 to 27 or 34, wherein said affective disorder is selected from the group consisting of major depression, generalized anxiety disorder and bipolar disorder.
43. The use or the method of claim 42, wherein said major depression is selected from the group consisting of major depression, dysthymia, atypical depression, premenstrual dysphoric disorder and seasonal affective disorder.
- 15 44. The use or the method of claim 42, wherein said generalized anxiety disorder is selected from the group consisting of panic disorder, phobias, agoraphobia, social phobia, specific phobia, obsessive-compulsive disorder, post-traumatic stress disorder, separation anxiety disorder, mania, hypomania and cyclothymic disorder.
- 20 45. The use or the method of claim 42, wherein said bipolar disorder is bipolar disorder type I or bipolar disorder type II.
46. A kit comprising the nucleic acid molecule of any one of claims 1 to 3, a vector of claim 4 or 5, a host of any one of claims 6 to 11, a polypeptide of claim 14, an antibody of claim 15 or 16, an aptamer of claim 17 and/or a primer or pair of primers of claim 18 or 19.
- 25 47. A method for identifying compounds which are capable of specifically interacting with the polypeptide of claim 14, comprising the steps of
 - 30 (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture of compounds to be tested; and
 - (b) determining whether said compound or a candidate mixture of compounds is capable of specifically interacting with said polypeptide.
48. A method for the characterization of compounds which are capable of altering characteristics of the polypeptide of claim 14, comprising the steps of
 - 35 (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture; and
 - (b) determining whether the compound or a candidate mixture alters a characteristic of the polypeptide of claim 14.
- 40 49. A method of screening for compounds which are capable of interacting with the polypeptide of claim 14, comprising the steps of
 - 45 (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture of compounds;
 - (b) measuring and/or detecting a response; and
 - (c) comparing said response to a standard response as measured in the absence of said candidate molecule.
- 50 50. A method for the production of a pharmaceutical composition comprising the steps of the method of any one of claims 47 to 49 and comprising a further step, wherein a derivative of said identified, characterized and/or screened molecule is generated.
51. A method for the production of a pharmaceutical composition comprising the steps of the method of any one of claims 47 to 50 and formulating the molecules identified, characterized, screened and/or derivatized in pharmaceutically acceptable form.
- 55 52. The method of claim 51, wherein the pharmaceutical composition to be produced further comprises neuroprotective substances, nootropic substances, brilliant blue, piperidine or piperazine derivatives thereof, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate,

3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate or β -adrenergic receptor modulators.

53. The method of any one of claims 47 to 52, wherein said compound(s) or candidate mixture(s) of compounds
comprise(s) antagonist(s), partial antagonist(s), partial agonist(s) and/or agonist(s) for an altered ATP-gated ion
channel P2X7R.

54. A method for diagnosing an affective disorder of an individual comprising:

- (a) isolating DNA from cells obtained from an individual;
- (b) determining all or part of the nucleotide composition of the P2X7R gene; and
- (c) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism(s) mutation
or allelic variation.

55. A method for diagnosing an affective disorder of an individual comprising:

- (a) isolating RNA from cells obtained from an individual;
- (b) converting said RNA into cDNA;
- (c) determining all or part of the nucleotide composition of the P2X7R gene; and
- (d) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism(s), mutation
or allelic variation.

56. A method for diagnosing an affective disorder of an individual comprising:

- (a) isolating RNA or protein from cells obtained from an individual ;
- (b) determining the levels of P2X7R RNA or protein; and
- (c) comparing the levels of P2X7R RNA or protein with the corresponding levels from a normal individual not
afflicted with an affective disorder.

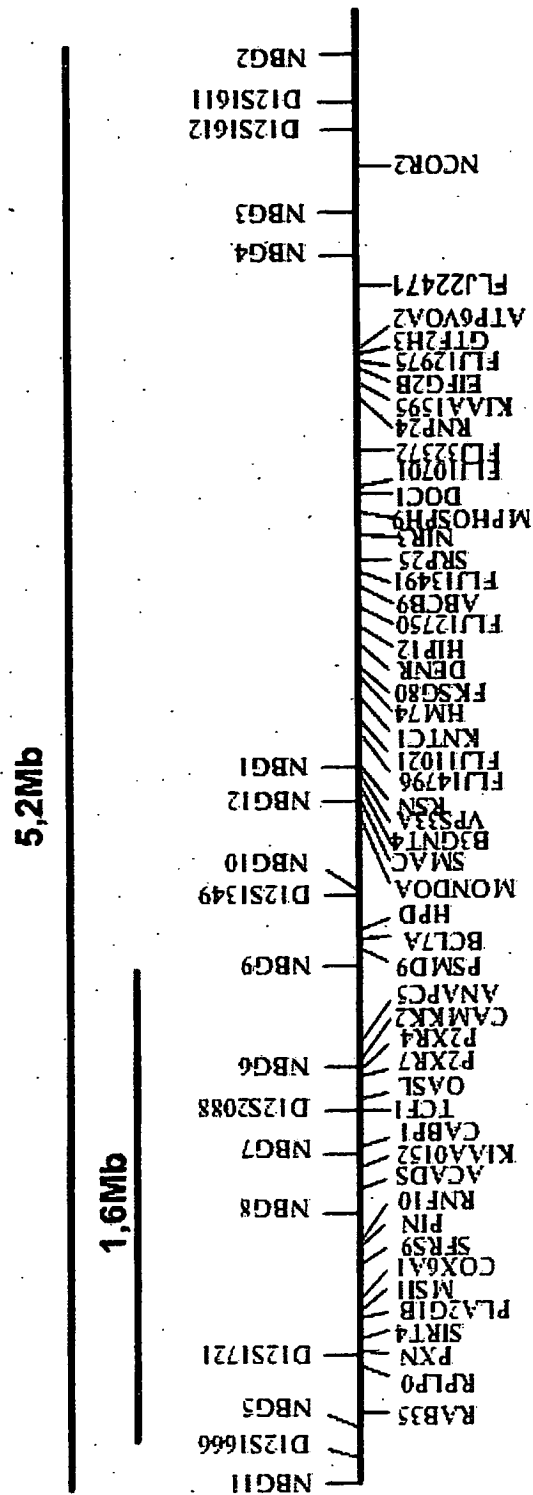


Figure 1a

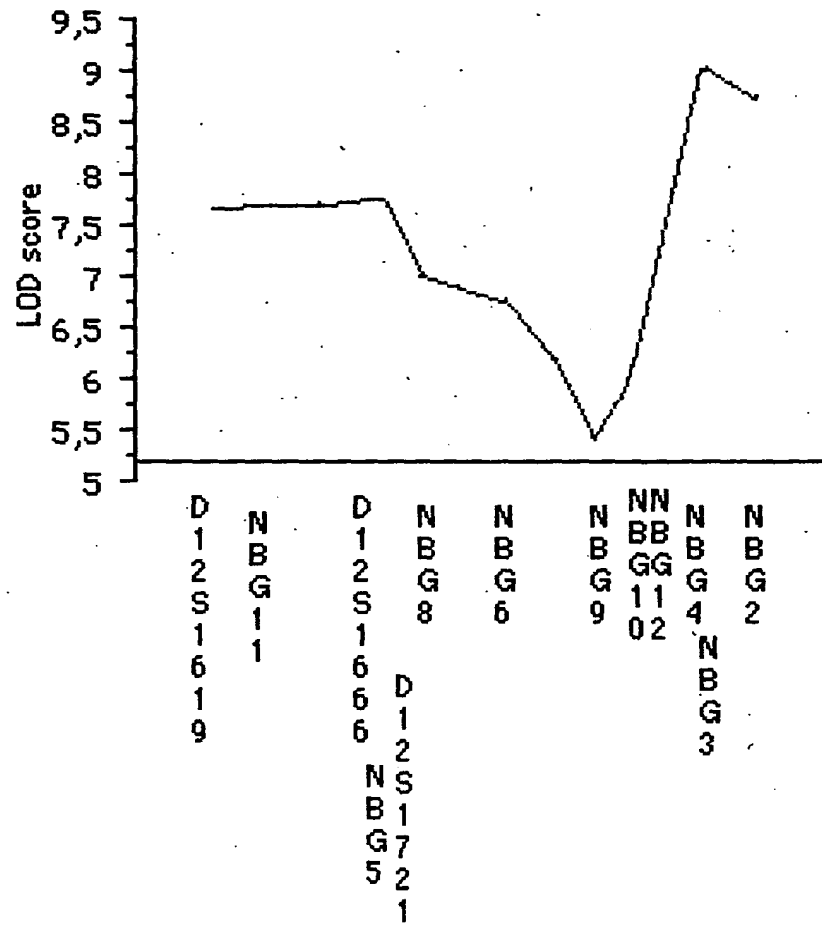


Figure 1b

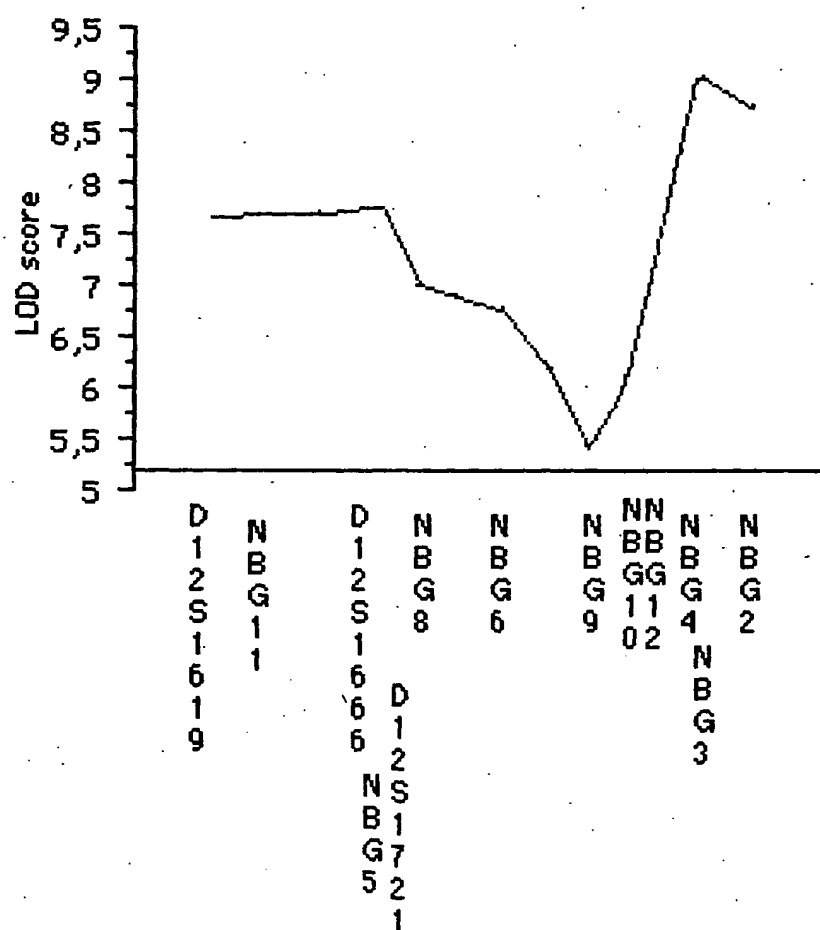


Figure 1c

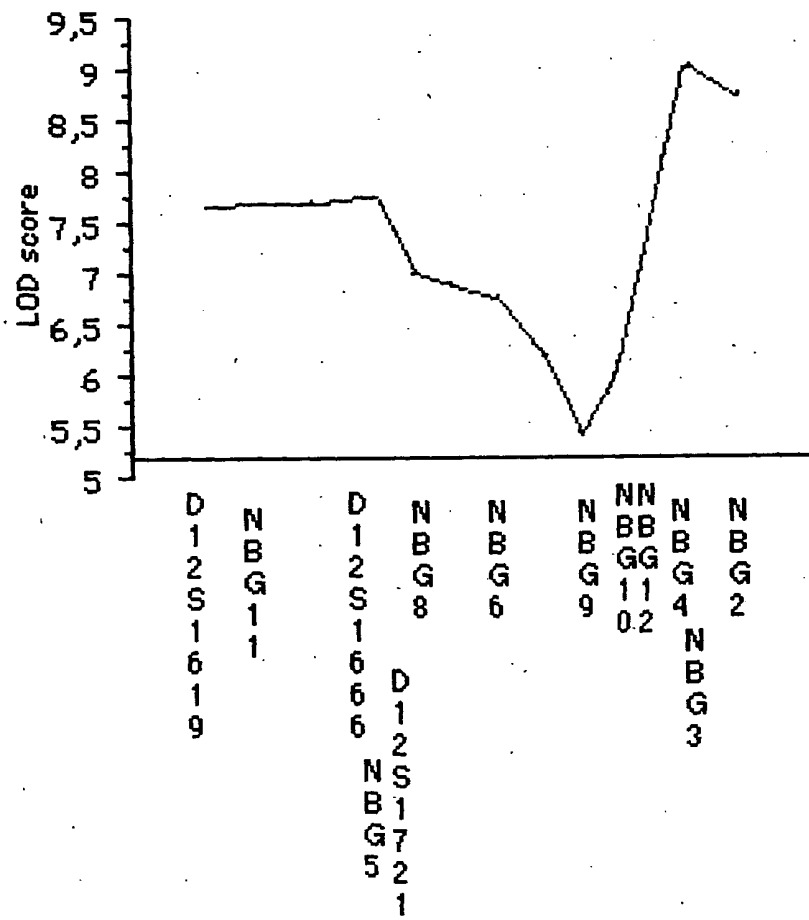


Figure 1d

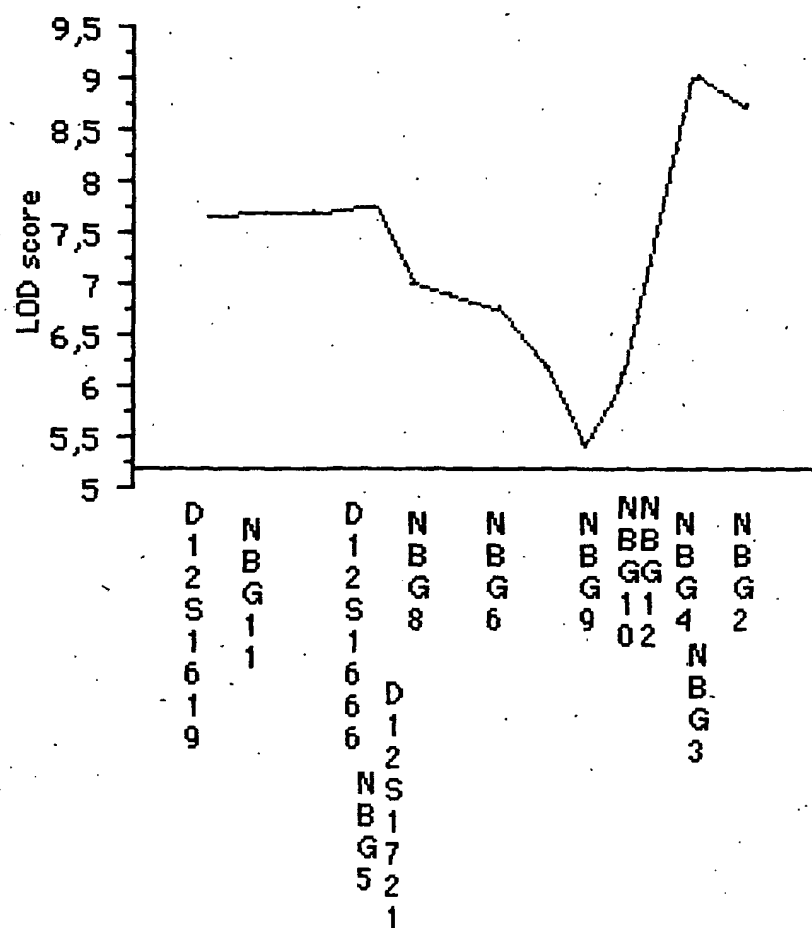


Figure 1e

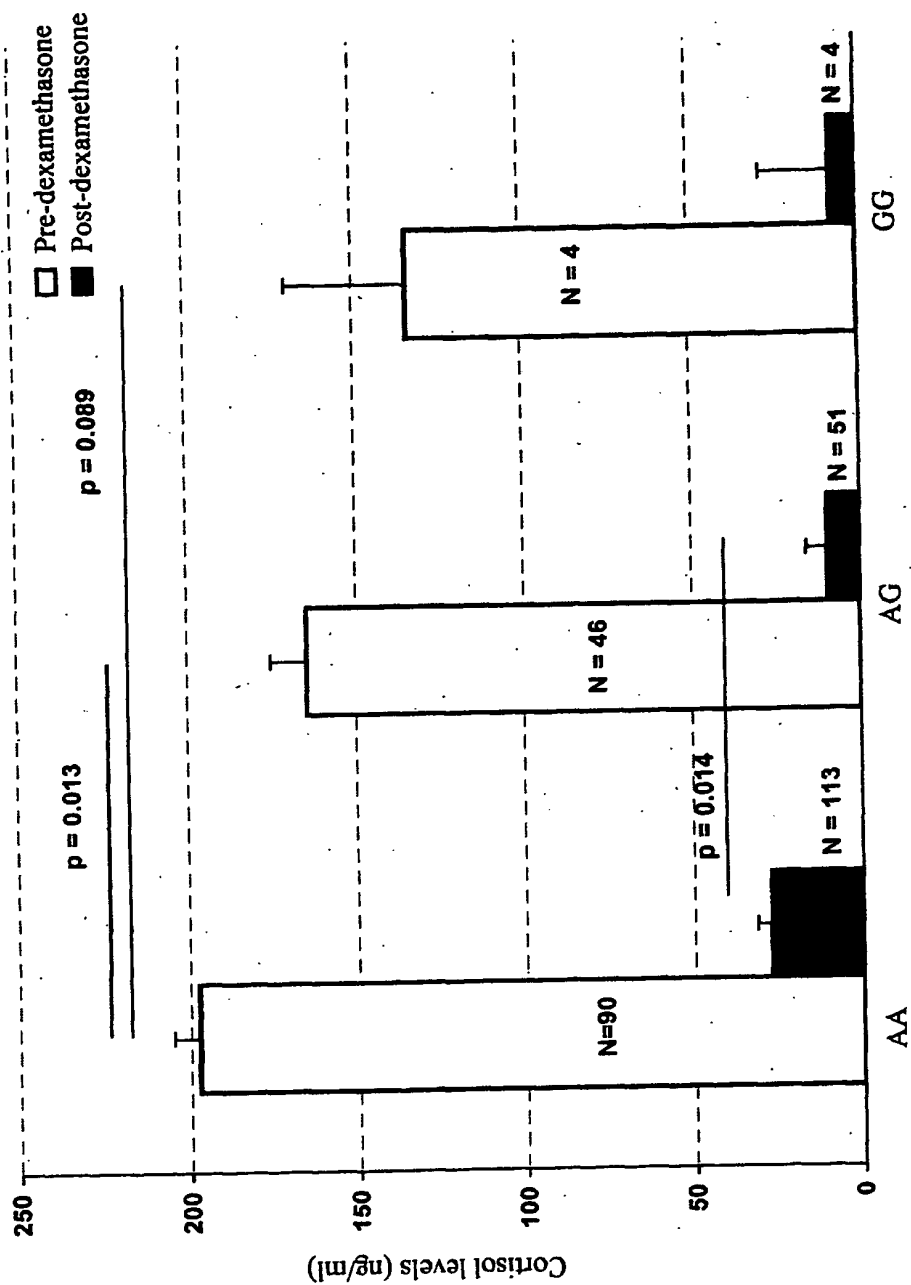


Figure 1f

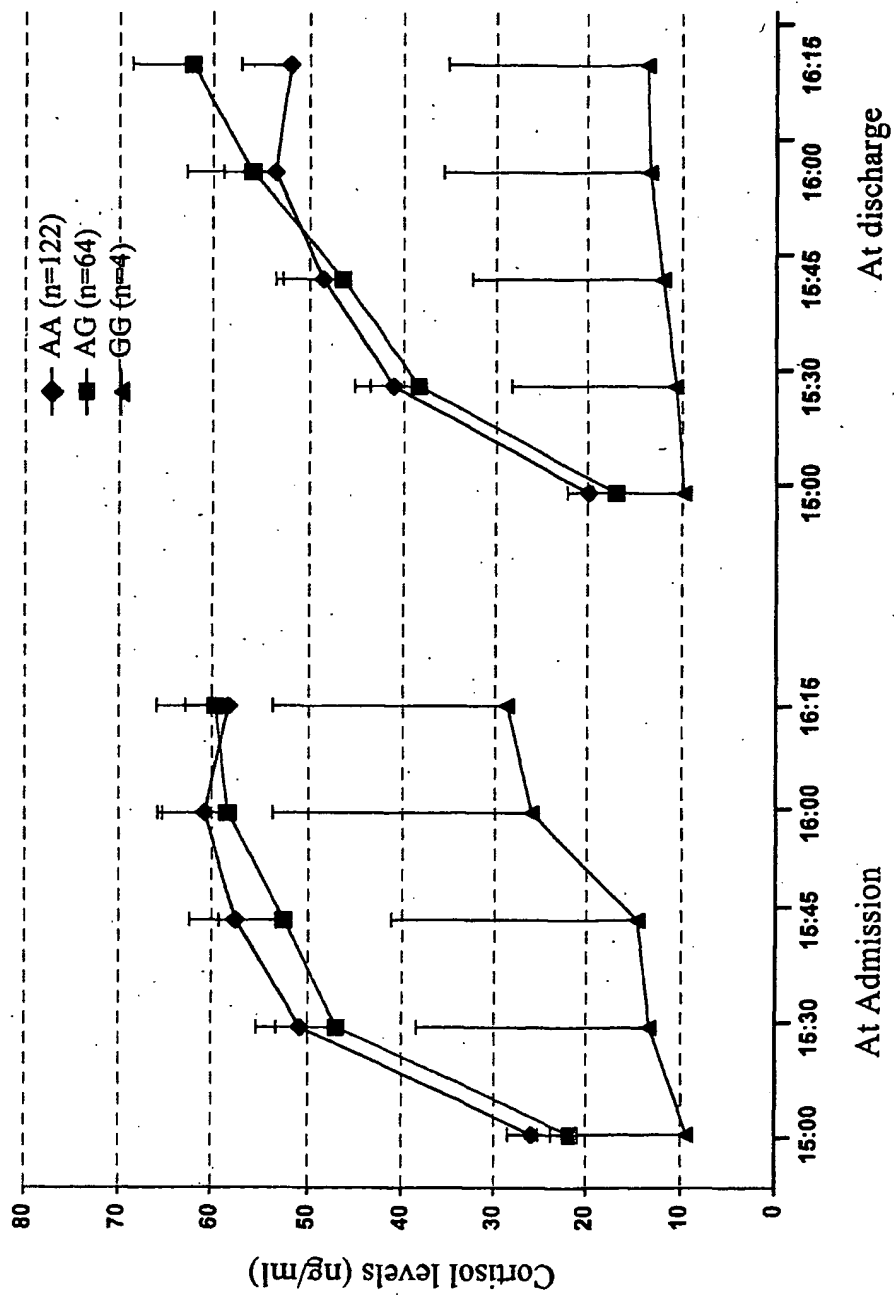


Figure 1g

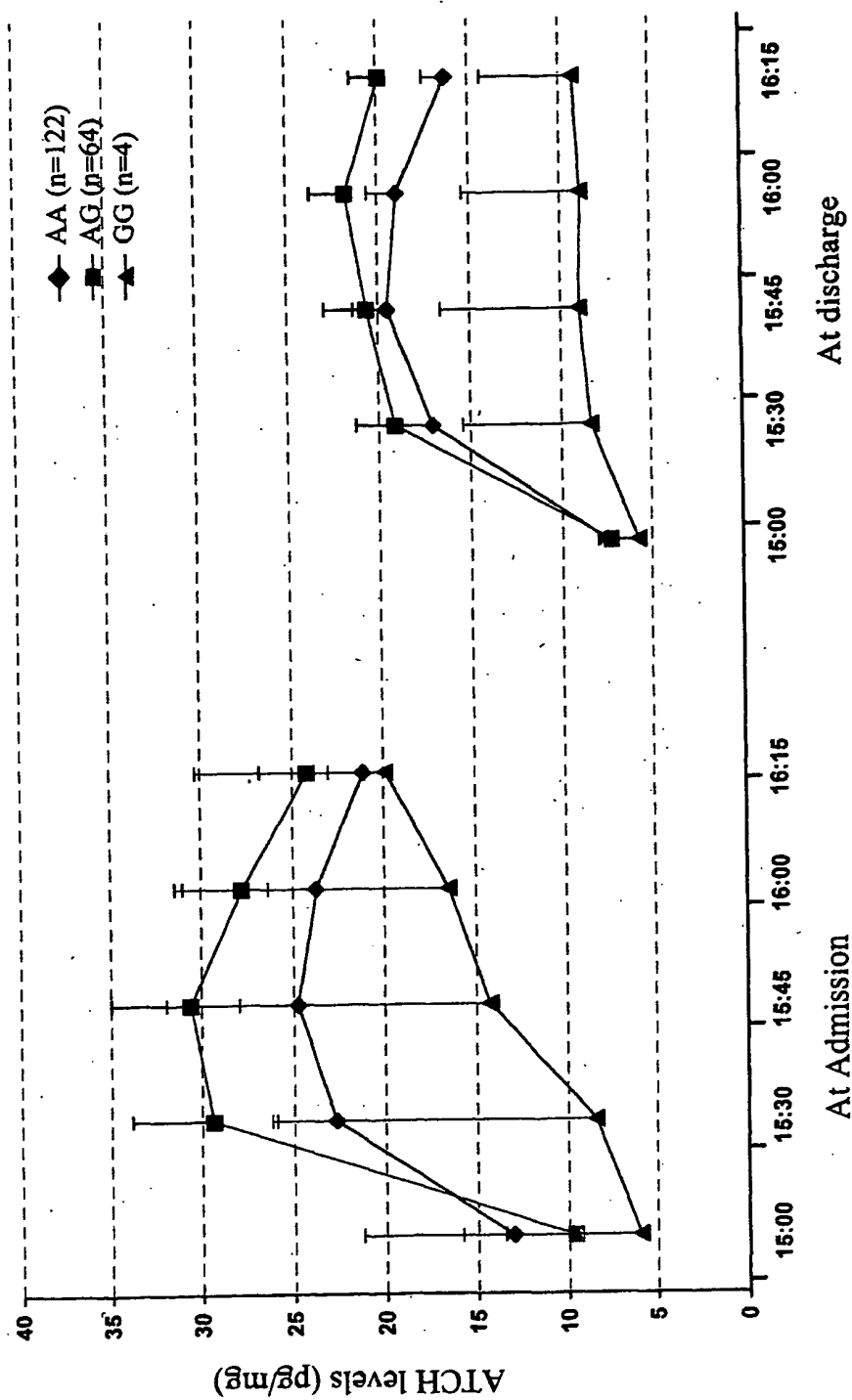


Figure 1h

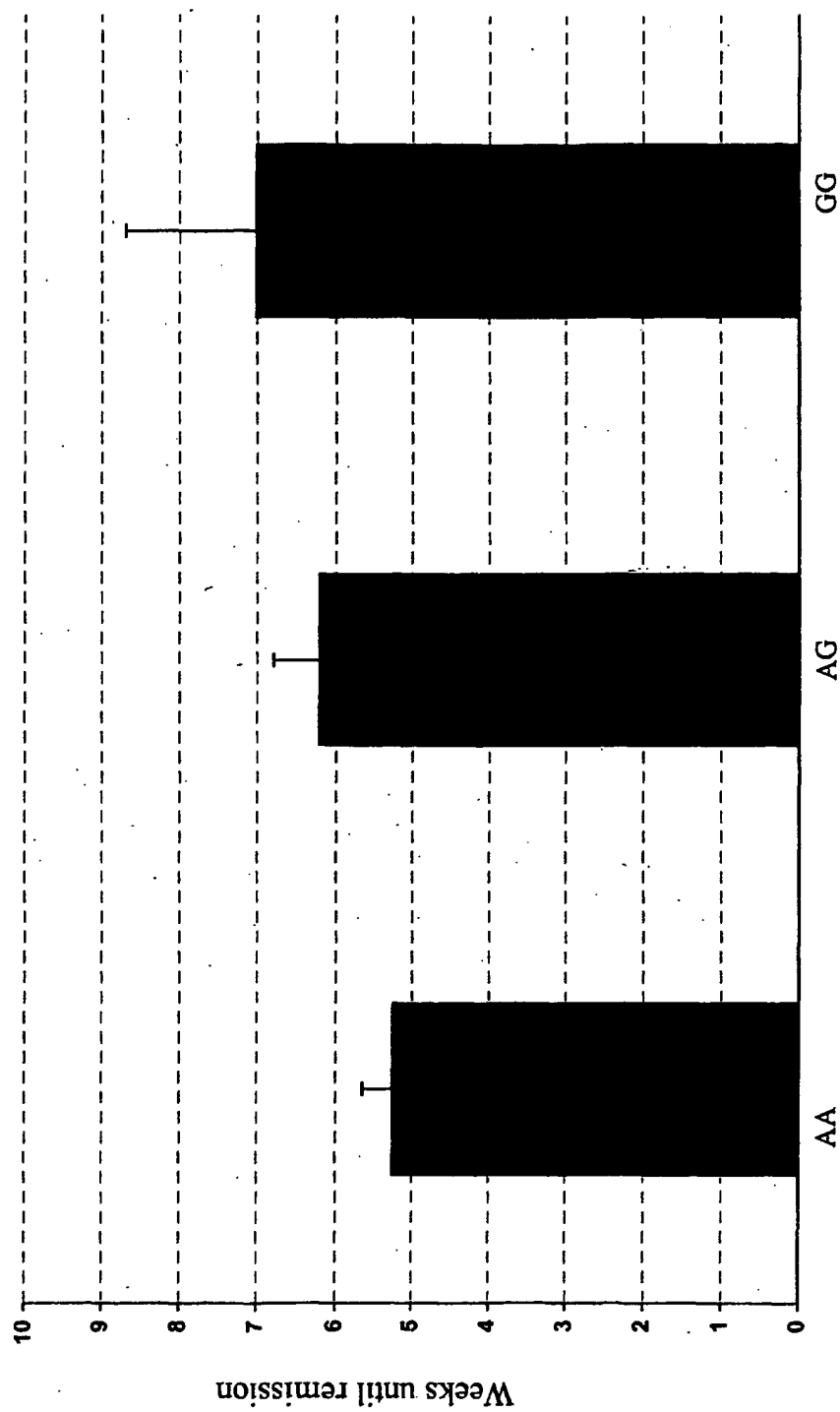


Figure 1i

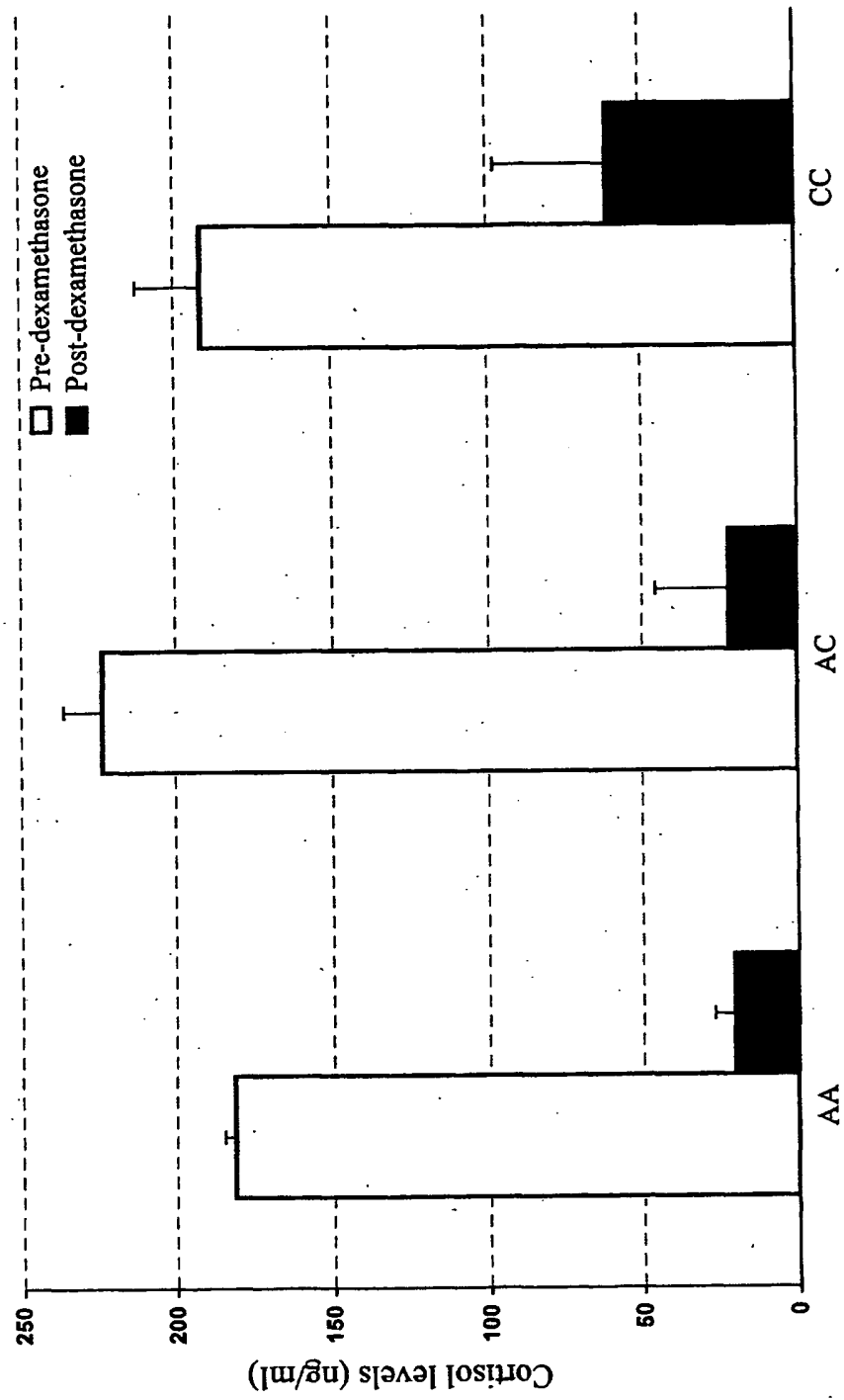


Figure 1j

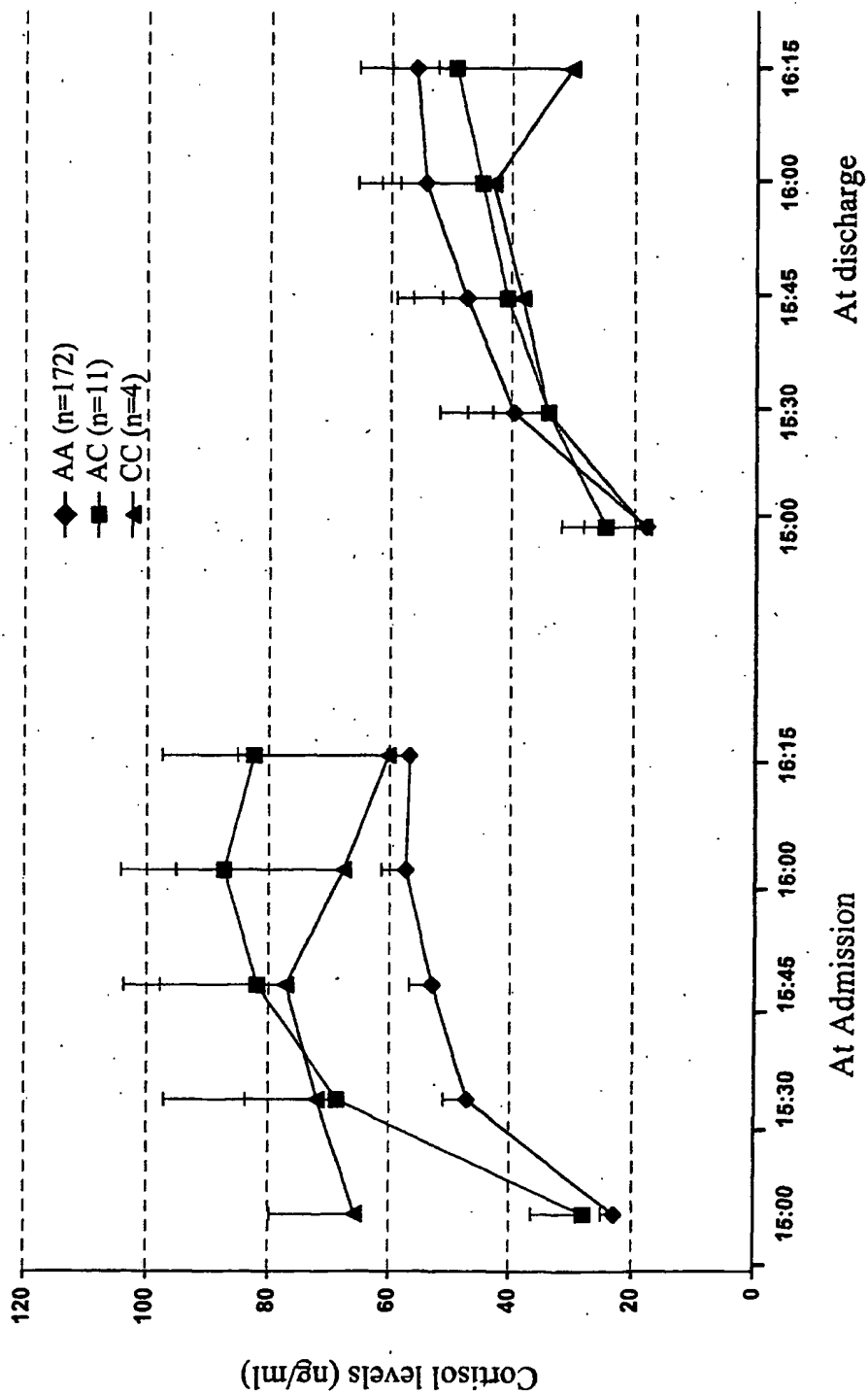


Figure 1k

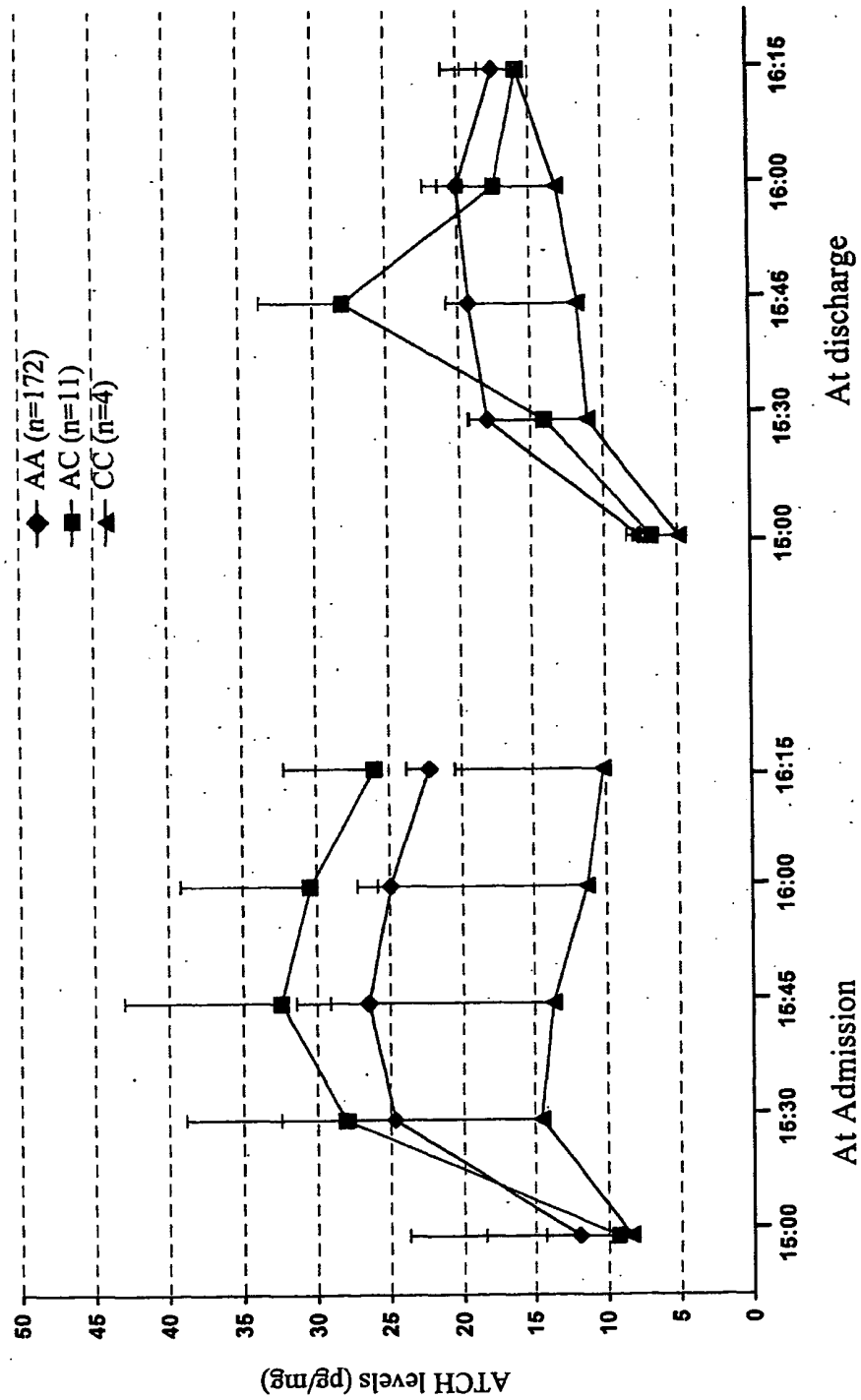


Figure 11

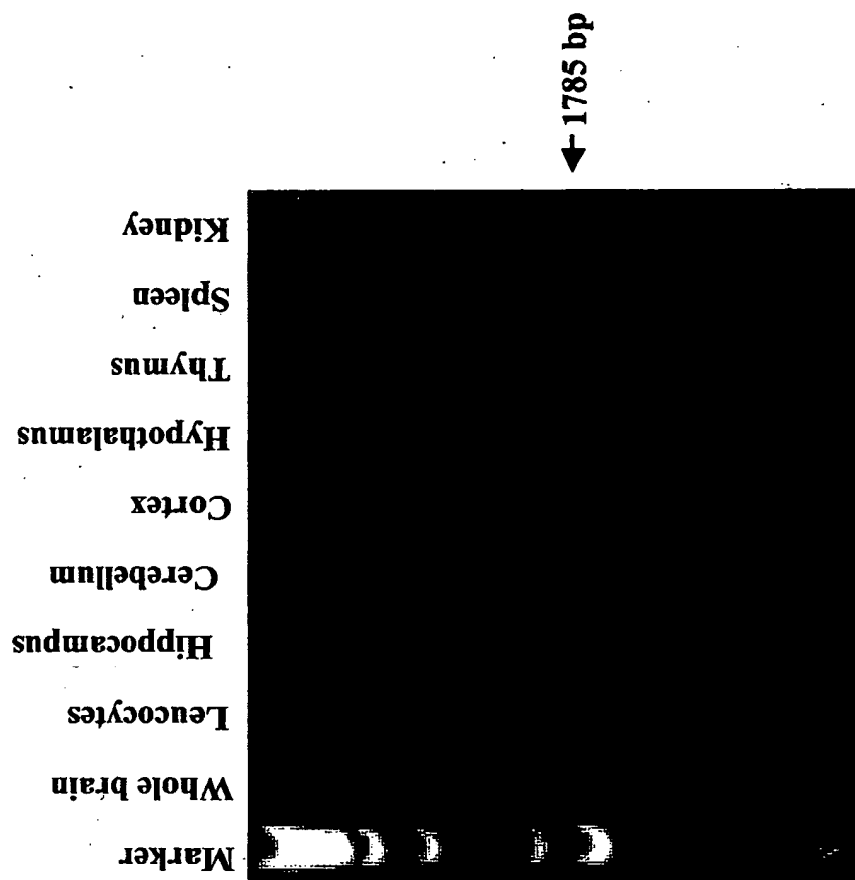


Figure 2

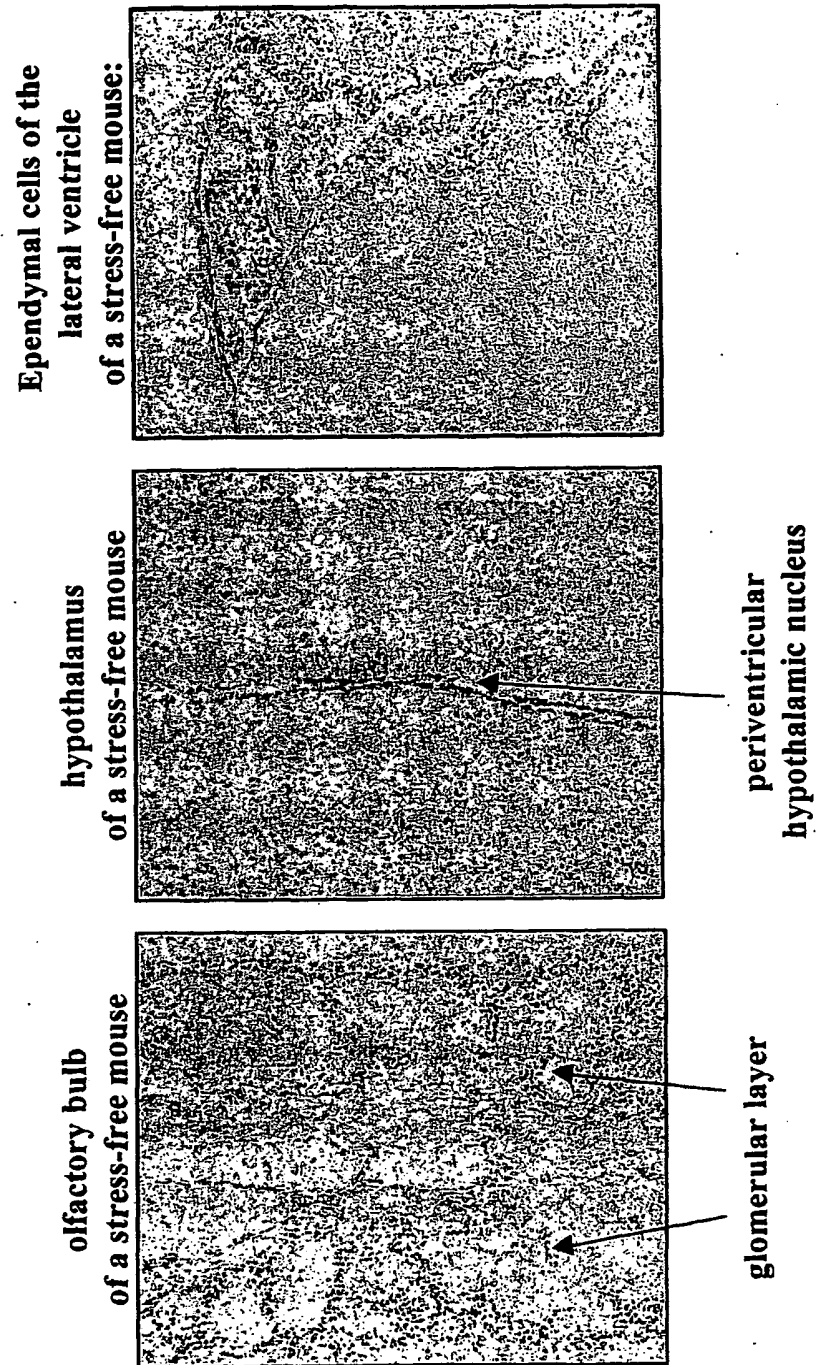


Figure 3

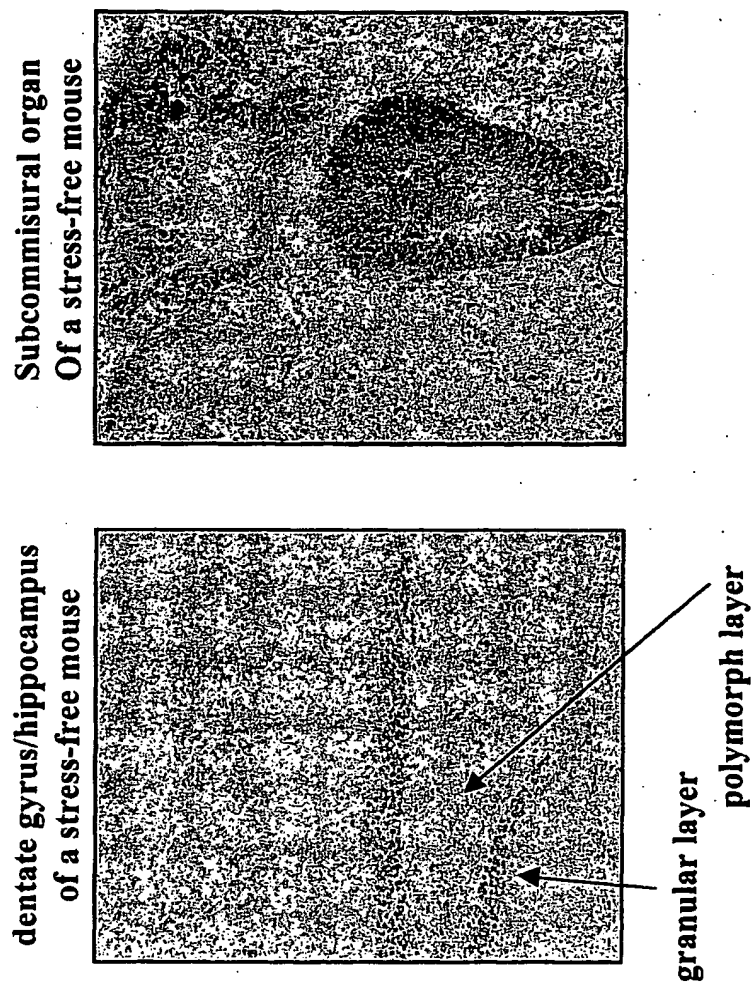


Figure 4

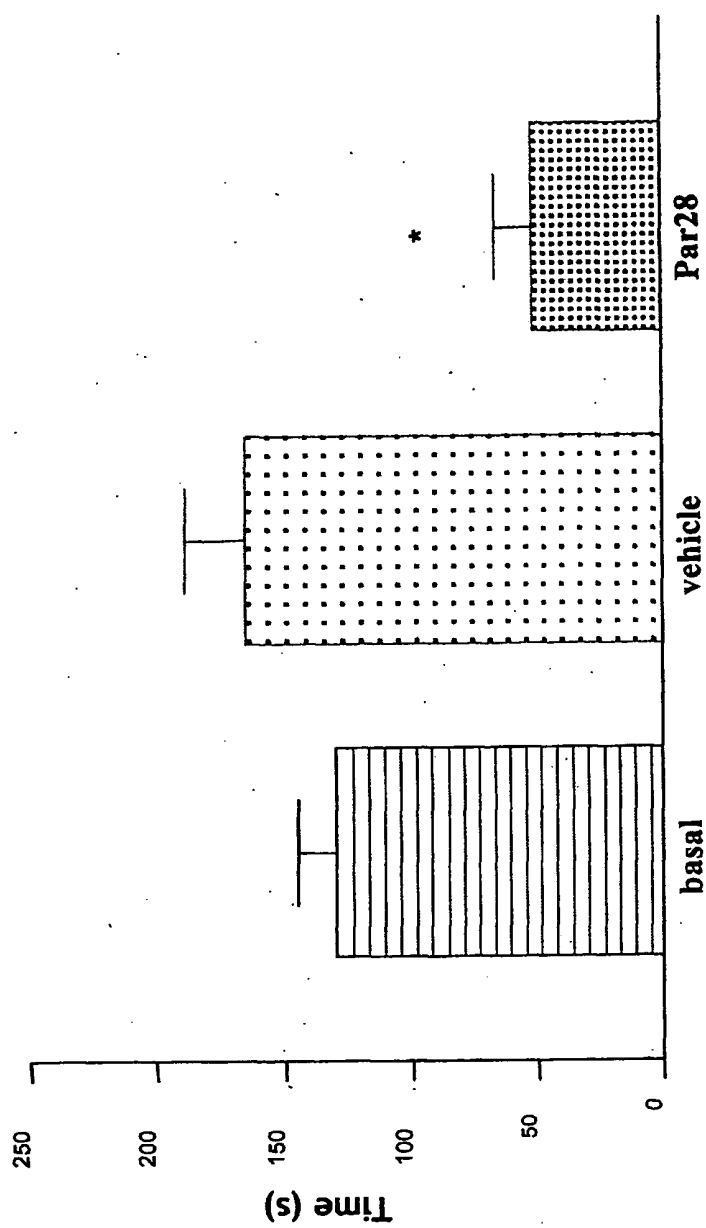


Figure 5

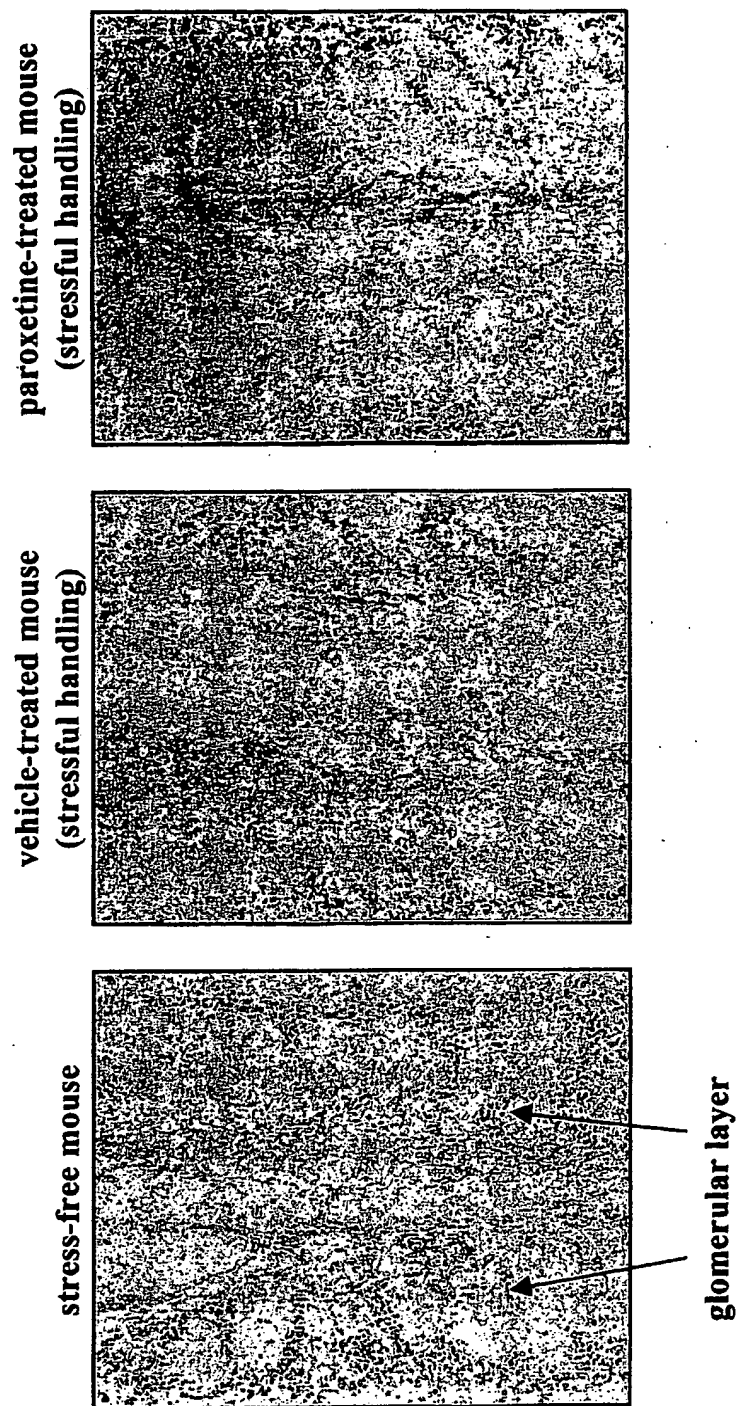


Figure 6

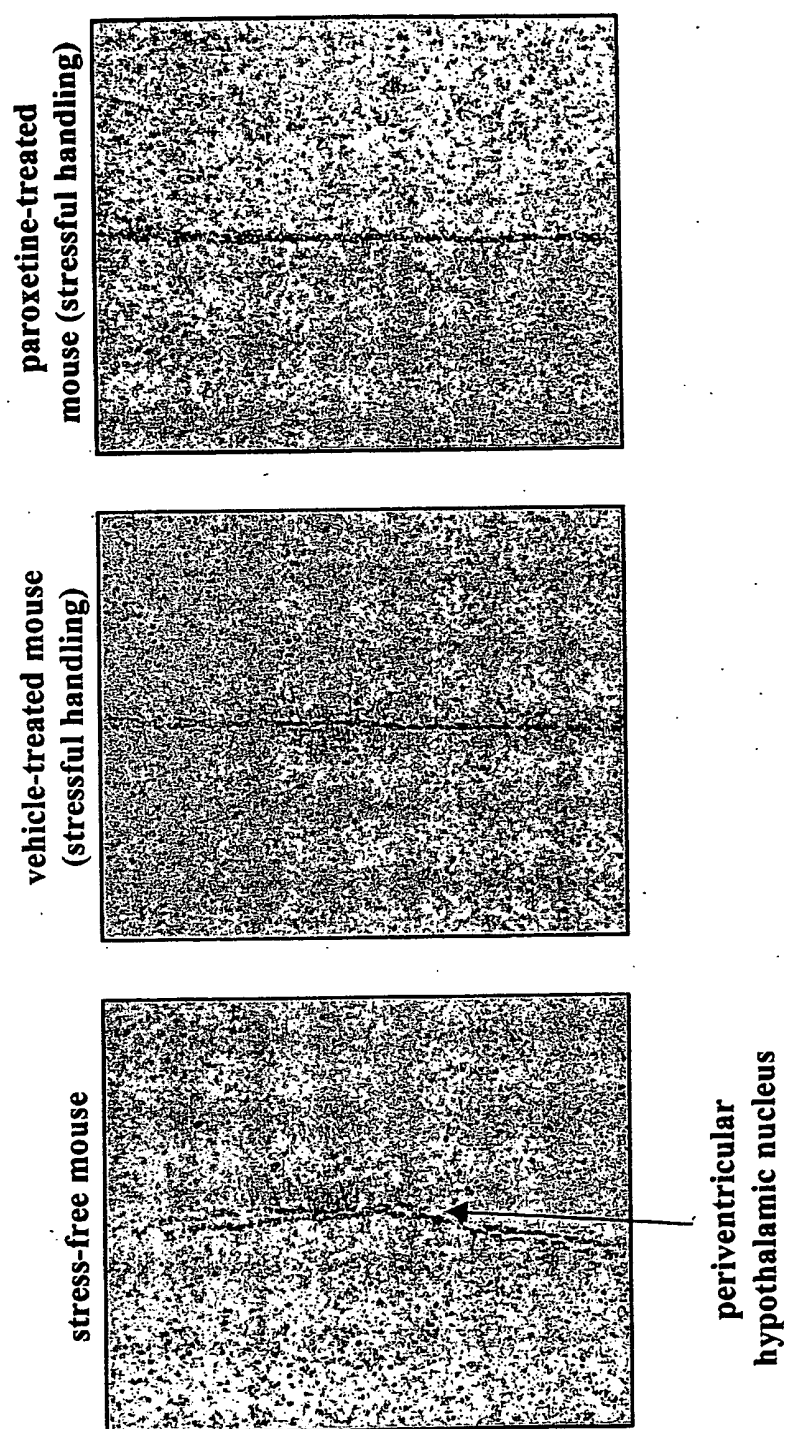


Figure 7

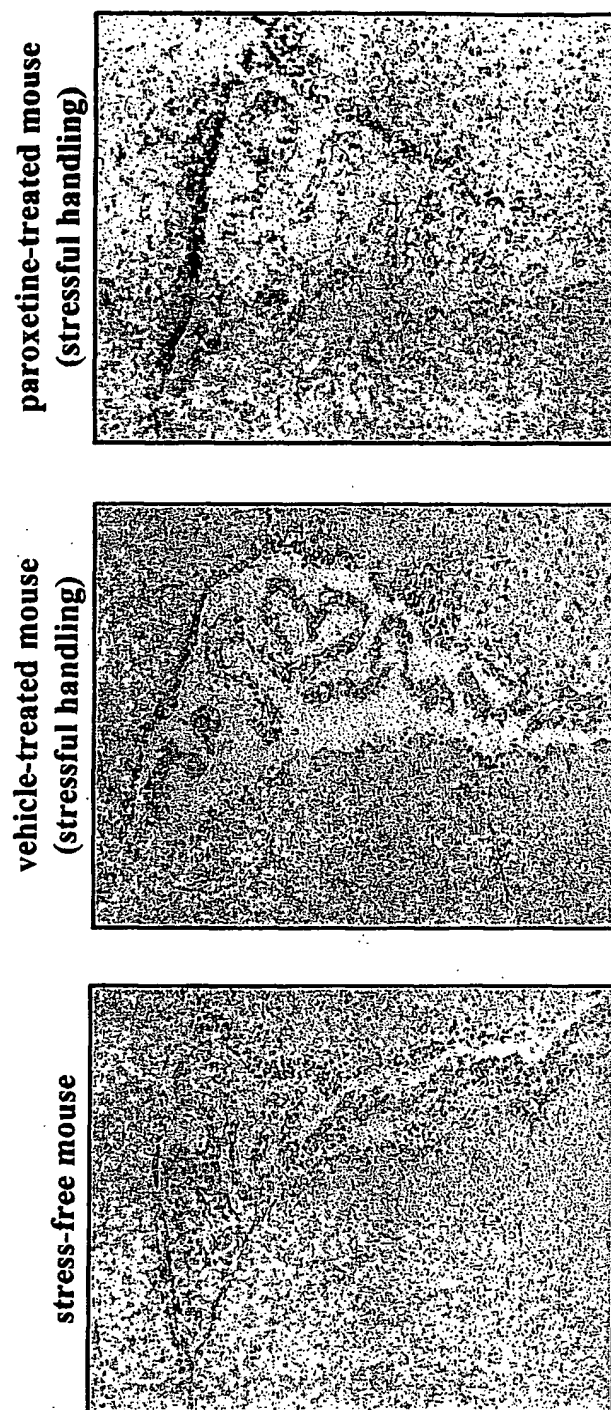


Figure 8



Figure 9

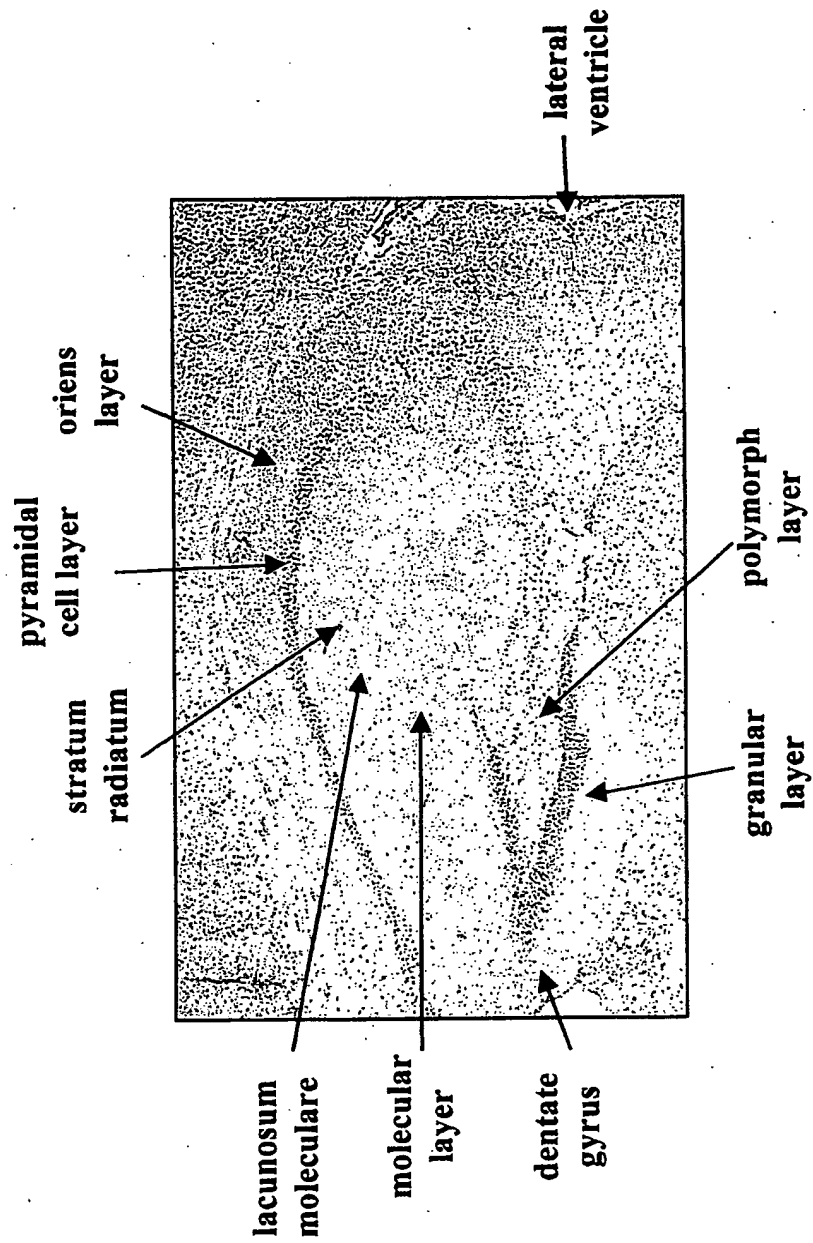


Figure 10

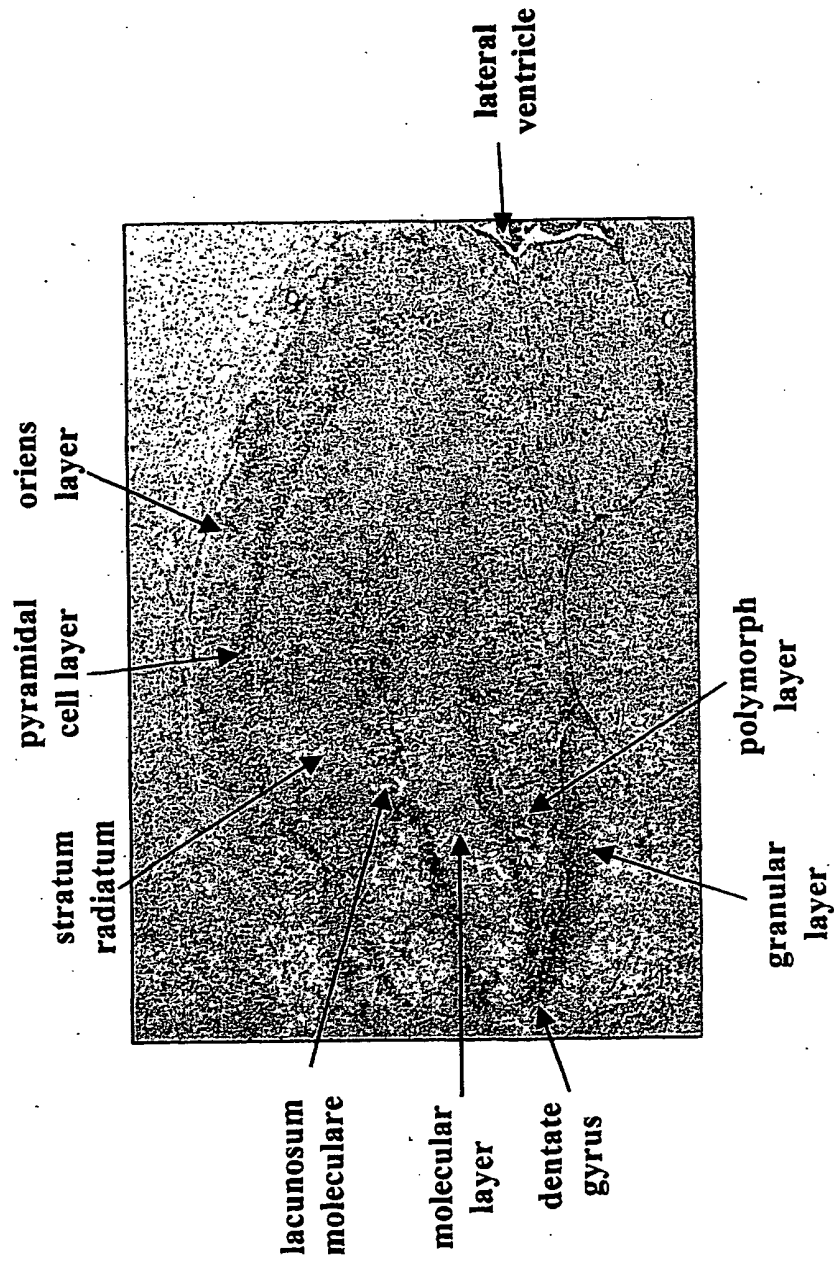


Figure 11

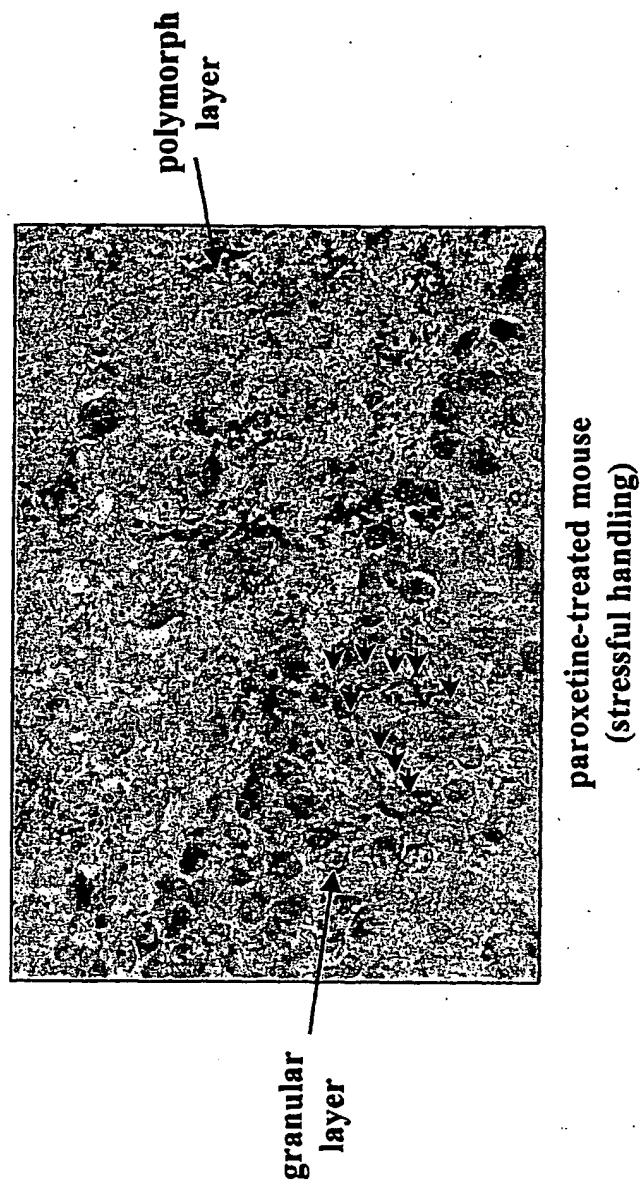


Figure 12

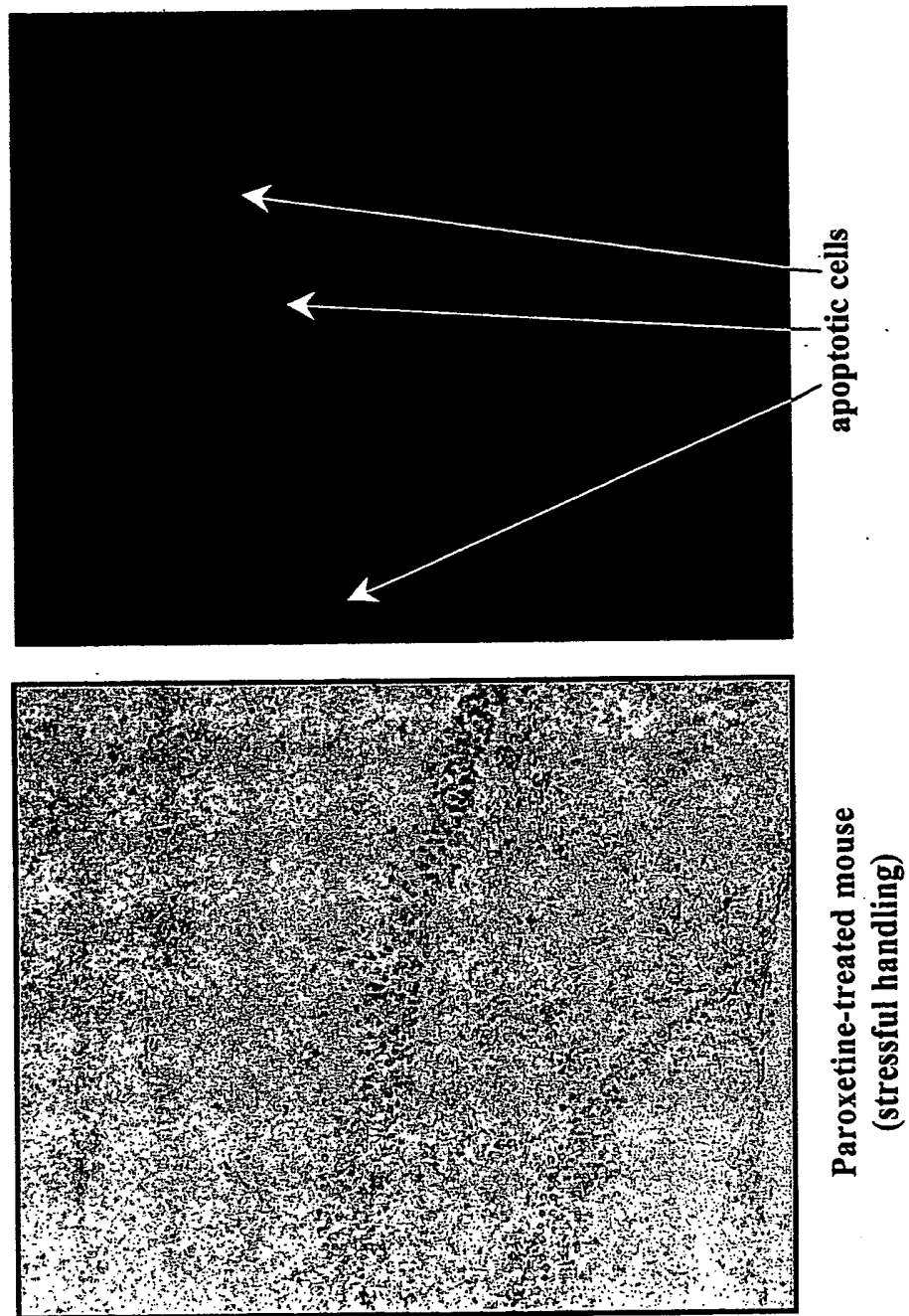


Figure 13

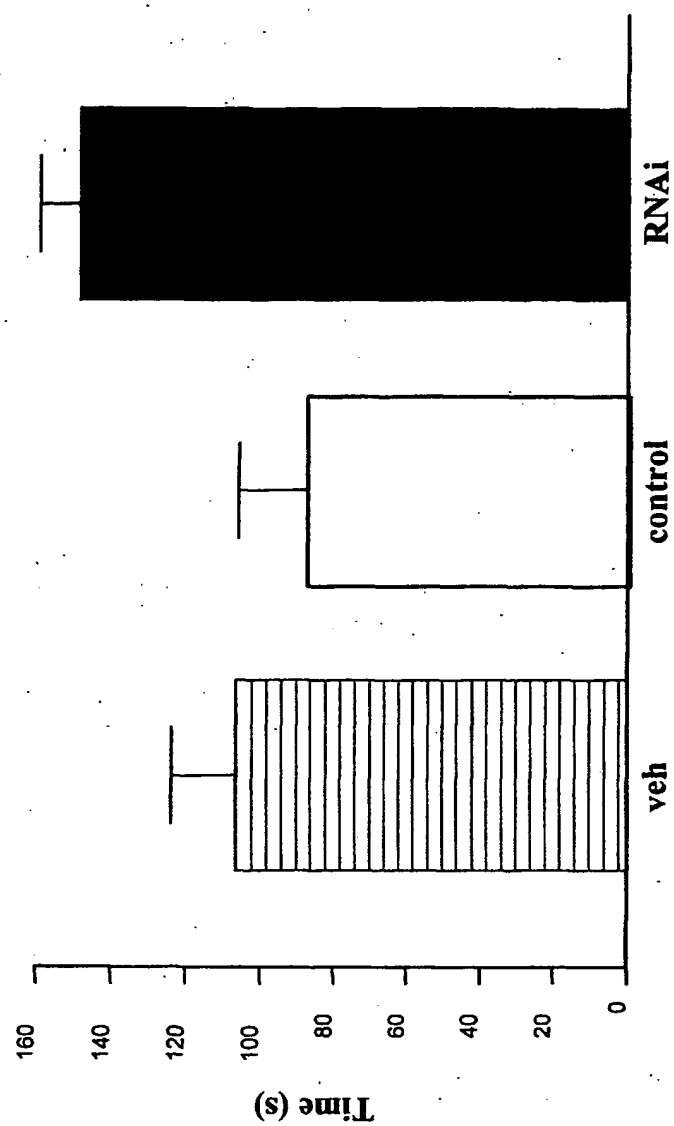


Figure 14

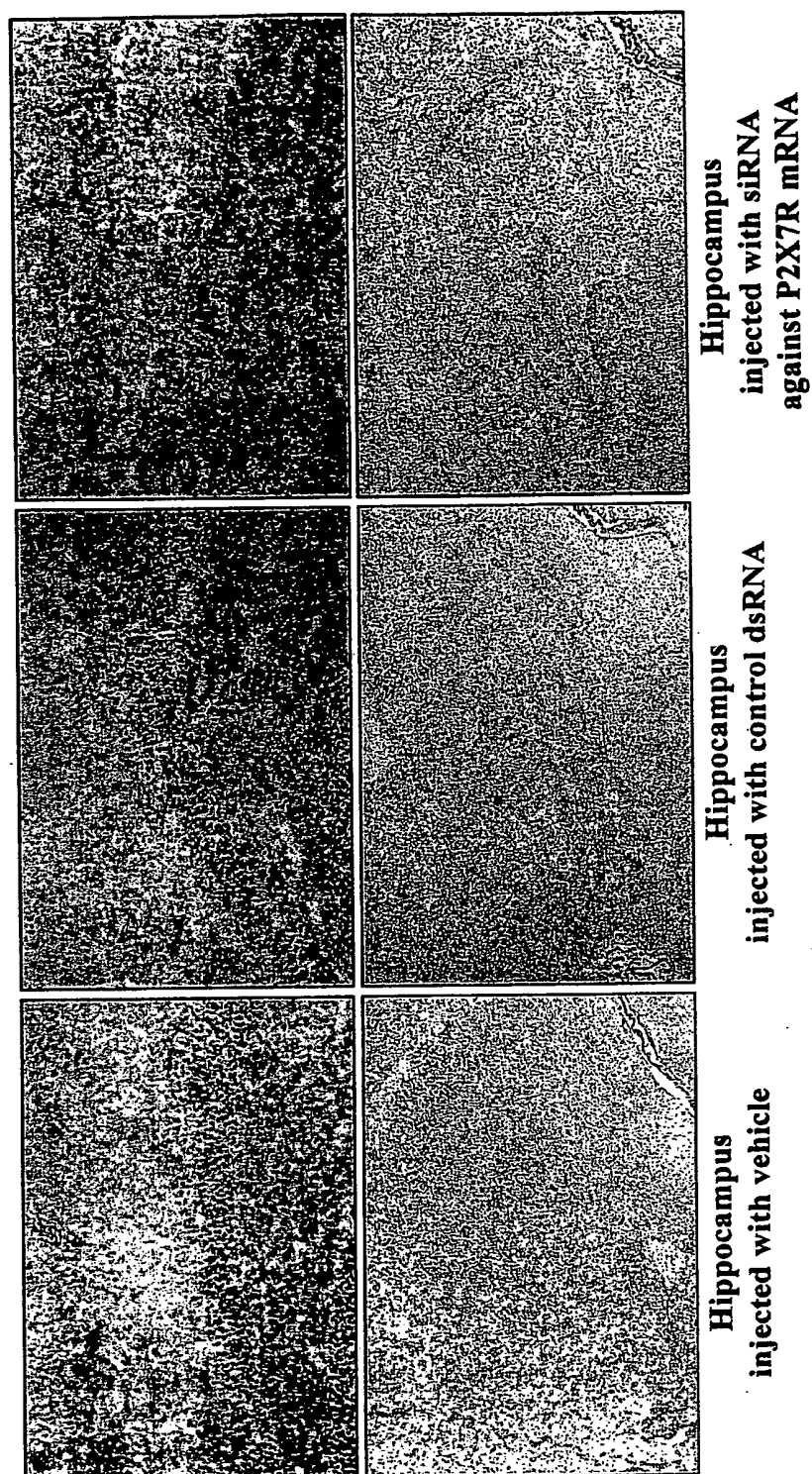


Figure 15

```

P2X7v01 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
P2X7v04 MPPVD-----AFPCLPFS---FALVSDKLYQRKEPVISS
P2X7v02 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
P2X7v03 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
      1.....10.....20.....30.....40.....50

P2X7v01 VHTKVKGIAEVKEEIVENGVKKLVHSVFDTADYTFPLQGNSEFFVMTNFKTEGQEQRLCP
P2X7v04 VHTKVKGIAEVKEEIVENGVKKLVHSVFDTADYTFPLQGNSEFFVMTNFKTEGQEQRLCP
P2X7v02 VHTKVKGIAEVKEEIVENGVKKLVHSVFDTADYTFPLQGNSEFFVMTNFKTEGQEQRLCP
P2X7v03 VHTKVKGIAEVKEEIVENGVKKLVHSVFDTADYTFPLQGNSEFFVMTNFKTEGQEQRLCP
      61.....70.....80.....90.....100.....110

```

Figure 16a

```

P2X7v01 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
P2X7v04 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
P2X7v02 EYPTRRTLCSDDRGCKKGWMDPQSKGLLS-----
P2X7v03 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
      121.....130.....140.....150.....160.....170

P2X7v01 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
P2X7v04 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
P2X7v02 -----
P2X7v03 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
      181.....190.....200.....210.....220.....230

```

Figure 16b

```

P2X7v01  NFSDVAIQGGIMGIEIYWDCNLD RWFHHC HCPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK
P2X7v04  NFSDVAIQGGIMGIEIYWDCNLD RWFHHC HCPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK
P2X7v02  -----
P2X7v03  NFSDVAIQGGIMGIEIYWDCNLD RWFHHC HCPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK
          241.....250.....260.....270.....280.....290

P2X7v01  ENNVEKRTLKVF GIRFDILVFGTGGKFDIIQLVVIIGSTLSYFGLAAVFIDFLIDTYSS
P2X7v04  ENNVEKRTLKVF GIRFDILVFGTGGKFDIIQLVVIIGSTLSYFGLAAVFIDFLIDTYSS
P2X7v02  -----
P2X7v03  ENNVEKRTLKVF GIRFDILVFGTGGKFDIIQLVVIIGSTLSYFGLVDRDSL FHALGKWFG
          301.....310.....320.....330.....340.....350

```

Figure 16c

P2X7v01	NCCRS	HIYPWCKCCQPCVV	NEYYRKKCESIVEPKPTLKYVSFVDESHIRMVNQQLLGRS
P2X7v04	NCCRS	HIYPWCKCCQPCVV	NEYYRKKCESIVEPKPTLKYVSFVDESHIRMVNQQLLGRS
P2X7v02			-----
P2X7v03	EGSD		-----
	361370.....380.....390.....400.....410	
P2X7v01	LQDV	KGQEVPRPAMDFTDLSRLPLALHDTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG	
P2X7v04	LQDV	KGQEVPRPAMDFTDLSRLPLALHDTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG	
P2X7v02			-----
P2X7v03			-----
	421430.....440.....450.....460.....470	

Figure 16d

P2X7v01	SCLPSQLPESHRCLEELCCRKKPGACITTSELFRLVLSRHLVLFLLLYQEPLALDVS
P2X7v04	SCLPSQLPESHRCLEELCCRKKPGACITTSELFRLVLSRHLVLFLLLYQEPLALDVS
P2X7v02	-----
P2X7v03	-----
	481.....490.....500.....510.....520.....530
P2X7v01	TNSRLRHCAIRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGOYSGFKSPY
P2X7v04	TNSRLRHCAIRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGOYSGFKSPY
P2X7v02	-----
P2X7v03	-----
	541.....550.....560.....570.....580.....590

Figure 16e

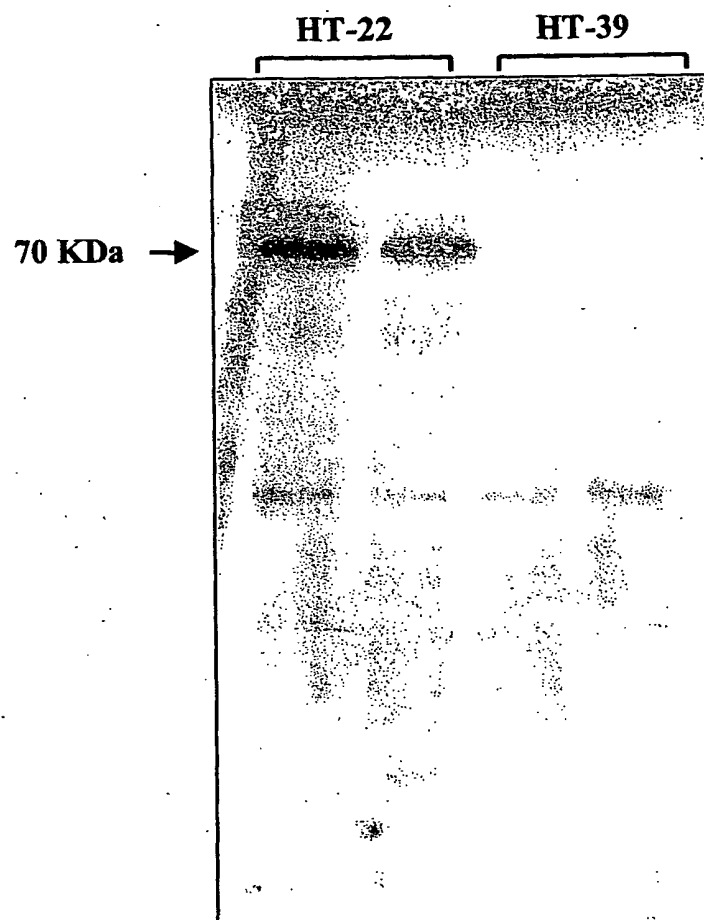


Figure 17

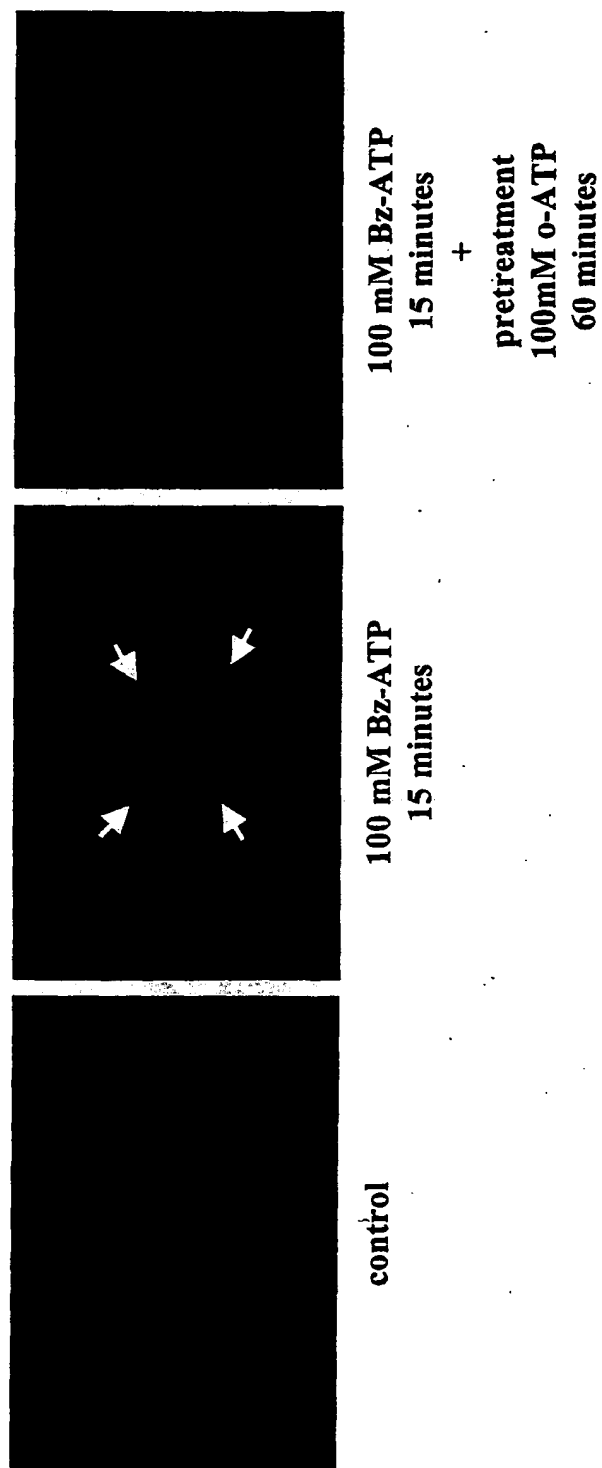


Figure 18

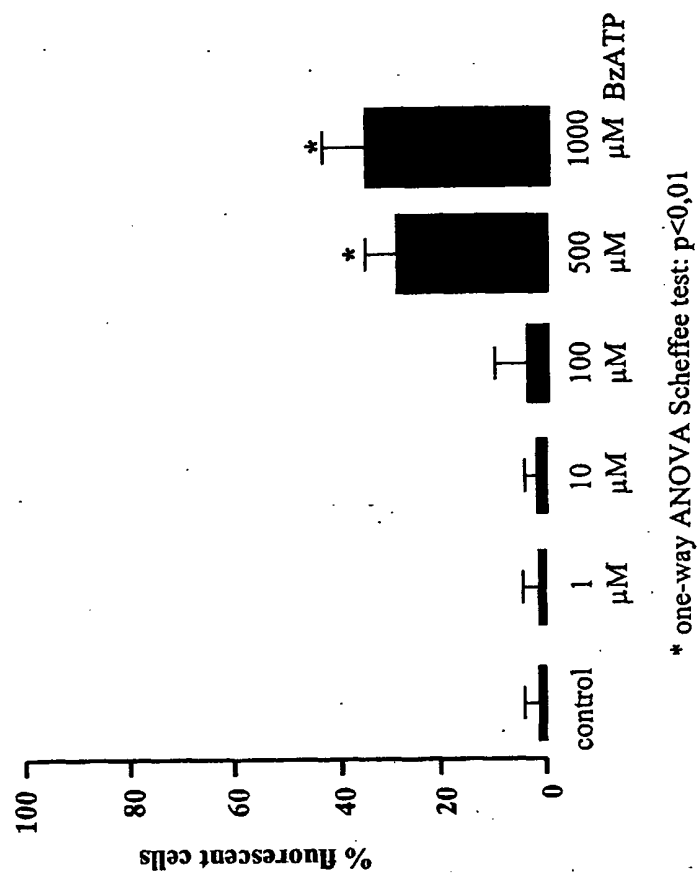


Figure 19a

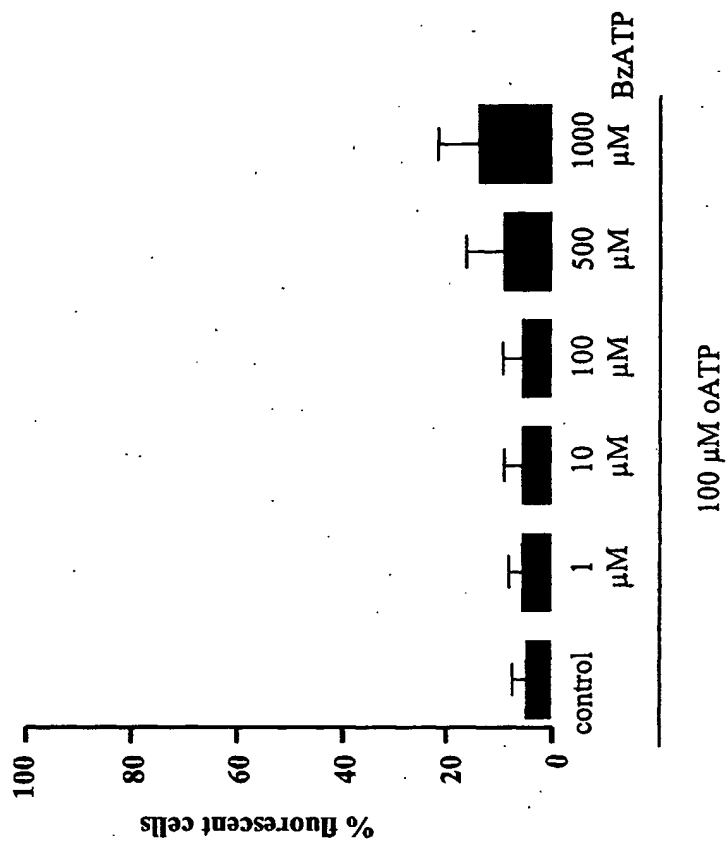


Figure 19b

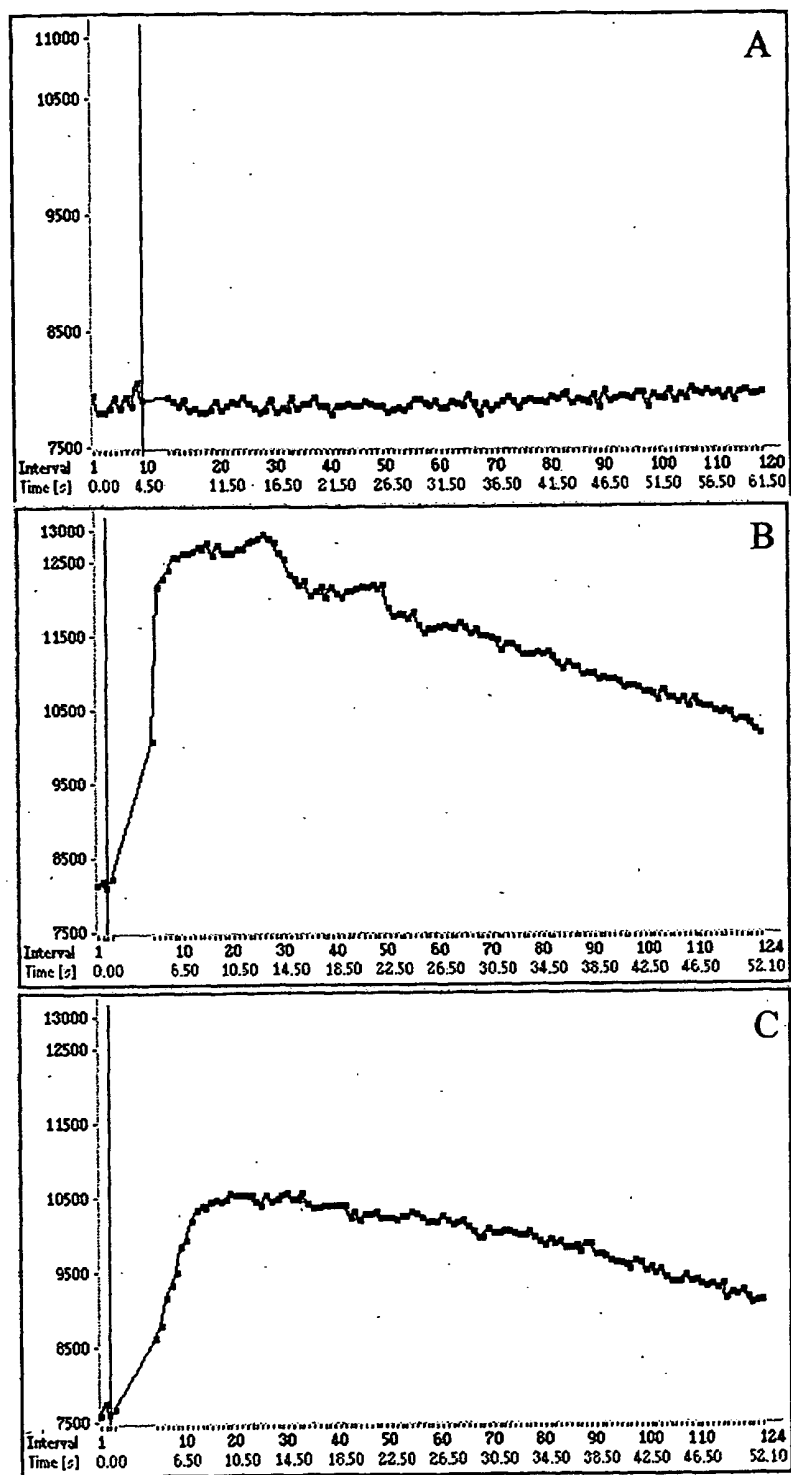


Figure 19c

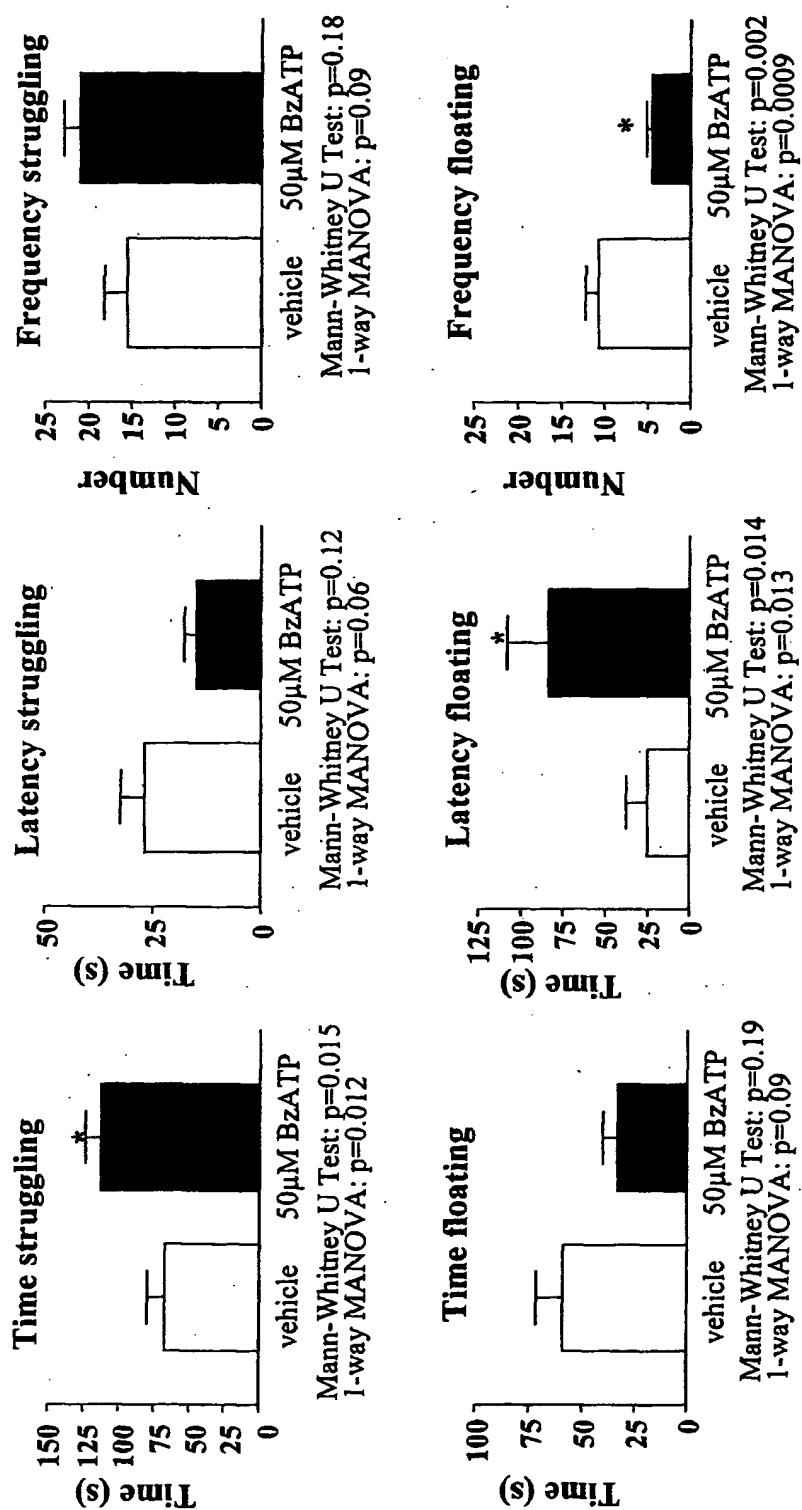


Figure 20

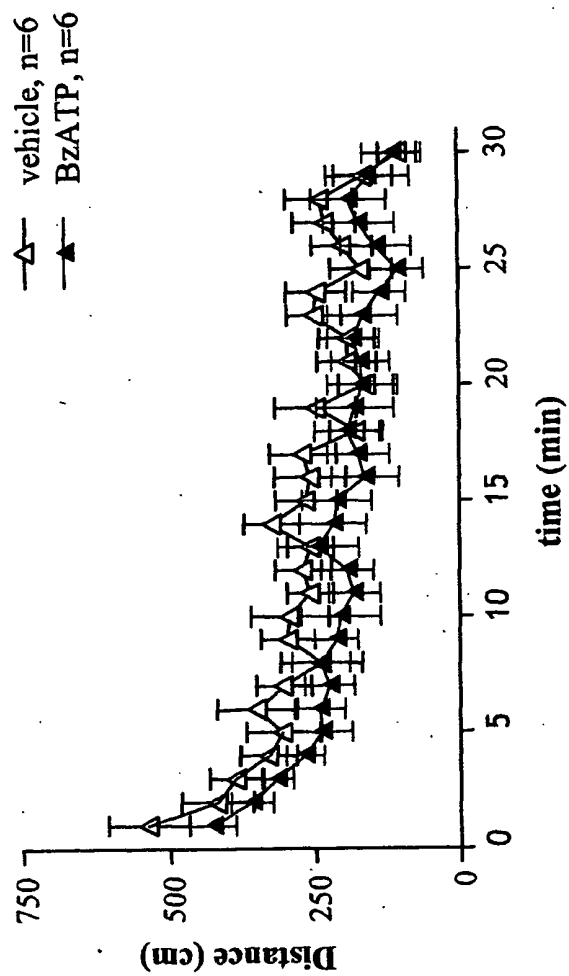


Figure 21

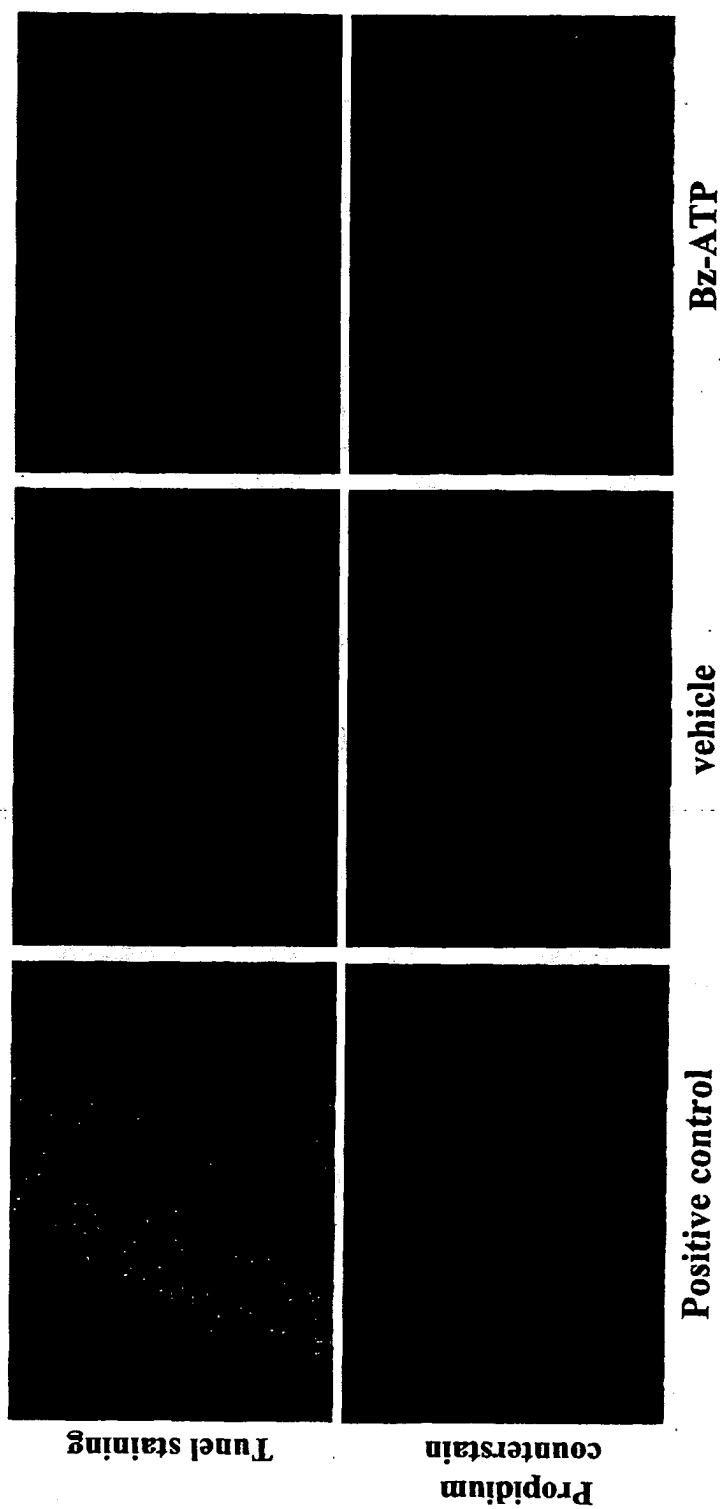


Figure 22

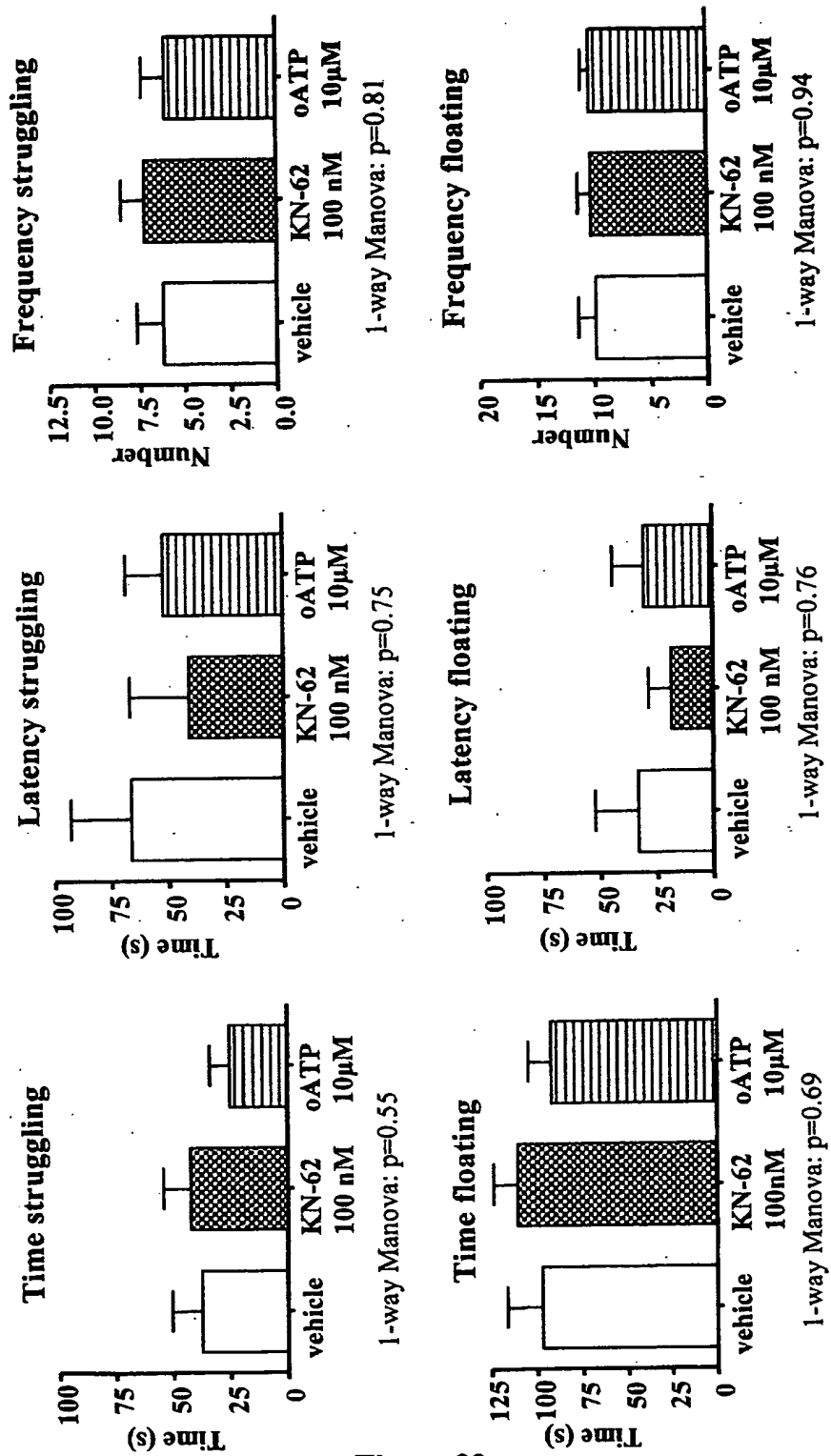


Figure 23

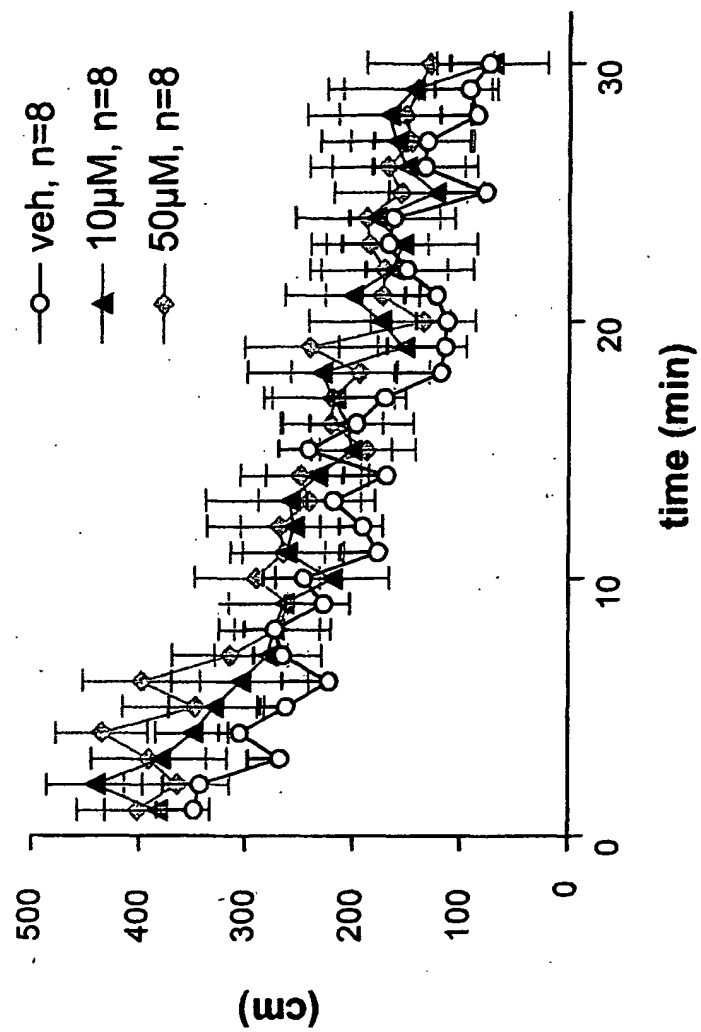
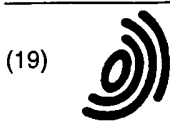


Figure 24



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11) **EP 1 469 072 A3**

(12)

EUROPEAN PATENT APPLICATION

(88) Date of publication A3:
24.11.2004 Bulletin 2004/48

(43) Date of publication A2:
20.10.2004 Bulletin 2004/43

(21) Application number: **04009160.5**

(22) Date of filing: **16.04.2004**

(51) Int Cl.7: **C12N 15/12, C12N 1/21,
C12N 5/10, C07K 16/28,
C12N 15/11, C12Q 1/68,
A61K 38/17, A61K 39/395,
A61K 31/7088, A61K 31/40,
G01N 33/68**

(84) Designated Contracting States:
**AT BE BG CH CY CZ DE DK EE ES FI FR GB GR
HU IE IT LI LU MC NL PL PT RO SE SI SK TR**
Designated Extension States:
AL HR LT LV MK

(30) Priority: **17.04.2003 EP 03008753
04.09.2003 EP 03019626**

(60) Divisional application:
04018640.5 / 1 473 367

(71) Applicant: **NeuroNova Aktiengesellschaft
80804 München (DE)**

(72) Inventors:
• **Barden, Nicholas**
Sainte-Foy, Québec G1W 3H1 (CA)
• **Sillaber, Inge**
80802 Munich (DE)
• **Paez-Pereda, Marcelo**
80809 Munich (DE)

(74) Representative: **VOSSIUS & PARTNER
Siebertstrasse 4
81675 München (DE)**

(54) **Means and methods for diagnosing and treating affective disorders**

(57) The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the

present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R.

The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases.

Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

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European Patent
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PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

EP 04 00 9160

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	EP 1 199 372 A (ASTRAZENECA AB) 24 April 2002 (2002-04-24) * the whole document *	28, 29, 32, 33, 47-51, 53	C12N15/12 C12N1/21 C12N5/10 C07K16/28 C12N15/11 C12Q1/68 A61K38/17 A61K39/395 A61K31/7088 A61K31/40 G01N33/68
A	DATABASE EMBL 14 May 1999 (1999-05-14), XP002284283 accession no. AC007546 Database accession no. AC007546 nucleotides 66559-66578 * the whole document *		
A	WO 01/62787 A (OXFORD GLYCOSCIENCES UK LTD ; HERATH HERATH MUDIYANSELAGE AT (GB); PAR) 30 August 2001 (2001-08-30)		
A	SANZ J M ET AL: "TENIDAP ENHANCES P2Z/P2X7 RECEPTOR SIGNALLING IN MACROPHAGES" EUROPEAN JOURNAL OF PHARMACOLOGY, AMSTERDAM, NL, vol. 355, no. 2/3, 1998, pages 235-244, XP001056968 ISSN: 0014-2999 * the whole document *	36-39	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
			C07K C12Q A61K G01N
INCOMPLETE SEARCH <p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>see sheet C</p>			
Place of search		Date of completion of the search	Examiner
The Hague		28 September 2004	Van der Schaal, C
CATEGORY OF CITED DOCUMENTS <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons</p> <p>& : member of the same patent family, corresponding document</p>			

EPO FORM 1503 03 02 (P4-C07)



European Patent
Office

INCOMPLETE SEARCH
SHEET C

Application Number
EP 04 00 9160

Although claims 30 34 42-45 are (partially) directed to a method of treatment of the human/animal body (Article 52(4) EPC), the search has been carried out and based on the alleged effects of the compound/composition.

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 04 00 9160

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
P,X	EP 1 310 493 A (PFIZER PROD INC) 14 May 2003 (2003-05-14) * page 16, line 31 * -----	36,42,43	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)



European Patent
Office

Application Number
EP 04 00 9160

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet 8

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☒ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

28-41 47-53 completely 1-12 17-20, 42-45 partially

☐ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:



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LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 04 00 9160

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: Claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 362, or fragments containing the substitution, nucleotides hybridizing with the mutated sequence.

Inventions 2-6 :Claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 532, 1100, 1122, 1171, 1702 respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Inventions 7-13: claims 1-19 partially

polypeptides according to SEQ 3 or 4 with substitution of amino acid residue 117,150, 186, 191, 270, 568 or 578 respectively, nucleotides or fragments thereof encoding the mutated polypeptide(fragments), nucleotides hybridizing with the mutated nucleotide sequence and antibodies against the mutated polypeptide sequence

Inventions 14 and 15: claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 32548 or 37633 respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Invention 16: claims 1-19 partially

polypeptides according to SEQ 3 or 4 with a deletion of amino acids 488-494, nucleotides or fragments thereof encoding the mutated polypeptide(fragments), nucleotides hybridizing with the mutated nucleotide sequence and antibodies against the mutated polypeptide sequence.

Inventions 17-39: claims 1-12 17-19 respectively



European Patent
Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number

EP 04 00 9160

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotides mentioned in claim 1(e) and 1(f) respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Invention 40. claims 21-27, 46 54-56 completely 20 42-45 partially

Use of P2X7R or its encoding nucleotides or variants thereof in diagnosis of affective disorder

Invention 41: claims 28-41 47-53 completely, claims 20 42-45 partially

Use of modulators of P2X7R activity as pharmaceutical against affective disorders

**ANNEX TO THE EUROPEAN SEARCH REPORT
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EP 04 00 9160

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